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(54) Title: HUMAN GENES AND GENE EXPRESSION PRODUCTS I			
(57) Abstract			
<p>This invention relates to novel human polynucleotides and variants thereof, their encoded polypeptides and variants thereof, to genes corresponding to these polynucleotides and to proteins expressed by the genes. The invention also relates to diagnostic and therapeutic agents employing such novel human polynucleotides, their corresponding genes or gene products, e.g., these genes and proteins, including probes, antisense constructs, and antibodies.</p>			

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NOVEL HUMAN GENES AND GENE EXPRESSION PRODUCTS ICross-References to Related Applications

This application is a continuation-in-part of U.S. provisional patent application serial
5 no. 60/068,755, filed December 23, 1997, and of U.S. provisional patent application serial
no. 60/080,664, filed April 3, 1998, and of U.S. provisional patent application serial no.
60/105,234, filed October 21, 1998, each of which applications are incorporated herein by
reference.

10 Field of the Invention

The present invention relates to novel polynucleotides, particularly to novel
polynucleotides of human origin that are expressed in a selected cell type, are differentially
expressed in one cell type relative to another cell type (e.g., in cancerous cells, or in cells of a
specific tissue origin) and/or share homology to polynucleotides encoding a gene product
15 having an identified functional domain and/or activity.

Background of the Invention

Identification of novel polynucleotides, particularly those that encode an expressed
gene product, is important in the advancement of drug discovery, diagnostic technologies,
20 and the understanding of the progression and nature of complex diseases such as cancer.
Identification of genes expressed in different cell types isolated from sources that differ in
disease state or stage, developmental stage, exposure to various environmental factors, the
tissue of origin, the species from which the tissue was isolated, and the like is key to
identifying the genetic factors that are responsible for the phenotypes associated with these
25 various differences

This invention provides novel human polynucleotides, the polypeptides encoded by
these polynucleotides, and the genes and proteins corresponding to these novel
polynucleotides.

30 Summary of the Invention

This invention relates to novel human polynucleotides and variants thereof, their
encoded polypeptides and variants thereof, to genes corresponding to these polynucleotides

WO 99/33982

PCT/US98/27610

and to proteins expressed by the genes. The invention also relates to diagnostic and therapeutic agents employing such novel human polynucleotides, their corresponding genes or gene products, *e.g.*, these genes and proteins, including probes, antisense constructs, and antibodies.

5 Accordingly, in one embodiment, the present invention features a library of polynucleotides, the library comprising the sequence information of at least one of SEQ ID NOS:1-844. In related aspects, the invention features a library provided on a nucleic acid array, or in a computer-readable format.

In one embodiment, the library is comprises a differentially expressed polynucleotide
10 comprising a sequence selected from the group consisting of SEQ ID NOS:9, 39, 42, 52, 62, 74, 119, 172, 317, and 379. In specific related embodiments, the library comprises: 1) a polynucleotide that is differentially expressed in a human breast cancer cell, where the polynucleotide comprises a sequence selected from the group consisting of SEQ ID NOS: 4, 9, 39, 42, 52, 62, 65, 66, 68, 74, 81, 114, 123, 144, 130, 157, 162, 172, 178, 183, 202, 214,
15 219, 223, 258, 298, 317, 338, 379, 384, 386, and 388; 2) a polynucleotide differentially expressed in a human colon cancer cell, where the polynucleotide comprises a sequence selected from the group consisting of SEQ ID NOS: 1, 39, 52, 97, 119, 134, 172, 176, 241, 288, 317, 357, 362, and 374; or 3) a polynucleotide differentially expressed in a human lung cancer cell, where the polynucleotide comprises a sequence selected from the group
20 consisting of SEQ ID NOS: 9, 34, 42, 62, 74, 106, 119, 135, 154, 160, 260, 308, 323, 349, 361, 369, 371, 379, 395, 381, and 400.

In another aspect, the invention features an isolated polynucleotide comprising a nucleotide sequence having at least 90% sequence identity to an identifying sequence of SEQ ID NOS:1-844 or a degenerate variant thereof. In related aspects, the
25 invention features recombinant host cells and vectors comprising the polynucleotides of the invention, as well as isolated polypeptides encoded by the polynucleotides of the invention and antibodies that specifically bind such polypeptides.

In one embodiment, the invention features an isolated polynucleotide comprising a sequence encoding a polypeptide of a protein family selected from the group consisting of:
30 4 transmembrane segments integral membrane proteins, 7 transmembrane receptors, ATPases associated with various cellular activities (AAA), eukaryotic aspartyl proteases,

WO 99/33982

PCT/US98/27610

GATA family of transcription factors, G-protein alpha subunit, phorbol esters/diacylglycerol binding proteins, protein kinase, protein phosphatase 2C, protein tyrosine phosphatase, trypsin, wnt family of developmental signaling proteins, and WW/rsp5/WWP domain containing proteins. In a specific related embodiment, the invention features a

- 5 polynucleotide comprising a sequence of one of SEQ ID NOS: 24, 41, 101, 157, 291, 305, 315, 341, 63, 116, 134, 136, 151, 384, 404, 308, 213, 367, 188, 251, 202, 315, 367, 397, 256, 382, 169, 23, 291, 324, 330, 341, 353, 188, 379, and 395.

- In another embodiment, the invention features a polynucleotide comprising a sequence encoding a polypeptide having a functional domain selected from the group
- 10 consisting of: Ank repeat, basic region plus leucine zipper transcription factors, bromodomain, EF-hand, SH3 domain, WD domain/G-beta repeats, zinc finger (C2H2 type), zinc finger (CCHC class), and zinc-binding metalloprotease domain. In a specific related embodiment, the invention features a polynucleotide comprising a sequence of one of SEQ ID NOS: 116, 251, 374, 97, 136, 242, 379, 306, 386, 18, 335, 61, 306, 386, 322, 306, and
- 15 395.

- In another aspect, the invention features a method of detecting differentially expressed genes correlated with a cancerous state of a mammalian cell, where the method comprises the step of detecting at least one differentially expressed gene product in a test sample derived from a cell suspected of being cancerous, where the gene product is encoded
- 20 by a gene corresponding to a sequence of at least one of SEQ ID NOS: 4, 9, 39, 42, 52, 62, 65, 66, 68, 74, 81, 114, 123, 144, 130, 157, 162, 172, 178, 183, 202, 214, 219, 223, 258, 298, 317, 338, 379, 384, 386, 388, 1, 39, 52, 97, 119, 134, 172, 176, 241, 288, 317, 357, 362, 374, 9, 34, 42, 62, 74, 106, 119, 135, 154, 160, 260, 308, 323, 349, 361, 369, 371, 379, 395, 381, and 400. Detection of the differentially expressed gene product is correlated with a
- 25 cancerous state of the cell from which the test sample was derived. In one embodiment, the detecting is by hybridization of the test sample to a reference array, wherein the reference array comprises an identifying sequence of at least one of SEQ ID NOS: 1-844.

- In one embodiment of the method of the invention, the cell is a breast tissue derived cell, and the differentially expressed gene product is encoded by a gene corresponding to a
- 30 sequence of at least one of SEQ ID NOS: 4, 9, 39, 42, 52, 62, 65, 66, 68, 74, 81, 114, 123,

WO 99/33982

PCT/US98/27610

144, 130, 157, 162, 172, 178, 183, 202, 214, 219, 223, 258, 298, 317, 338, 379, 384, 386, and 388.

In another embodiment of the method of the invention, the cell is a colon tissue derived cell, and differentially expressed gene product is encoded by a gene corresponding to a sequence of at least one of SEQ ID NOS: 1, 39, 52, 97, 119, 134, 172, 176, 241, 288, 317, 357, 362, and 374.

In yet another embodiment of the method of the invention, the cell is a lung tissue derived cell, and differentially expressed gene product is encoded by a gene corresponding to a sequence of at least one of SEQ ID NOS: 9, 34, 42, 62, 74, 106, 119, 135, 154, 160, 260, 308, 323, 349, 361, 369, 371, 379, 395, 381, and 400.

Other aspects and embodiments of the invention will be readily apparent to the ordinarily skilled artisan upon reading the description provided herein.

Detailed Description of the Invention

The invention relates to polynucleotides comprising the disclosed nucleotide sequences, to full length cDNA, mRNA and genes corresponding to these sequences, and to polypeptides and proteins encoded by these polynucleotides and genes.

Also included are polynucleotides that encode polypeptides and proteins encoded by the polynucleotides of the Sequence Listing. The various polynucleotides that can encode these polypeptides and proteins differ because of the degeneracy of the genetic code, in that most amino acids are encoded by more than one triplet codon. The identity of such codons is well-known in this art, and this information can be used for the construction of the polynucleotides within the scope of the invention.

Polynucleotides encoding polypeptides and proteins that are variants of the polypeptides and proteins encoded by the polynucleotides and related cDNA and genes are also within the scope of the invention. The variants differ from wild type protein in having one or more amino acid substitutions that either enhance, add, or diminish a biological activity of the wild type protein. Once the amino acid change is selected, a polynucleotide encoding that variant is constructed according to the invention.

The following detailed description describes the polynucleotide compositions encompassed by the invention, methods for obtaining cDNA or genomic DNA encoding a full-length gene product, expression of these polynucleotides and genes, identification of

WO 99/33982

PCT/US98/27610

structural motifs of the polynucleotides and genes, identification of the function of a gene product encoded by a gene corresponding to a polynucleotide of the invention, use of the provided polynucleotides as probes and in mapping and in tissue profiling, use of the corresponding polypeptides and other gene products to raise antibodies, and use of the polynucleotides and their encoded gene products for therapeutic and diagnostic purposes.

I. Polynucleotide Compositions

The scope of the invention with respect to polynucleotide compositions includes, but is not necessarily limited to, polynucleotides having a sequence set forth in any one of SEQ ID NOS:1-844; polynucleotides obtained from the biological materials described herein or other biological sources (particularly human sources) by hybridization under stringent conditions (particularly conditions of high stringency); genes corresponding to the provided polynucleotides; variants of the provided polynucleotides and their corresponding genes, particularly those variants that retain a biological activity of the encoded gene product (e.g., a biological activity ascribed to a gene product corresponding to the provided polynucleotides as a result of the assignment of the gene product to a protein family(ies) and/or identification of a functional domain present in the gene product). Other nucleic acid compositions contemplated by and within the scope of the present invention will be readily apparent to one of ordinary skill in the art when provided with the disclosure here.

The invention features polynucleotides that are expressed in cells of human tissue, specifically human colon, breast, and/or lung tissue. Novel nucleic acid compositions of the invention of particular interest comprise a sequence set forth in any one of SEQ ID NOS:1-844 or an identifying sequence thereof. An "identifying sequence" is a contiguous sequence of residues at least about 10 nt to about 20 nt in length, usually at least about 50 nt to about 100 nt in length, that uniquely identifies a polynucleotide sequence, e.g., exhibits less than 90%, usually less than about 80% to about 85% sequence identity to any contiguous nucleotide sequence of more than about 20 nt. Thus, the subject novel nucleic acid compositions include full length cDNAs or mRNAs that encompass an identifying sequence of contiguous nucleotides from any one of SEQ ID NOS:1-844.

The polynucleotides of the invention also include polynucleotides having sequence similarity or sequence identity. Nucleic acids having sequence similarity are detected by

WO 99/33982

PCT/US98/27610

hybridization under low stringency conditions, for example, at 50°C and 10XSSC (0.9 M saline/0.09 M sodium citrate) and remain bound when subjected to washing at 55°C in 1XSSC. Sequence identity can be determined by hybridization under stringent conditions, for example, at 50°C or higher and 0.1XSSC (9 mM saline/0.9 mM sodium citrate).

- 5 Hybridization methods and conditions are well known in the art, see, *e.g.*, U.S. Patent No. 5,707,829. Nucleic acids that are substantially identical to the provided polynucleotide sequences, *e.g.* allelic variants, genetically altered versions of the gene, *etc.*, bind to the provided polynucleotide sequences (SEQ ID NOS:1-844) under stringent hybridization conditions. By using probes, particularly labeled probes of DNA sequences, one can isolate
- 10 homologous or related genes. The source of homologous genes can be any species, *e.g.* primate species, particularly human; rodents, such as rats and mice, canines, felines, bovines, ovines, equines, yeast, nematodes, *etc.*

- Preferably, hybridization is performed using at least 15 contiguous nucleotides of at least one of SEQ ID NOS: 1-844. That is, when at least 15 contiguous nucleotides of one of
- 15 the disclosed SEQ ID NOS. is used as a probe, the probe will preferentially hybridize with a gene or mRNA (of the biological material) comprising the complementary sequence, allowing the identification and retrieval of the nucleic acids of the biological material that uniquely hybridize to the selected probe. Probes from more than one SEQ ID NO. will hybridize with the same gene or mRNA if the cDNA from which they were derived
- 20 corresponds to one mRNA. Probes of more than 15 nucleotides can be used, but 15 nucleotides represents enough sequence for unique identification.

- The polynucleotides of the invention also include naturally occurring variants of the nucleotide sequences (*e.g.*, degenerate variants, allelic variants, *etc.*). Variants of the polynucleotides of the invention are identified by hybridization of putative variants with
- 25 nucleotide sequences disclosed herein, preferably by hybridization under stringent conditions. For example, by using appropriate wash conditions, variants of the polynucleotides of the invention can be identified where the allelic variant exhibits at most about 25-30% base pair mismatches relative to the selected polynucleotide probe. In general, allelic variants contain 15-25% base pair mismatches, and can contain as little as even 5-15%, or 2-5%, or 1-2%
- 30 base pair mismatches, as well as a single base-pair mismatch.

WO 99/33982

PCT/US98/27610

The invention also encompasses homologs corresponding to the polynucleotides of SEQ ID NOS:1-844, where the source of homologous genes can be any mammalian species, *e.g.*, primate species, particularly human; rodents, such as rats, canines, felines, bovines, ovines, equines, yeast, nematodes, etc. Between mammalian species, *e.g.*, human and mouse, homologs have substantial sequence similarity, *e.g.*, at least 75% sequence identity, usually at least 90%, more usually at least 95% between nucleotide sequences. Sequence similarity is calculated based on a reference sequence, which may be a subset of a larger sequence, such as a conserved motif, coding region, flanking region, *etc.* A reference sequence will usually be at least about 18 contiguous nt long, more usually at least about 30 nt long, and may extend to the complete sequence that is being compared. Algorithms for sequence analysis are known in the art, such as BLAST, described in Altschul *et al.*, *J. Mol. Biol.* (1990) 215:403-10.

In general, variants of the invention have a sequence identity greater than at least about 65%, preferably at least about 75%, more preferably at least about 85%, and can be greater than at least about 90% or more as determined by the Smith-Waterman homology search algorithm as implemented in MPSRCH program (Oxford Molecular). For the purposes of this invention, a preferred method of calculating percent identity is the Smith-Waterman algorithm, using the following. Global DNA sequence identity must be greater than 65% as determined by the Smith-Waterman homology search algorithm as implemented in MPSRCH program (Oxford Molecular) using an affine gap search with the following search parameters: gap open penalty, 12; and gap extension penalty, 1.

The subject nucleic acids can be cDNAs or genomic DNAs, as well as fragments thereof, particularly fragments that encode a biologically active gene product and/or are useful in the methods disclosed herein (*e.g.*, in diagnosis, as a unique identifier of a differentially expressed gene of interest, *etc.*). The term "cDNA" as used herein is intended to include all nucleic acids that share the arrangement of sequence elements found in native mature mRNA species, where sequence elements are exons and 3' and 5' non-coding regions. Normally mRNA species have contiguous exons, with the intervening introns, when present, being removed by nuclear RNA splicing, to create a continuous open reading frame encoding a polypeptide of the invention.

WO 99/33982

PCT/US98/27610

A genomic sequence of interest comprises the nucleic acid present between the initiation codon and the stop codon, as defined in the listed sequences, including all of the introns that are normally present in a native chromosome. It can further include the 3 and 5 untranslated regions found in the mature mRNA. It can further include specific transcriptional and translational regulatory sequences, such as promoters, enhancers, *etc.*, including about 1 kb, but possibly more, of flanking genomic DNA at either the 5 and 3 end of the transcribed region. The genomic DNA can be isolated as a fragment of 100 kbp or smaller; and substantially free of flanking chromosomal sequence. The genomic DNA flanking the coding region, either 3 and 5, or internal regulatory sequences as sometimes found in introns, contains sequences required for proper tissue, stage-specific, or disease-state specific expression.

The nucleic acid compositions of the subject invention can encode all or a part of the subject differentially expressed polypeptides. Double or single stranded fragments can be obtained from the DNA sequence by chemically synthesizing oligonucleotides in accordance with conventional methods, by restriction enzyme digestion, by PCR amplification, *etc.* Isolated polynucleotides and polynucleotide fragments of the invention comprise at least about 10, about 15, about 20, about 35, about 50, about 100, about 150 to about 200, about 250 to about 300, or about 350 contiguous nucleotides selected from the polynucleotide sequences as shown in SEQ ID NOS:1-844. For the most part, fragments will be of at least 15 nt, usually at least 18 nt or 25 nt, and up to at least about 50 contiguous nt in length or more. In a preferred embodiment, the polynucleotide molecules comprise a contiguous sequence of at least twelve nucleotides selected from the group consisting of the polynucleotides shown in SEQ ID NOS:1-844.

Probes specific to the polynucleotides of the invention can be generated using the polynucleotide sequences disclosed in SEQ ID NOS:1-844. The probes are preferably at least about 12, 15, 16, 18, 20, 22, 24, or 25 nucleotide fragment of a corresponding contiguous sequence of SEQ ID NOS:1-844, and can be less than 2, 1, 0.5, 0.1, or 0.05 kb in length. The probes can be synthesized chemically or can be generated from longer polynucleotides using restriction enzymes. The probes can be labeled, for example, with a radioactive, biotinylated, or fluorescent tag. Preferably, probes are designed based upon an identifying sequence of a polynucleotide of one of SEQ ID NOS:1-844. More preferably,

WO 99/33982

PCT/US98/27610

probes are designed based on a contiguous sequence of one of the subject polynucleotides that remain unmasked following application of a masking program for masking low complexity (*e.g.*, XBLAST) to the sequence., *i.e.*, one would select an unmasked region, as indicated by the polynucleotides outside the poly-n stretches of the masked sequence

5 produced by the masking program.

The polynucleotides of the subject invention are isolated and obtained in substantial purity, generally as other than an intact chromosome. Usually, the polynucleotides, either as DNA or RNA, will be obtained substantially free of other naturally-occurring nucleic acid sequences, generally being at least about 50%, usually at least about 90% pure and are

10 typically "recombinant", *e.g.*, flanked by one or more nucleotides with which it is not normally associated on a naturally occurring chromosome.

The polynucleotides of the invention can be provided as a linear molecule or within a circular molecule. They can be provided within autonomously replicating molecules (vectors) or within molecules without replication sequences. They can be regulated by their

15 own or by other regulatory sequences, as is known in the art. The polynucleotides of the invention can be introduced into suitable host cells using a variety of techniques which are available in the art, such as transferrin polycation-mediated DNA transfer, transfection with naked or encapsulated nucleic acids, liposome-mediated DNA transfer, intracellular transportation of DNA-coated latex beads, protoplast fusion, viral infection, electroporation,

20 gene gun, calcium phosphate-mediated transfection, and the like.

The subject nucleic acid compositions can be used to, for example, produce polypeptides, as probes for the detection of mRNA of the invention in biological samples (*e.g.*, extracts of human cells) to generate additional copies of the polynucleotides, to generate ribozymes or antisense oligonucleotides, and as single stranded DNA probes or as

25 triple-strand forming oligonucleotides. The probes described herein can be used to, for example, determine the presence or absence of the polynucleotide sequences as shown in SEQ ID NOS:1-844 or variants thereof in a sample. These and other uses are described in more detail below.

WO 99/33982

PCT/US98/27610

Use of Polynucleotides to Obtain Full-Length cDNA and Full-Length Human Gene and Promoter Region

Full-length cDNA molecules comprising the disclosed polynucleotides are obtained as follows. A polynucleotide having a sequence of one of SEQ ID NOS:1-844, or a portion thereof comprising at least 12, 15, 18, or 20 nucleotides, is used as a hybridization probe to detect hybridizing members of a cDNA library using probe design methods, cloning methods, and clone selection techniques such as those described in U.S. Patent No. 5,654,173. Libraries of cDNA are made from selected tissues, such as normal or tumor tissue, or from tissues of a mammal treated with, for example, a pharmaceutical agent. Preferably, the tissue is the same as the tissue from which the polynucleotides of the invention were isolated, as both the polynucleotides described herein and the cDNA represent expressed genes. Most preferably, the cDNA library is made from the biological material described herein in the Examples. Alternatively, many cDNA libraries are available commercially. (Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual*, 2nd Ed., (1989) Cold Spring Harbor Press, Cold Spring Harbor, NY). The choice of cell type for library construction can be made after the identity of the protein encoded by the gene corresponding to the polynucleotide of the invention is known. This will indicate which tissue and cell types are likely to express the related gene, and thus represent a suitable source for the mRNA for generating the cDNA. Where the provided polynucleotides are isolated from cDNA libraries, the libraries are prepared from mRNA of human colon cells, more preferably, human colon cancer cells, even more preferably, from a highly metastatic colon cell, Km12L4-A.

Techniques for producing and probing nucleic acid sequence libraries are described, for example, in Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual*, 2nd Ed., (1989) Cold Spring Harbor Press, Cold Spring Harbor, NY. The cDNA can be prepared by using primers based on sequence from SEQ ID NOS:1-844. In one embodiment, the cDNA library can be made from only poly-adenylated mRNA. Thus, poly-T primers can be used to prepare cDNA from the mRNA.

Members of the library that are larger than the provided polynucleotides, and preferably that encompass the complete coding sequence of the native message, are obtained. In order to confirm that the entire cDNA has been obtained, RNA protection experiments

WO 99/33982

PCT/US98/27610

are performed as follows. Hybridization of a full-length cDNA to an mRNA will protect the RNA from RNase degradation. If the cDNA is not full length, then the portions of the mRNA that are not hybridized will be subject to RNase degradation. This is assayed, as is known in the art, by changes in electrophoretic mobility on polyacrylamide gels, or by detection of released monoribonucleotides. Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual, 2nd Ed.*, (1989) Cold Spring Harbor Press, Cold Spring Harbor, NY. In order to obtain additional sequences 5' to the end of a partial cDNA, 5' RACE (PCR Protocols: A Guide to Methods and Applications, (1990) Academic Press, Inc.) is performed.

Genomic DNA is isolated using the provided polynucleotides in a manner similar to the isolation of full-length cDNAs. Briefly, the provided polynucleotides, or portions thereof, are used as probes to libraries of genomic DNA. Preferably, the library is obtained from the cell type that was used to generate the polynucleotides of the invention, but this is not essential. Most preferably, the genomic DNA is obtained from the biological material described herein in the Examples. Such libraries can be in vectors suitable for carrying large segments of a genome, such as P1 or YAC, as described in detail in Sambrook *et al.*, 9.4-9.30. In addition, genomic sequences can be isolated from human BAC libraries, which are commercially available from Research Genetics, Inc., Huntsville, Alabama, USA, for example. In order to obtain additional 5' or 3' sequences, chromosome walking is performed, as described in Sambrook *et al.*, such that adjacent and overlapping fragments of genomic DNA are isolated. These are mapped and pieced together, as is known in the art, using restriction digestion enzymes and DNA ligase.

Using the polynucleotide sequences of the invention, corresponding full-length genes can be isolated using both classical and PCR methods to construct and probe cDNA libraries. Using either method, Northern blots, preferably, are performed on a number of cell types to determine which cell lines express the gene of interest at the highest level. Classical methods of constructing cDNA libraries are taught in Sambrook *et al.*, *supra*. With these methods, cDNA can be produced from mRNA and inserted into viral or expression vectors. Typically, libraries of mRNA comprising poly(A) tails can be produced with poly(T) primers. Similarly, cDNA libraries can be produced using the instant sequences as primers.

PCR methods are used to amplify the members of a cDNA library that comprise the desired insert. In this case, the desired insert will contain sequence from the full length

WO 99/33982

PCT/US98/27610

cDNA that corresponds to the instant polynucleotides. Such PCR methods include gene trapping and RACE methods. Gene trapping entails inserting a member of a cDNA library into a vector. The vector then is denatured to produce single stranded molecules. Next, a substrate-bound probe, such a biotinylated oligo, is used to trap cDNA inserts of interest.

- 5 Biotinylated probes can be linked to an avidin-bound solid substrate. PCR methods can be used to amplify the trapped cDNA. To trap sequences corresponding to the full length genes, the labeled probe sequence is based on the polynucleotide sequences of the invention. Random primers or primers specific to the library vector can be used to amplify the trapped cDNA. Such gene trapping techniques are described in Gruber *et al.*, WO 95/04745 and
- 10 Gruber *et al.*, U.S. Pat. No. 5,500,356. Kits are commercially available to perform gene trapping experiments from, for example, Life Technologies, Gaithersburg, Maryland, USA.

- “Rapid amplification of cDNA ends,” or RACE, is a PCR method of amplifying cDNAs from a number of different RNAs. The cDNAs are ligated to an oligonucleotide linker, and amplified by PCR using two primers. One primer is based on sequence from the
- 15 instant polynucleotides, for which full length sequence is desired, and a second primer comprises sequence that hybridizes to the oligonucleotide linker to amplify the cDNA. A description of this methods is reported in WO 97/19110. In preferred embodiments of RACE, a common primer is designed to anneal to an arbitrary adaptor sequence ligated to cDNA ends (Apte and Siebert, *Biotechniques* (1993) 15:890-893; Edwards *et al.*, *Nuc. Acids*
- 20 *Res.* (1991) 19:5227-5232). When a single gene-specific RACE primer is paired with the common primer, preferential amplification of sequences between the single gene specific primer and the common primer occurs. Commercial cDNA pools modified for use in RACE are available.

- Another PCR-based method generates full-length cDNA library with anchored ends without needing specific knowledge of the cDNA sequence. The method uses lock-docking
- 25 primers (I-VI), where one primer, poly TV (I-III) locks over the polyA tail of eukaryotic mRNA producing first strand synthesis and a second primer, polyGH (IV-VI) locks onto the polyC tail added by terminal deoxynucleotidyl transferase (TdT). This method is described in WO 96/40998.

- 30 The promoter region of a gene generally is located 5' to the initiation site for RNA polymerase II. Hundreds of promoter regions contain the “TATA” box, a sequence such as

WO 99/33982

PCT/US98/27610

TATTA or TATAA, which is sensitive to mutations. The promoter region can be obtained by performing 5' RACE using a primer from the coding region of the gene. Alternatively, the cDNA can be used as a probe for the genomic sequence, and the region 5' to the coding region is identified by "walking up." If the gene is highly expressed or differentially expressed, the promoter from the gene can be of use in a regulatory construct for a heterologous gene.

Once the full-length cDNA or gene is obtained, DNA encoding variants can be prepared by site-directed mutagenesis, described in detail in Sambrook *et al.*, 15.3-15.63. The choice of codon or nucleotide to be replaced can be based on disclosure herein on optional changes in amino acids to achieve altered protein structure and/or function.

As an alternative method to obtaining DNA or RNA from a biological material, nucleic acid comprising nucleotides having the sequence of one or more polynucleotides of the invention can be synthesized. Thus, the invention encompasses nucleic acid molecules ranging in length from 15 nucleotides (corresponding to at least 15 contiguous nucleotides of one of SEQ ID NOS: 1-844) up to a maximum length suitable for one or more biological manipulations, including replication and expression, of the nucleic acid molecule. The invention includes but is not limited to (a) nucleic acid having the size of a full gene, and comprising at least one of SEQ ID NOS: 1-844; (b) the nucleic acid of (a) also comprising at least one additional gene, operably linked to permit expression of a fusion protein; (c) an expression vector comprising (a) or (b); (d) a plasmid comprising (a) or (b); and (e) a recombinant viral particle comprising (a) or (b). Once provided with the polynucleotides disclosed herein, construction or preparation of (a) - (e) are well within the skill in the art.

The sequence of a nucleic acid comprising at least 15 contiguous nucleotides of at least any one of SEQ ID NOS: 1-844, preferably the entire sequence of at least any one of SEQ ID NOS: 1-844, is not limited and can be any sequence of A, T, G, and/or C (for DNA) and A, U, G, and/or C (for RNA) or modified bases thereof, including inosine and pseudouridine. The choice of sequence will depend on the desired function and can be dictated by coding regions desired, the intron-like regions desired, and the regulatory regions desired. Where the entire sequence of any one of SEQ ID NOS: 1-844 is within the nucleic acid, the nucleic acid obtained is referred to herein as a polynucleotide comprising the sequence of any one of SEQ ID NOS: 1-844.

II. Expression of Polypeptide Encoded by Full-Length cDNA or Full-Length Gene

The provided polynucleotide (e.g., a polynucleotide having a sequence of one of SEQ ID NOS:1-844), the corresponding cDNA, or the full-length gene is used to express a partial or complete gene product.

Constructs of polynucleotides having sequences of SEQ ID NOS:1-844 can be generated synthetically. Alternatively, single-step assembly of a gene and entire plasmid from large numbers of oligodeoxyribonucleotides is described by, e.g., Stemmer *et al.*, *Gene (Amsterdam)* (1995) 164(1):49-53. In this method, assembly PCR (the synthesis of long DNA sequences from large numbers of oligodeoxyribonucleotides (oligos)) is described. The method is derived from DNA shuffling (Stemmer, *Nature* (1994) 370:389-391), and does not rely on DNA ligase, but instead relies on DNA polymerase to build increasingly longer DNA fragments during the assembly process. For example, a 1.1-kb fragment containing the TEM-1 beta-lactamase-encoding gene (bla) can be assembled in a single reaction from a total of 56 oligos, each 40 nucleotides (nt) in length. The synthetic gene can be PCR amplified and cloned in a vector containing the tetracycline-resistance gene (Tc-R) as the sole selectable marker. Without relying on ampicillin (Ap) selection, 76% of the Tc-R colonies were Ap-R, making this approach a general method for the rapid and cost-effective synthesis of any gene.

Appropriate polynucleotide constructs are purified using standard recombinant DNA techniques as described in, for example, Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual, 2nd Ed.*, (1989) Cold Spring Harbor Press, Cold Spring Harbor, NY, and under current regulations described in United States Dept. of HHS, National Institute of Health (NIH) Guidelines for Recombinant DNA Research. The gene product encoded by a polynucleotide of the invention is expressed in any expression system, including, for example, bacterial, yeast, insect, amphibian and mammalian systems. Suitable vectors and host cells are described in U.S. Patent No. 5,654,173.

Bacteria. Expression systems in bacteria include those described in Chang *et al.*, *Nature* (1978) 275:615; Goeddel *et al.*, *Nature* (1979) 281:544; Goeddel *et al.*, *Nucleic Acids Res.* (1980) 8:4057; EP 0 036,776; U.S. Patent No. 4,551,433; DeBoer *et al.*, *Proc. Natl. Acad. Sci. (USA)* (1983) 80:21-25; and Siebenlist *et al.*, *Cell* (1980) 20:269.

WO 99/33982

PCT/US98/27610

- Yeast. Expression systems in yeast include those described in Hinnen *et al.*, *Proc. Natl. Acad. Sci. (USA)* (1978) 75:1929; Ito *et al.*, *J. Bacteriol.* (1983) 153:163; Kurtz *et al.*, *Mol. Cell. Biol.* (1986) 6:142; Kunze *et al.*, *J. Basic Microbiol.* (1985) 25:141; Gleeson *et al.*, *J. Gen. Microbiol.* (1986) 132:3459; Roggenkamp *et al.*, *Mol. Gen. Genet.* (1986) 202:302; Das *et al.*, *J. Bacteriol.* (1984) 158:1165; De Louvencourt *et al.*, *J. Bacteriol.* (1983) 154:737; Van den Berg *et al.*, *Bio/Technology* (1990) 8:135; Kunze *et al.*, *J. Basic Microbiol.* (1985) 25:141; Cregg *et al.*, *Mol. Cell. Biol.* (1985) 5:3376; U.S. Patent Nos. 4,837,148 and 4,929,555; Beach and Nurse, *Nature* (1981) 300:706; Davidow *et al.*, *Curr. Genet.* (1985) 10:380; Gaillardin *et al.*, *Curr. Genet.* (1985) 10:49; Ballance *et al.*, *Biochem. Biophys. Res. Commun.* (1983) 112:284-289; Tilburn *et al.*, *Gene* (1983) 26:205-221; Yelton *et al.*, *Proc. Natl. Acad. Sci. (USA)* (1984) 81:1470-1474; Kelly and Hynes, *EMBO J.* (1985) 4:475479; EP 0 244,234; and WO 91/00357.

- Insect Cells. Expression of heterologous genes in insects is accomplished as described in U.S. Patent No. 4,745,051; Friesen *et al.*, "The Regulation of Baculovirus Gene Expression", in: *The Molecular Biology Of Baculoviruses* (1986) (W. Doerfler, ed.); EP 0 127,839; EP 0 155,476; and Vlcek *et al.*, *J. Gen. Virol.* (1988) 69:765-776; Miller *et al.*, *Ann. Rev. Microbiol.* (1988) 42:177; Carbonell *et al.*, *Gene* (1988) 73:409; Maeda *et al.*, *Nature* (1985) 315:592-594; Lebacqz-Verheyden *et al.*, *Mol. Cell. Biol.* (1988) 8:3129; Smith *et al.*, *Proc. Natl. Acad. Sci. (USA)* (1985) 82:8844; Miyajima *et al.*, *Gene* (1987) 58:273; and Martin *et al.*, *DNA* (1988) 7:99. Numerous baculoviral strains and variants and corresponding permissive insect host cells from hosts are described in Luckow *et al.*, *Bio/Technology* (1988) 6:47-55, Miller *et al.*, *Generic Engineering* (1986) 8:277-279, and Maeda *et al.*, *Nature* (1985) 315:592-594.

- Mammalian Cells. Mammalian expression is accomplished as described in Dijkema *et al.*, *EMBO J.* (1985) 4:761, Gorman *et al.*, *Proc. Natl. Acad. Sci. (USA)* (1982) 79:6777, Boshart *et al.*, *Cell* (1985) 41:521 and U.S. Patent No. 4,399,216. Other features of mammalian expression are facilitated as described in Ham and Wallace, *Meth. Enz.* (1979) 58:44, Barnes and Sato, *Anal. Biochem.* (1980) 102:255, U.S. Patent Nos. 4,767,704, 4,657,866, 4,927,762, 4,560,655, WO 90/103430, WO 87/00195, and U.S. RE 30,985.

- Polynucleotide molecules comprising a polynucleotide sequence provided herein propagated by placing the molecule in a vector. Viral and non-viral vectors are used,

WO 99/33982

PCT/US98/27610

including plasmids. The choice of plasmid will depend on the type of cell in which propagation is desired and the purpose of propagation. Certain vectors are useful for amplifying and making large amounts of the desired DNA sequence. Other vectors are suitable for expression in cells in culture. Still other vectors are suitable for transfer and expression in cells in a whole animal or person. The choice of appropriate vector is well within the skill of the art. Many such vectors are available commercially. The partial or full-length polynucleotide is inserted into a vector typically by means of DNA ligase attachment to a cleaved restriction enzyme site in the vector. Alternatively, the desired nucleotide sequence can be inserted by homologous recombination *in vivo*. Typically this is accomplished by attaching regions of homology to the vector on the flanks of the desired nucleotide sequence. Regions of homology are added by ligation of oligonucleotides, or by polymerase chain reaction using primers comprising both the region of homology and a portion of the desired nucleotide sequence, for example.

The polynucleotides set forth in SEQ ID NOS:1-844 or their corresponding full-length polynucleotides are linked to regulatory sequences as appropriate to obtain the desired expression properties. These can include promoters (attached either at the 5' end of the sense strand or at the 3' end of the antisense strand), enhancers, terminators, operators, repressors, and inducers. The promoters can be regulated or constitutive. In some situations it may be desirable to use conditionally active promoters, such as tissue-specific or developmental stage-specific promoters. These are linked to the desired nucleotide sequence using the techniques described above for linkage to vectors. Any techniques known in the art can be used.

When any of the above host cells, or other appropriate host cells or organisms, are used to replicate and/or express the polynucleotides or nucleic acids of the invention, the resulting replicated nucleic acid, RNA, expressed protein or polypeptide, is within the scope of the invention as a product of the host cell or organism. The product is recovered by any appropriate means known in the art.

Once the gene corresponding to a selected polynucleotide is identified, its expression can be regulated in the cell to which the gene is native. For example, an endogenous gene of a cell can be regulated by an exogenous regulatory sequence as disclosed in U.S. Patent No. 5,641,670.

III. Identification of Functional and Structural Motifs of Novel Genes

A. Screening Polynucleotide Sequences and Amino Acid Sequences Against Publicly Available Databases

5 Translations of the nucleotide sequence of the provided polynucleotides, cDNAs or full genes can be aligned with individual known sequences. Similarity with individual sequences can be used to determine the activity of the polypeptides encoded by the polynucleotides of the invention. For example, sequences that show similarity with a chemokine sequence can exhibit chemokine activities. Also, sequences exhibiting similarity
10 with more than one individual sequence can exhibit activities that are characteristic of either or both individual sequences.

The full length sequences and fragments of the polynucleotide sequences of the nearest neighbors can be used as probes and primers to identify and isolate the full length sequence corresponding to provided polynucleotides. The nearest neighbors can indicate a
15 tissue or cell type to be used to construct a library for the full-length sequences corresponding to the provided polynucleotides..

Typically, a selected polynucleotide is translated in all six frames to determine the best alignment with the individual sequences. The sequences disclosed herein in the Sequence Listing are in a 5' to 3' orientation and translation in three frames can be sufficient
20 (with a few specific exceptions as described in the Examples). These amino acid sequences are referred to, generally, as query sequences, which will be aligned with the individual sequences. Databases with individual sequences are described in "Computer Methods for Macromolecular Sequence Analysis" *Methods in Enzymology* (1996) 266, Doolittle, Academic Press, Inc., a division of Harcourt Brace & Co., San Diego, California, USA.
25 Databases include Genbank, EMBL, and DNA Database of Japan (DDBJ).

Query and individual sequences can be aligned using the methods and computer programs described above, and include BLAST, available over the world wide web at <http://www.ncbi.nlm.nih.gov/BLAST/>. Another alignment algorithm is Fasta, available in the Genetics Computing Group (GCG) package, Madison, Wisconsin, USA, a wholly owned
30 subsidiary of Oxford Molecular Group, Inc. Other techniques for alignment are described in Doolittle, *supra*. Preferably, an alignment program that permits gaps in the sequence is

WO 99/33982

PCT/US98/27610

utilized to align the sequences. The Smith-Waterman is one type of algorithm that permits gaps in sequence alignments. See *Meth. Mol. Biol.* (1997) 70: 173-187. Also, the GAP program using the Needleman and Wunsch alignment method can be utilized to align sequences. An alternative search strategy uses MPSRCH software, which runs on a

- 5 MASPAR computer. MPSRCH uses a Smith-Waterman algorithm to score sequences on a massively parallel computer. This approach improves ability to identify sequences that are distantly related matches, and is especially tolerant of small gaps and nucleotide sequence errors. Amino acid sequences encoded by the provided polynucleotides can be used to search both protein and DNA databases.

- 10 Results of individual and query sequence alignments can be divided into three categories, high similarity, weak similarity, and no similarity. Individual alignment results ranging from high similarity to weak similarity provide a basis for determining polypeptide activity and/or structure. Parameters for categorizing individual results include: percentage of the alignment region length where the strongest alignment is found, percent sequence
15 identity, and p value.

- The percentage of the alignment region length is calculated by counting the number of residues of the individual sequence found in the region of strongest alignment, e.g., contiguous region of the individual sequence that contains the greatest number of residues that are identical to the residues of the corresponding region of the aligned query sequence.
- 20 This number is divided by the total residue length of the query sequence to calculate a percentage. For example, a query sequence of 20 amino acid residues might be aligned with a 20 amino acid region of an individual sequence. The individual sequence might be identical to amino acid residues 5, 9-15, and 17-19 of the query sequence. The region of strongest alignment is thus the region stretching from residue 9-19, an 11 amino acid stretch.
- 25 The percentage of the alignment region length is: 11 (length of the region of strongest alignment) divided by (query sequence length) 20 or 55%.

- Percent sequence identity is calculated by counting the number of amino acid matches between the query and individual sequence and dividing total number of matches by the number of residues of the individual sequences found in the region of strongest
30 alignment. Thus, the percent identity in the example above would be 10 matches divided by 11 amino acids, or approximately, 90.9%

WO 99/33982

PCT/US98/27610

P value is the probability that the alignment was produced by chance. For a single alignment, the p value can be calculated according to Karlin *et al.*, *Proc. Natl. Acad. Sci.* (1990) 87:2264 and Karlin *et al.*, *Proc. Natl. Acad. Sci.* (1993) 90. The p value of multiple alignments using the same query sequence can be calculated using an heuristic approach described in Altschul *et al.*, *Nat. Genet.* (1994) 6:119. Alignment programs such as BLAST program can calculate the p value.

Another factor to consider for determining identity or similarity is the location of the similarity or identity. Strong local alignment can indicate similarity even if the length of alignment is short. Sequence identity scattered throughout the length of the query sequence also can indicate a similarity between the query and profile sequences. The boundaries of the region where the sequences align can be determined according to Doolittle, *supra*; BLAST or FAST programs; or by determining the area where sequence identity is highest.

High Similarity. In general, in alignment results considered to be of high similarity, the percent of the alignment region length is typically at least about 55% of total length query sequence; more typically, at least about 58%; even more typically, at least about 60% of the total residue length of the query sequence. Usually, percent length of the alignment region can be as much as about 62%; more usually, as much as about 64%; even more usually, as much as about 66%. Further, for high similarity, the region of alignment, typically, exhibits at least about 75% of sequence identity; more typically, at least about 78%; even more typically, at least about 80% sequence identity. Usually, percent sequence identity can be as much as about 82%; more usually, as much as about 84%; even more usually, as much as about 86%.

The p value is used in conjunction with these methods. If high similarity is found, the query sequence is considered to have high similarity with a profile sequence when the p value is less than or equal to about 10^{-2} ; more usually, less than or equal to about 10^{-3} ; even more usually, less than or equal to about 10^{-4} . More typically, the p value is no more than about 10^{-5} ; more typically, no more than or equal to about 10^{-10} ; even more typically, no more than or equal to about 10^{-15} for the query sequence to be considered high similarity.

Weak Similarity. In general, where alignment results considered to be of weak similarity, there is no minimum percent length of the alignment region nor minimum length of alignment. A better showing of weak similarity is considered when the region of

WO 99/33982

PCT/US98/27610

alignment is, typically, at least about 15 amino acid residues in length; more typically, at least about 20; even more typically; at least about 25 amino acid residues in length. Usually, length of the alignment region can be as much as about 30 amino acid residues; more usually, as much as about 40; even more usually, as much as about 60 amino acid residues.

- 5 Further, for weak similarity, the region of alignment, typically, exhibits at least about 35% of sequence identity; more typically, at least about 40%; even more typically; at least about 45% sequence identity. Usually, percent sequence identity can be as much as about 50%; more usually, as much as about 55%; even more usually, as much as about 60%.

- If low similarity is found, the query sequence is considered to have weak similarity
10 with a profile sequence when the p value is usually less than or equal to about 10^{-2} ; more usually; less than or equal to about 10^{-3} ; even more usually; less than or equal to about 10^{-4} . More typically, the p value is no more than about 10^{-5} ; more usually; no more than or equal to about 10^{-10} ; even more usually; no more than or equal to about 10^{-15} for the query sequence to be considered weak similarity.

- 15 Similarity Determined by Sequence Identity Alone. Sequence identity alone can be used to determine similarity of a query sequence to an individual sequence and can indicate the activity of the sequence. Such an alignment, preferably, permits gaps to align sequences. Typically, the query sequence is related to the profile sequence if the sequence identity over the entire query sequence is at least about 15%; more typically, at least about 20%; even
20 more typically, at least about 25%; even more typically, at least about 50%. Sequence identity alone as a measure of similarity is most useful when the query sequence is usually, at least 80 residues in length; more usually, 90 residues; even more usually, at least 95 amino acid residues in length. More typically, similarity can be concluded based on sequence identity alone when the query sequence is preferably 100 residues in length; more preferably,
25 120 residues in length; even more preferably, 150 amino acid residues in length.

Determining Activity from Alignments with Profile and Multiple Aligned Sequences.

- Translations of the provided polynucleotides can be aligned with amino acid profiles that define either protein families or common motifs. Also, translations of the provided polynucleotides can be aligned to multiple sequence alignments (MSA) comprising the
30 polypeptide sequences of members of protein families or motifs. Similarity or identity with profile sequences or MSAs can be used to determine the activity of the gene products (e.g.,

WO 99/33982

PCT/US98/27610

polypeptides) encoded by the provided polynucleotides or corresponding cDNA or genes.

For example, sequences that show an identity or similarity with a chemokine profile or MSA can exhibit chemokine activities.

- Profiles can designed manually by (1) creating an MSA, which is an alignment of the amino acid sequence of members that belong to the family and (2) constructing a statistical representation of the alignment. Such methods are described, for example, in Birney *et al.*, *Nucl. Acid Res.* (1996) 24(14): 2730-2739. MSAs of some protein families and motifs are publicly available. For example, <http://genome.wustl.edu/Pfam/> includes MSAs of 547 different families and motifs. These MSAs are described also in Sonnhammer *et al.*, *Proteins* (1997) 28: 405-420. Other sources over the world wide web include the site at <http://www.embl-heidelberg.de/argos/ali/ali.html>; alternatively, a message can be sent to ALI@EMBL-HEIDELBERG.DE for the information. A brief description of these MSAs is reported in Pascarella *et al.*, *Prot. Eng.* (1996) 9(3):249-251. Techniques for building profiles from MSAs are described in Sonnhammer *et al.*, *supra*; Birney *et al.*, *supra*; and "Computer Methods for Macromolecular Sequence Analysis," *Methods in Enzymology* (1996) 266, Doolittle, Academic Press, Inc., a division of Harcourt Brace & Co., San Diego, California, USA.

- Similarity between a query sequence and a protein family or motif can be determined by (a) comparing the query sequence against the profile and/or (b) aligning the query sequence with the members of the family or motif. Typically, a program such as Searchwise is used to compare the query sequence to the statistical representation of the multiple alignment, also known as a profile. The program is described in Birney *et al.*, *supra*. Other techniques to compare the sequence and profile are described in Sonnhammer *et al.*, *supra* and Doolittle, *supra*.

- Next, methods described by Feng *et al.*, *J. Mol. Evol.* (1987) 25:351 and Higgins *et al.*, *CABIOS* (1989) 5:151 can be used align the query sequence with the members of a family or motif, also known as a MSA. Computer programs, such as PILEUP, can be used. See Feng *et al.*, *infra*. In general, the following factors are used to determine if a similarity between a query sequence and a profile or MSA exists: (1) number of conserved residues found in the query sequence, (2) percentage of conserved residues found in the query sequence, (3) number of frameshifts, and (4) spacing between conserved residues.

WO 99/33982

PCT/US98/27610

Some alignment programs that both translate and align sequences can make any number of frameshifts when translating the nucleotide sequence to produce the best alignment. The fewer frameshifts needed to produce an alignment, the stronger the similarity or identity between the query and profile or MSAs. For example, a weak

5 similarity resulting from no frameshifts can be a better indication of activity or structure of a query sequence, than a strong similarity resulting from two frameshifts. Preferably, three or fewer frameshifts are found in an alignment; more preferably two or fewer frameshifts; even more preferably, one or fewer frameshifts; even more preferably, no frameshifts are found in an alignment of query and profile or MSAs.

10 Conserved residues are those amino acids found at a particular position in all or some of the family or motif members. For example, most chemokines contain four conserved cysteines. Alternatively, a position is considered conserved if only a certain class of amino acids is found in a particular position in all or some of the family members. For example, the N-terminal position can contain a positively charged amino acid, such as lysine, arginine,
15 or histidine.

Typically, a residue of a polypeptide is conserved when a class of amino acids or a single amino acid is found at a particular position in at least about 40% of all class members; more typically, at least about 50%; even more typically, at least about 60% of the members. Usually, a residue is conserved when a class or single amino acid is found in at least about
20 70% of the members of a family or motif; more usually, at least about 80%; even more usually, at least about 90%; even more usually, at least about 95%.

A residue is considered conserved when three unrelated amino acids are found at a particular position in the some or all of the members; more usually, two unrelated amino acids. These residues are conserved when the unrelated amino acids are found at particular
25 positions in at least about 40% of all class member; more typically, at least about 50%; even more typically, at least about 60% of the members. Usually, a residue is conserved when a class or single amino acid is found in at least about 70% of the members of a family or motif; more usually, at least about 80%; even more usually, at least about 90%; even more usually, at least about 95%.

30 A query sequence has similarity to a profile or MSA when the query sequence comprises at least about 25% of the conserved residues of the profile or MSA; more usually,

WO 99/33982

PCT/US98/27610

at least about 30%; even more usually; at least about 40%. Typically, the query sequence has a stronger similarity to a profile sequence or MSA when the query sequence comprises at least about 45% of the conserved residues of the profile or MSA; more typically, at least about 50%; even more typically; at least about 55%.

5 B. Screening Polynucleotide and Amino Acid Sequences Against Protein Profiles

The identify and function of the gene that correlates to a polynucleotide described herein can be determined by screening the polynucleotides or their corresponding amino acid sequences against profiles of protein families. Such profiles focus on common structural motifs among proteins of each family. Publicly available profiles are described above in Section IVA. Additional or alternative profiles are described below.

In comparing a novel polynucleotide with known sequences, several alignment tools are available. Examples include PileUp, which creates a multiple sequence alignment, and is described in Feng *et al.*, *J. Mol. Evol.* (1987) 25:351. Another method, GAP, uses the alignment method of Needleman *et al.*, *J. Mol. Biol.* (1970) 48:443. GAP is best suited for global alignment of sequences. A third method, BestFit, functions by inserting gaps to maximize the number of matches using the local homology algorithm of Smith *et al.*, *Adv. Appl. Math.* (1981) 2:482. Exemplary protein profiles are provided below and in the examples.

20 Chemokines. Chemokines are a family of proteins that have been implicated in lymphocyte trafficking, inflammatory diseases, angiogenesis, hematopoiesis, and viral infection. See, for example, Rollins, *Blood* (1997) 90(3):909-928, and Wells *et al.*, *J. Leuk. Biol.* (1997) 61:545-550. U.S. Patent No. 5,605,817 discloses DNA encoding a chemokine expressed in fetal spleen. U.S. Patent No. 5,656,724 discloses chemokine-like proteins and methods of use. U.S. Patent No. 5,602,008 discloses DNA encoding a chemokine expressed by liver.

Chemokine mutants are polypeptides having an amino acid sequence that possesses at least one amino acid substitution, addition, or deletion as compared to native chemokines. Fragments possess the same amino acid sequence of the native chemokines; mutants can lack the amino and/or carboxyl terminal sequences. Fusions are mutants, fragments, or native chemokines that also include amino and/or carboxyl terminal amino acid extensions.

WO 99/33982

PCT/US98/27610

The number or type of the amino acid changes is not critical, nor is the length or number of the amino acid deletions, or amino acid extensions that are incorporated in the chemokines as compared to the native chemokine amino acid sequences. A polynucleotide encoding one of these variant polypeptides will retain at least about 80% amino acid identity with at least one known chemokine. Preferably, these polypeptides will retain at least about 85% amino acid sequence identity, more preferably, at least about 90%; even more preferably, at least about 95%. In addition, the variants exhibit at least 80%; preferably about 90%; more preferably about 95% of at least one activity exhibited by a native chemokine, which includes immunological, biological, receptor binding, and signal transduction functions.

Assays for chemotaxis relating to neutrophils are described in Walz *et al.*, *Biochem. Biophys. Res. Commun.* (1987) 149:755, Yoshimura *et al.*, *Proc. Natl. Acad. Sci. (USA)* (1987) 84:9233, and Schroder *et al.*, *J. Immunol.* (1987) 139:3474; to lymphocytes, Larsen *et al.*, *Science* (1989) 243:1464, Carr *et al.*, *Proc. Natl. Acad. Sci. (USA)* (1994) 91:3652; to tumor-infiltrating lymphocytes, Liao *et al.*, *J. Exp. Med.* (1995) 182:1301; to hematopoietic progenitors, Aiuti *et al.*, *J. Exp. Med.* (1997) 185:111; to monocytes, Valente *et al.*, *Biochem.* (1988) 27:4162; and to natural killer cells, Loetscher *et al.*, *J. Immunol.* (1996) 156:322, and Allavena *et al.*, *Eur. J. Immunol.* (1994) 24:3233.

Assays for determining the biological activity of attracting eosinophils are described in Dahinden *et al.*, *J. Exp. Med.* (1994) 179:751, Weber *et al.*, *J. Immunol.* (1995) 154:4166, and Noso *et al.*, *Biochem. Biophys. Res. Commun.* (1994) 200:1470; for attracting dendritic cells, Sozzani *et al.*, *J. Immunol.* (1995) 155:3292; for attracting basophils, in Dahinden *et al.*, *J. Exp. Med.* (1994) 179:751, Alam *et al.*, *J. Immunol.* (1994) 152:1298, Alam *et al.*, *J. Exp. Med.* (1992) 176:781; and for activating neutrophils, Maghazaci *et al.*, *Eur. J. Immunol.* (1996) 26:315, and Taub *et al.*, *J. Immunol.* (1995) 155:3877. Native chemokines can act as mitogens for fibroblasts, assayed as described in Mullenbach *et al.*, *J. Biol. Chem.* (1986) 261:719.

Native chemokines exhibit binding activity with a number of receptors. Description of such receptors and assays to detect binding are described in, for example, Murphy *et al.*, *Science* (1991) 253:1280; Combadiere *et al.*, *J. Biol. Chem.* (1995) 270:29671; Daugherty *et al.*, *J. Exp. Med.* (1996) 183:2349; Samson *et al.*, *Biochem.* (1996) 35:3362; Raport *et al.*, *J.*

WO 99/33982

PCT/US98/27610

Biol. Chem. (1996) 271:17161; Combadiere *et al.*, *J. Leukoc. Biol.* (1996) 60:147; Baba *et al.*, *J. Biol. Chem.* (1997) 23:14893; Yosida *et al.*, *J. Biol. Chem.* (1997) 272:13803; Arvanitakis *et al.*, *Nature* (1997) 385:347, and other assays are known in the art.

Assays for kinase activation of chemokines are described by Yen *et al.*, *J. Leukoc.*

- 5 *Biol.* (1997) 61:529; Dubois *et al.*, *J. Immunol.* (1996) 156:1356; Turner *et al.*, *J. Immunol.* (1995) 155:2437. Assays for inhibition of angiogenesis or cell proliferation are described in Maione *et al.*, *Science* (1990) 247:77. Glycosaminoglycan production can be induced by native chemokines, assayed as described in Castor *et al.*, *Proc. Natl. Acad. Sci. (USA)* (1983) 80:765. Chemokine-mediated histamine release from basophils is assayed as described in
- 10 Dahinden *et al.*, *J. Exp. Med.* (1989) 170:1787; and White *et al.*, *Immunol. Lett.* (1989) 22:151. Heparin binding is described in Luster *et al.*, *J. Exp. Med.* (1995) 182:219.

Chemokines can possess dimerization activity, which can be assayed according to Burrows *et al.*, *Biochem.* (1994) 33:12741; and Zhang *et al.*, *Mol. Cell. Biol.* (1995) 15:4851.

- Native chemokines can play a role in the inflammatory response of viruses. This activity
- 15 can be assayed as described in Bleul *et al.*, *Nature* (1996) 382:829; and Oberlin *et al.*, *Nature* (1996) 382:833. Exocytosis of monocytes can be promoted by native chemokines. The assay for such activity is described in Uguccioni *et al.*, *Eur. J. Immunol.* (1995) 25:64. Native chemokines also can inhibit hematopoietic stem cell proliferation. The method for testing for such activity is reported in Graham *et al.*, *Nature* (1990) 344:442.

- 20 **Death Domain Proteins.** Several protein families contain death domain motifs (Feinstein and Kimchi, *TIBS Letters* (1995) 20:242). Some death domain containing proteins are implicated in cytotoxic intracellular signaling (Cleveland *et al.*, *Cell* (1995) 81:479; Pan *et al.*, *Science* (1997) 276:111; Duan *et al.*, *Nature* (1997) 385:86-89, and Chinnaiyan *et al.*, *Science* (1996) 274:990). U.S. Patent No. 5,563,039 describes a protein
- 25 homologous to TRADD (Tumor Necrosis Factor Receptor-1 Associated Death Domain containing protein), and modifications of the active domain of TRADD that retain the functional characteristics of the protein, as well as apoptosis assays for testing the function of such death domain containing proteins. U.S. Patent No. 5,658,883 discloses biologically active TGF- β 1 peptides. U.S. Patent No. 5,674,734 discloses RIP, which contains a C-
- 30 terminal death domain and an N-terminal kinase domain.

WO 99/33982

PCT/US98/27610

Leukemia Inhibitory Factor (LIF). An LIF profile is constructed from sequences of leukemia inhibitor factor, CT-1 (cardiotrophin-1), CNTF (ciliary neurotrophic factor), OSM (oncostatin M), and IL-6 (interleukin-6). This profile encompasses a family of secreted cytokines that have pleiotropic effects on many cell types including hepatocytes, osteoclasts, neuronal cells and cardiac myocytes, and can be used to detect additional genes encoding such proteins. These molecules are all structurally related and share a common co-receptor gp130 which mediates intracellular signal transduction by cytoplasmic tyrosine kinases such as src.

Novel proteins related to this family are also likely to be secreted, to activate gp130 and to function in the development of a variety of cell types. Thus new members of this family would be candidates to be developed as growth or survival factors for the cell types that they stimulate. For more details on this family of cytokines, see Pennica *et al*, *Cytokine and Growth Factor Reviews* (1996) 7:81-91. U.S. Patent No. 5,420,247 discloses LIF receptor and fusion proteins. U.S. Patent No. 5,443,825 discloses human LIF.

Angiopoietin. Angiopoietin-1 is a secreted ligand of the TIE-2 tyrosine kinase; it functions as an angiogenic factor critical for normal vascular development. Angiopoietin-2 is a natural antagonist of angiopoietin-1 and thus functions as an anti-angiogenic factor. These two proteins are structurally similar and activate the same receptor (Folkman *et al*, *Cell* (1996) 87:1153, and Davis *et al*, *Cell* (1996) 87:1161). The angiopoietin molecules are composed of two domains: a coiled-coil region and a region related to fibrinogen. The fibrinogen domain is found in many molecules including ficolin and tesascin, and is well defined structurally with many members.

Receptor Protein-Tyrosine Kinases. Receptor Protein-Tyrosine Kinases or RPTKs are described in Lindberg, *Annu. Rev. Cell Biol.* (1994) 10:251-337.

Growth Factors: (Epidermal Growth Factor) EGF and (Fibroblast Growth Factor) FGF. For a discussion of growth factor superfamilies, see *Growth Factors: A Practical Approach*, (Appendix A1) (1993) McKay and Leigh, Oxford University Press, NY, 237-243. U.S. Patent No. 4,444,760 discloses acidic brain fibroblast growth factor, which is active in the promotion of cell division and wound healing. U.S. Patent No. 5,439,818 discloses DNA encoding human recombinant basic fibroblast growth factor, which is active in wound healing. U.S. Patent No. 5,604,293 discloses recombinant human basic fibroblast growth

WO 99/33982

PCT/US98/27610

factor, which is useful for wound healing. U.S. Patent No. 5,410,832 discloses brain-derived and recombinant acidic fibroblast growth factor, which act as mitogens for mesoderm and neuroectoderm-derived cells in culture, and promote wound healing in soft tissue, cartilaginous tissue and musculo-skeletal tissue. U.S. Patent No. 5,387,673 discloses

- 5 biologically active fragments of FGF.

Proteins of the TNF Family. A profile derived from the TNF family is created by aligning sequences of the following TNF family members: nerve growth factor (NGF), lymphotoxin, Fas ligand, tumor necrosis factor (TNF α), CD40 ligand, TRAIL, α 40 ligand, 4-1BB ligand, CD27 ligand, and CD30 ligand. The profile is designed to identify sequences

10 of proteins that constitute new members or homologues of this family of proteins. U.S. Patent No. 5,606,023 discloses mutant TNF proteins; U.S. Patent No. 5,597,899 and U.S. Patent No. 5,486,463 disclose TNF muteins; and U.S. Patent No. 5,652,353 discloses DNA encoding TNF α muteins.

- Members of the TNF family of proteins have been show in vitro to multimerize, as
- 15 described in Burrows *et al.*, *Biochem.* (1994) 33:12741 and Zhang *et al.*, *Mol. Cell. Biol.* (1995) 15:4851 and bind receptors as described in Browning *et al.*, *J. Immunol.* (1994) 147:1230, Androlewicz *et al.*, *J. Biol. Chem.* (1992) 267:2542, and Crowe *et al.*, *Science* (1994) 264:707.

- In vivo, TNFs proteolytically cleave a target protein as described in Kriegel *et al.*,
- 20 *Cell* (1988) 53:45 and Mohler *et al.*, *Nature* (1994) 370:218 and demonstrate cell proliferation and differentiation activity. T-cell or thymocyte proliferation is assayed as described in Armitage *et al.*, *Eur. J. Immunol.* (1992) 22:447; Current Protocols in Immunology, ed. J.E. Coligan *et al.*, 3.1-3.19; Takai *et al.*, *J. Immunol.* (1986) 137:3494-3500, Bertagnoli *et al.*, *J. Immunol.* (1990) 145:1706, Bertagnoli *et al.*, *J. Immunol.* (1991)
- 25 133:327, Bertagnoli *et al.*, *J. Immunol.* (1992) 149:3778, and Bowman *et al.*, *J. Immunol.* (1994) 152:1756. B cell proliferation and Ig secretion are assayed as described in Maliszewski, *J. Immunol.* (1990) 144:3028, and Assays for B Cell Function: In Vitro Antibody Production, Mond and Brunswick, Current Protocols in Immunol., Coligan Ed vol 1 pp 3.8.1-3.8.16, John Wiley and Sons, Toronto 1994, Kehrl *et al.*, *Science* (1987) 238:1144
- 30 and Boussiotis *et al.*, *PNAS USA* (1994) 91:7007. Other in vivo activities include upregulation of cell surface antigens, upregulation of costimulatory molecules, and cellular

WO 99/33982

PCT/US98/27610

aggregation/adhesion as described in Barrett *et al.*, *J. Immunol.* (1991) 146:1722; Bjorck *et al.*, *Eur. J. Immunol.* (1993) 23:1771; Clark *et al.*, *Annu Rev. Immunol.* (1991) 9:97; Ranheim *et al.*, *J. Exp. Med.* (1994) 177:925; Yellin, *J. Immunol.* (1994) 153:666; and Gruss *et al.*, *Blood* (1994) 84:2305.

- 5 Proliferation and differentiation of hematopoietic and lymphopoietic cells has also been shown in vivo for TNFs, using assays for embryonic differentiation and hematopoiesis as described in Johansson *et al.*, *Cellular Biology* (1995) 15:141, Keller *et al.*, *Mol. Cell. Biol.* (1993) 13:473, McClanahan *et al.*, *Blood* (1993) 81:2903 and using assays to detect stem cell survival and differentiation as described in Culture of Hematopoietic Cells,
- 10 Freshney *et al.* eds, pp 1-21, 23-29, 139-162, 163-179, and 265-268, Wiley-Liss, Inc., New York, NY, 1994, and Hirajama *et al.*, *PNAS USA* (1992) 89:5907.

- In vivo activities of TNFs also include lymphocyte survival and apoptosis, assayed as described in Darzynkewicz *et al.*, *Cytometry* (1992) 13:795; Gorczyca *et al.*, *Leukemia* (1993) 7:659; Itoh *et al.*, *Cell* (1991) 66:233; Zacharduk, *J. Immunol.* (1990) 145:4037; Zamaï *et al.*, *Cytometry* (1993) 14:891; and Gorczyca *et al.*, *Int'l J. Oncol.* (1992) 1:639. Some
- 15 members of the TNF family are cleaved from the cell surface; others remain membrane bound. The three-dimensional structure of TNF is discussed in Sprang and Eck, Tumor Necrosis Factors; *supra*.

- TNF proteins include a transmembrane domain. The protein is cleaved into a shorter
- 20 soluble version, as described in Kriegler *et al.*, *Cell* (1988) 53:45, Perez *et al.*, *Cell* (1990) 63:251, and Shaw *et al.*, *Cell* (1986) 46:659. The transmembrane domain is between amino acid 46 and 77 and the cytoplasmic domain is between position 1 and 45 on the human form of TNF α . The 3-dimensional motifs of TNF include a sandwich of two pleated β sheets. Each sheet is composed of anti-parallel β strands. β strands facing each other on opposite
- 25 sites of the sandwich are connected by short polypeptide loops, as described in Van Ostade *et al.*, *Protein Engineering* (1994) 7(1):5, and Sprang *et al.*, Tumor Necrosis Factors; *supra*. Residues of the TNF family proteins that are involved in the β sheet secondary structure have been identified as described in Van Ostade *et al.*, *Protein Eng.* (1994) 7(1):5, and Sprang *et al.*, *supra*.

- 30 TNF receptors are disclosed in U.S. Patent No. 5,395,760. A profile derived from the TNF receptor family is created by aligning sequences of the TNF receptor family, including

WO 99/33982

PCT/US98/27610

Apo1/Fas, TNFR I and II, death receptor 3 (DR3), CD40, ox40, CD27, and CD30. Thus, the profile is designed to identify from the polynucleotides of the invention sequences of proteins that constitute new members or homologues of this family of proteins.

- Tumor necrosis factor receptors exist in two forms in humans: p55 TNFR and p75 TNFR, both of which provide intracellular signals upon binding with a ligand. The extracellular domains of these receptor proteins are cysteine rich. The receptors can remain membrane bound, although some forms of the receptors are cleaved forming soluble receptors. The regulation, diagnostic, prognostic, and therapeutic value of soluble TNF receptors is discussed in Aderka, *Cytokine and Growth Factor Reviews*, (1996) 7(3):231.
- PDGF Family. U.S. Patent No. 5,326,695 discloses platelet derived growth factor agonists; bioactive portions of PDGF-B are used as agonists. U.S. Patent No. 4,845,075 discloses biologically active B-chain homodimers, and also includes variants and derivatives of the PDGF-B chain. U.S. Patent No. 5,128,321 discloses PDGF analogs and methods of use. Proteins having the same bioactivity as PDGF are disclosed, including A and B chain proteins.

- Kinase (Including MKK) Family. U.S. Patent No. 5,650,501 discloses serine/threonine kinase, associated with mitotic and meiotic cell division; the protein has a kinase domain in its N-terminal and 3 PEST regions in the C-terminus. U.S. Patent No. 5,605,825 discloses human PAK65, a serine protein kinase.

- The foregoing discussion provides a few examples of the protein profiles that can be compared with the polynucleotides of the invention. One skilled in the art can use these and other protein profiles to identify the genes that correlate with the provided polynucleotides.

C. Identification of Secreted & Membrane-Bound Polypeptides

- Both secreted and membrane-bound polypeptides of the present invention are of particular interest. For example, levels of secreted polypeptides can be assayed in body fluids that are convenient, such as blood, urine, prostatic fluid and semen. Membrane-bound polypeptides are useful for constructing vaccine antigens or inducing an immune response. Such antigens would comprise all or part of the extracellular region of the membrane-bound polypeptides. Because both secreted and membrane-bound polypeptides comprise a fragment of contiguous hydrophobic amino acids, hydrophobicity predicting algorithms can be used to identify such polypeptides.

WO 99/33982

PCT/US98/27610

A signal sequence is usually encoded by both secreted and membrane-bound polypeptide genes to direct a polypeptide to the surface of the cell. The signal sequence usually comprises a stretch of hydrophobic residues. Such signal sequences can fold into helical structures. Membrane-bound polypeptides typically comprise at least one transmembrane region that possesses a stretch of hydrophobic amino acids that can transverse the membrane. Some transmembrane regions also exhibit a helical structure. Hydrophobic fragments within a polypeptide can be identified by using computer algorithms. Such algorithms include Hopp & Woods, *Proc. Natl. Acad. Sci. USA* (1981) 78:3824-3828; Kyte & Doolittle, *J. Mol. Biol.* (1982) 157: 105-132; and RAOAR algorithm, Degli Esposti *et al.*, *Eur. J. Biochem.* (1990) 190: 207-219.

Another method of identifying secreted and membrane-bound polypeptides is to translate the polynucleotides of the invention in all six frames and determine if at least 8 contiguous hydrophobic amino acids are present. Those translated polypeptides with at least 8; more typically, 10; even more typically, 12 contiguous hydrophobic amino acids are considered to be either a putative secreted or membrane bound polypeptide. Hydrophobic amino acids include alanine, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, threonine, tryptophan, tyrosine, and valine.

IV. Identification of the Function of an Expression Product of a Full-Length Gene Corresponding to a Polynucleotide

Ribozymes, antisense constructs, and dominant negative mutants can be used to determine function of the expression product of a gene corresponding to a polynucleotide provided herein. These methods and compositions are particularly useful where the provided novel polynucleotide exhibits no significant or substantial homology to a sequence encoding a gene of known function. Antisense molecules and ribozymes can be constructed from synthetic polynucleotides. Typically, the phosphoramidite method of oligonucleotide synthesis is used. See Beaucage *et al.*, *Tet. Lett.* (1981) 22:1859 and U.S. Patent No. 4,668,777. Automated devices for synthesis are available to create oligonucleotides using this chemistry. Examples of such devices include Biosearch 8600, Models 392 and 394 by Applied Biosystems, a division of Perkin-Elmer Corp., Foster City, California, USA; and Expedite by Perceptive Biosystems, Framingham, Massachusetts, USA. Synthetic RNA,

WO 99/33982

PCT/US98/27610

phosphate analog oligonucleotides, and chemically derivatized oligonucleotides can also be produced, and can be covalently attached to other molecules. RNA oligonucleotides can be synthesized, for example, using RNA phosphoramidites. This method can be performed on an automated synthesizer, such as Applied Biosystems, Models 392 and 394, Foster City, California, USA. See Applied Biosystems User Bulletin 53 and Ogilvie *et al.*, *Pure & Applied Chem.* (1987) 59:325.

Phosphorothioate oligonucleotides can also be synthesized for antisense construction. A sulfurizing reagent, such as tetraethylthiuram disulfide (TETD) in acetonitrile can be used to convert the internucleotide cyanoethyl phosphite to the phosphorothioate triester within 15 minutes at room temperature. TETD replaces the iodine reagent, while all other reagents used for standard phosphoramidite chemistry remain the same. Such a synthesis method can be automated using Models 392 and 394 by Applied Biosystems, for example.

Oligonucleotides of up to 200 nucleotides can be synthesized, more typically, 100 nucleotides, more typically 50 nucleotides; even more typically 30 to 40 nucleotides. These synthetic fragments can be annealed and ligated together to construct larger fragments. See, for example, Sambrook *et al.*, *supra*.

A. Ribozymes

Trans-cleaving catalytic RNAs (ribozymes) are RNA molecules possessing endoribonuclease activity. Ribozymes are specifically designed for a particular target, and the target message must contain a specific nucleotide sequence. They are engineered to cleave any RNA species site-specifically in the background of cellular RNA. The cleavage event renders the mRNA unstable and prevents protein expression. Importantly, ribozymes can be used to inhibit expression of a gene of unknown function for the purpose of determining its function in an in vitro or in vivo context, by detecting the phenotypic effect.

One commonly used ribozyme motif is the hammerhead, for which the substrate sequence requirements are minimal. Design of the hammerhead ribozyme is disclosed in Usman *et al.*, *Current Opin. Struct. Biol.* (1996) 6:527. Usman also discusses the therapeutic uses of ribozymes. Ribozymes can also be prepared and used as described in Long *et al.*, *FASEB J.* (1993) 7:25; Symons, *Ann. Rev. Biochem.* (1992) 61:641; Perrotta *et al.*, *Biochem.* (1992) 31:16; Ojwang *et al.*, *Proc. Natl. Acad. Sci. (USA)* (1992) 89:10802; and U.S. Patent No. 5,254,678. Ribozyme cleavage of HIV-I RNA is described in U.S.

WO 99/33982

PCT/US98/27610

Patent No. 5,144,019; methods of cleaving RNA using ribozymes is described in U.S. Patent No. 5,116,742; and methods for increasing the specificity of ribozymes are described in U.S. Patent No. 5,225,337 and Koizumi *et al.*, *Nucleic Acid Res.* (1989) 17:7059. Preparation and use of ribozyme fragments in a hammerhead structure are also described by Koizumi *et al.*, *Nucleic Acids Res.* (1989) 17:7059. Preparation and use of ribozyme fragments in a hairpin structure are described by Chowrira and Burke, *Nucleic Acids Res.* (1992) 20:2835. Ribozymes can also be made by rolling transcription as described in Daubendiek and Kool, *Nat. Biotechnol.* (1997) 15(3):273.

The hybridizing region of the ribozyme can be modified or can be prepared as a branched structure as described in Horn and Urdea, *Nucleic Acids Res.* (1989) 17:6959. The basic structure of the ribozymes can also be chemically altered in ways familiar to those skilled in the art, and chemically synthesized ribozymes can be administered as synthetic oligonucleotide derivatives modified by monomeric units. In a therapeutic context, liposome mediated delivery of ribozymes improves cellular uptake, as described in Birikh *et al.*, *Eur. J. Biochem.* (1997) 245:1.

Using the polynucleotide sequences of the invention and methods known in the art, ribozymes are designed to specifically bind and cut the corresponding mRNA species. Ribozymes thus provide a means to inhibit the expression of any of the proteins encoded by the disclosed polynucleotides or their full-length genes. The full-length gene need not be known in order to design and use specific inhibitory ribozymes. In the case of a polynucleotide or full-length cDNA of unknown function, ribozymes corresponding to that nucleotide sequence can be tested in vitro for efficacy in cleaving the target transcript. Those ribozymes that effect cleavage in vitro are further tested in vivo. The ribozyme can also be used to generate an animal model for a disease, as described in Birikh *et al.*, *supra*. An effective ribozyme is used to determine the function of the gene of interest by blocking its transcription and detecting a change in the cell. Where the gene is found to be a mediator in a disease, an effective ribozyme is designed and delivered in a gene therapy for blocking transcription and expression of the gene.

Therapeutic and functional genomic applications of ribozymes proceed beginning with knowledge of a portion of the coding sequence of the gene to be inhibited. Thus, for many genes, a partial polynucleotide sequence provides adequate sequence for constructing

WO 99/33982

PCT/US98/27610

an effective ribozyme. A target cleavage site is selected in the target sequence, and a ribozyme is constructed based on the 5' and 3' nucleotide sequences that flank the cleavage site. Retroviral vectors are engineered to express monomeric and multimeric hammerhead ribozymes targeting the mRNA of the target coding sequence. These monomeric and multimeric ribozymes are tested in vitro for an ability to cleave the target mRNA. A cell line is stably transduced with the retroviral vectors expressing the ribozymes, and the transduction is confirmed by Northern blot analysis and reverse-transcription polymerase chain reaction (RT-PCR). The cells are screened for inactivation of the target mRNA by such indicators as reduction of expression of disease markers or reduction of the gene product of the target mRNA.

B. Antisense

Antisense nucleic acids are designed to specifically bind to RNA, resulting in the formation of RNA-DNA or RNA-RNA hybrids, with an arrest of DNA replication, reverse transcription or messenger RNA translation. Antisense polynucleotides based on a selected polynucleotide sequence can interfere with expression of the corresponding gene. Antisense polynucleotides are typically generated within the cell by expression from antisense constructs that contain the antisense strand as the transcribed strand. Antisense polynucleotides based on the disclosed polynucleotides will bind and/or interfere with the translation of mRNA comprising a sequence complementary to the antisense polynucleotide. The expression products of control cells and cells treated with the antisense construct are compared to detect the protein product of the gene corresponding to the polynucleotide upon which the antisense construct is based. The protein is isolated and identified using routine biochemical methods.

One rationale for using antisense methods to determine the function of the gene corresponding to a disclosed polynucleotide is the biological activity of antisense therapeutics. Antisense therapy for a variety of cancers is in clinical phase and has been discussed extensively in the literature. Reed reviewed antisense therapy directed at the Bcl-2 gene in tumors; gene transfer-mediated overexpression of Bcl-2 in tumor cell lines conferred resistance to many types of cancer drugs. (Reed, J.C., *N.C.I.* (1997) 89:988). The potential for clinical development of antisense inhibitors of *ras* is discussed by Cowser, L.M., *Anti-Cancer Drug Design* (1997) 12:359. Additional important antisense targets include

WO 99/33982

PCT/US98/27610

leukemia (Geurtz, A.M., *Anti-Cancer Drug Design* (1997) 12:341); human C-ref kinase (Monia, B.P., *Anti-Cancer Drug Design* (1997) 12:327); and protein kinase C (McGraw *et al.*, *Anti-Cancer Drug Design* (1997) 12:315).

Given the extensive background literature and clinical experience in antisense therapy, one skilled in the art can use selected polynucleotides of the invention as additional potential therapeutics. The choice of polynucleotide can be narrowed by first testing them for binding to "hot spot" regions of the genome of cancerous cells. If a polynucleotide is identified as binding to a "hot spot", testing the polynucleotide as an antisense compound in the corresponding cancer cells clearly is warranted.

Ogunbiyi *et al.*, *Gastroenterology* (1997) 113(3):761 describe prognostic use of allelic loss in colon cancer; Barks *et al.*, *Genes, Chromosomes, and Cancer* (1997) 19(4):278 describe increased chromosome copy number detected by FISH in malignant melanoma; Nishizake *et al.*, *Genes, Chromosomes, and Cancer* (1997) 19(4):267 describe genetic alterations in primary breast cancer and their metastases and direct comparison using modified comparative genome hybridization; and Elo *et al.*, *Cancer Research* (1997) 57(16):3356 disclose that loss of heterozygosity at 16z24.1-q24.2 is significantly associated with metastatic and aggressive behavior of prostate cancer.

C. Dominant Negative Mutations

As an alternative method for identifying function of the gene corresponding to a polynucleotide disclosed herein, dominant negative mutations are readily generated for corresponding proteins that are active as homomultimers. A mutant polypeptide will interact with wild-type polypeptides (made from the other allele) and form a non-functional multimer. Thus, a mutation is in a substrate-binding domain, a catalytic domain, or a cellular localization domain. Preferably, the mutant polypeptide will be overproduced. Point mutations are made that have such an effect. In addition, fusion of different polypeptides of various lengths to the terminus of a protein can yield dominant negative mutants. General strategies are available for making dominant negative mutants (see, *e.g.*, Herskowitz, *Nature* (1987) 329:219). Such techniques can be used to create loss of function mutations, which are useful for determining protein function.

V. Construction of Polypeptides of the Invention and Variants Thereof

The polypeptides of the invention include those encoded by the disclosed polynucleotides. These polypeptides can also be encoded by nucleic acids that, by virtue of the degeneracy of the genetic code, are not identical in sequence to the disclosed

- 5 polynucleotides. Thus, the invention includes within its scope a polypeptide encoded by a polynucleotide having the sequence of any one of SEQ ID NOS: 1-844 or a variant thereof.

In general, the term "polypeptide" as used herein refers to both the full length polypeptide encoded by the recited polynucleotide, the polypeptide encoded by the gene represented by the recited polynucleotide, as well as portions or fragments thereof.

- 10 "Polypeptides" also includes variants of the naturally occurring proteins, where such variants are homologous or substantially similar to the naturally occurring protein, and can be of an origin of the same or different species as the naturally occurring protein (*e.g.*, human, murine, or some other species that naturally expresses the recited polypeptide, usually a mammalian species). In general, variant polypeptides have a sequence that has at
15 least about 80%, usually at least about 90%, and more usually at least about 98% sequence identity with a differentially expressed polypeptide of the invention, as measured by BLAST using the parameters described above. The variant polypeptides can be naturally or non-naturally glycosylated, *i.e.*, the polypeptide has a glycosylation pattern that differs from the glycosylation pattern found in the corresponding naturally occurring protein.

- 20 The invention also encompasses homologs of the disclosed polypeptides (or fragments thereof) where the homologs are isolated from other species, *i.e.* other animal or plant species, where such homologs, usually mammalian species, *e.g.* rodents, such as mice, rats; domestic animals, *e.g.*, horse, cow, dog, cat; and humans. By homolog is meant a polypeptide having at least about 35%, usually at least about 40% and more usually at least
25 about 60% amino acid sequence identity a particular differentially expressed protein as identified above, where sequence identity is determined using the BLAST algorithm, with the parameters described *supra*.

- In general, the polypeptides of the subject invention are provided in a non-naturally occurring environment, *e.g.* are separated from their naturally occurring environment. In
30 certain embodiments, the subject protein is present in a composition that is enriched for the protein as compared to a control. As such, purified polypeptide is provided, where by

WO 99/33982

PCT/US98/27610

purified is meant that the protein is present in a composition that is substantially free of non-differentially expressed polypeptides, where by substantially free is meant that less than 90%, usually less than 60% and more usually less than 50% of the composition is made up of non-differentially expressed polypeptides.

Also within the scope of the invention are variants; variants of polypeptides include mutants, fragments, and fusions. Mutants can include amino acid substitutions, additions or deletions. The amino acid substitutions can be conservative amino acid substitutions or substitutions to eliminate non-essential amino acids, such as to alter a glycosylation site, a phosphorylation site or an acetylation site, or to minimize misfolding by substitution or deletion of one or more cysteine residues that are not necessary for function. Conservative amino acid substitutions are those that preserve the general charge, hydrophobicity/hydrophilicity, and/or steric bulk of the amino acid substituted. For example, substitutions between the following groups are conservative: Gly/Ala, Val/Ile/Leu, Asp/Glu, Lys/Arg, Asn/Gln, Ser/Cys, Thr, and Phe/Trp/Tyr.

Variants can be designed so as to retain biological activity of a particular region of the protein (e.g., a functional domain and/or, where the polypeptide is a member of a protein family, a region associated with a consensus sequence). In a non-limiting example, Osawa *et al.*, *Biochem. Mol. Int.* (1994) 34:1003, discusses the actin binding region of a protein from several different species. The actin binding regions of these species are considered homologous based on the fact that they have amino acids that fall within "homologous residue groups." Homologous residues are judged according to the following groups (using single letter amino acid designations): STAG; ILVMF; HRK; DEQN; and FYW. For example, and S, a T, an A or a G can be in a position and the function (in this case actin binding) is retained.

Additional guidance on amino acid substitution is available from studies of protein evolution. Go *et al.*, *Int. J. Peptide Protein Res.* (1980) 15:211, classified amino acid residue sites as interior or exterior depending on their accessibility. More frequent substitution on exterior sites was confirmed to be general in eight sets of homologous protein families regardless of their biological functions and the presence or absence of a prosthetic group. Virtually all types of amino acid residues had higher mutabilities on the exterior than in the interior. No correlation between mutability and polarity was observed of amino acid

WO 99/33982

PCT/US98/27610

residues in the interior and exterior, respectively. Amino acid residues were classified into one of three groups depending on their polarity: polar (Arg, Lys, His, Gln, Asn, Asp. and Glu); weak polar (Ala, Pro, Gly, Thr, and Ser), and nonpolar (Cys, Val, Met, Ile, Leu, Phe, Tyr, and Trp). Amino acid replacements during protein evolution were very conservative: 88% and 76% of them in the interior or exterior, respectively, were within the same group of the three. Inter-group replacements are such that weak polar residues are replaced more often by nonpolar residues in the interior and more often by polar residues on the exterior.

Additional guidance for production of polypeptide variants is provided in Querol *et al.*, *Prot. Eng.* (1996) 9:265, which provides general rules for amino acid substitutions to enhance protein thermostability. New glycosylation sites can be introduced as discussed in Olsen and Thomsen, *J. Gen. Microbiol.* (1991) 137:579. An additional disulfide bridge can be introduced, as discussed by Perry and Wetzel, *Science* (1984) 226:555; Pantoliano *et al.*, *Biochemistry* (1987) 26:2077; Matsumura *et al.*, *Nature* (1989) 342:291; Nishikawa *et al.*, *Protein Eng.* (1990) 3:443; Takagi *et al.*, *J. Biol. Chem.* (1990) 265:6874; Clarke *et al.*, *Biochemistry* (1993) 32:4322; and Wakarchuk *et al.*, *Protein Eng.* (1994) 7:1379. Metal binding sites can be introduced, according to Toma *et al.*, *Biochemistry* (1991) 30:97, and Haezlerbrouck *et al.*, *Protein Eng.* (1993) 6:643. Substitutions with prolines in loops can be made according to Masul *et al.*, *Appl. Env. Microbiol.* (1994) 60:3579; and Hardy *et al.*, *FEBS Lett.* 317:89.

Cysteine-depleted muteins are considered variants within the scope of the invention. These variants can be constructed according to methods disclosed in U.S. Patent No. 4,959,314, which discloses substitution of cysteines with other amino acids, and methods for assaying biological activity and effect of the substitution. Such methods are suitable for proteins according to this invention that have cysteine residues suitable for such substitutions, for example to eliminate disulfide bond formation.

Variants also include fragments of the polypeptides disclosed herein, particularly biologically active fragments and/or fragments corresponding to functional domains. Fragments of interest will typically be at least about 10 aa to at least about 15 aa in length, usually at least about 50 aa in length, and can be as long as 300 aa in length or longer, but will usually not exceed about 1000 aa in length, where the fragment will have a stretch of

WO 99/33982

PCT/US98/27610

amino acids that is identical to a polypeptide encoded by a polynucleotide having a sequence of any SEQ ID NOS:1-844, or a homolog thereof.

The protein variants described herein are encoded by polynucleotides that are within the scope of the invention. The genetic code can be used to select the appropriate codons to construct the corresponding variants.

VI. Computer-Related Embodiments

In general, a library of polynucleotides is a collection of sequence information, which information is provided in either biochemical form (*e.g.*, as a collection of polynucleotide molecules), or in electronic form (*e.g.*, as a collection of polynucleotide sequences stored in a computer-readable form, as in a computer system and/or as part of a computer program).

The sequence information of the polynucleotides can be used in a variety of ways, *e.g.*, as a resource for gene discovery, as a representation of sequences expressed in a selected cell type (*e.g.*, cell type markers), and/or as markers of a given disease or disease state. In general, a disease marker is a representation of a gene product that is present in all affected by disease either at an increased or decreased level relative to a normal cell (*e.g.*, a cell of the same or similar type that is not substantially affected by disease). For example, a polynucleotide sequence in a library can be a polynucleotide that represents an mRNA, polypeptide, or other gene product encoded by the polynucleotide, that is either overexpressed or underexpressed in a breast ductal cell affected by cancer relative to a normal (*i.e.*, substantially disease-free) breast cell.

The nucleotide sequence information of the library can be embodied in any suitable form, *e.g.*, electronic or biochemical forms. For example, a library of sequence information embodied in electronic form includes an accessible computer data file (or, in biochemical form, a collection of nucleic acid molecules) that contains the representative nucleotide sequences of genes that are differentially expressed (*e.g.*, overexpressed or underexpressed) as between, for example, i) a cancerous cell and a normal cell; ii) a cancerous cell and a dysplastic cell; iii) a cancerous cell and a cell affected by a disease or condition other than cancer; iv) a metastatic cancerous cell and a normal cell and/or non-metastatic cancerous cell; v) a malignant cancerous cell and a non-malignant cancerous cell (or a normal cell) and/or vi) a dysplastic cell relative to a normal cell. Other combinations and comparisons of

WO 99/33982

PCT/US98/27610

cells affected by various diseases or stages of disease will be readily apparent to the ordinarily skilled artisan. Biochemical embodiments of the library include a collection of nucleic acids that have the sequences of the genes in the library, where the nucleic acids can correspond to the entire gene in the library or to a fragment thereof, as described in greater detail below.

The polynucleotide libraries of the subject invention include sequence information of a plurality of polynucleotide sequences, where at least one of the polynucleotides has a sequence of any of SEQ ID NOS:1-844. By plurality is meant at least 2, usually at least 3 and can include up to all of SEQ ID NOS:1-844. The length and number of polynucleotides in the library will vary with the nature of the library, *e.g.*, if the library is an oligonucleotide array, a cDNA array, a computer database of the sequence information, etc.

Where the library is an electronic library, the nucleic acid sequence information can be present in a variety of media. "Media" refers to a manufacture, other than an isolated nucleic acid molecule, that contains the sequence information of the present invention. Such a manufacture provides the genome sequence or a subset thereof in a form that can be examined by means not directly applicable to the sequence as it exists in a nucleic acid. For example, the nucleotide sequence of the present invention, *e.g.* the nucleic acid sequences of any of the polynucleotides of SEQ ID NOS:1-844, can be recorded on computer readable media, *e.g.* any medium that can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media, such as a floppy disc, a hard disc storage medium, and a magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as magnetic/optical storage media. One of skill in the art can readily appreciate how any of the presently known computer readable mediums can be used to create a manufacture comprising a recording of the present sequence information. "Recorded" refers to a process for storing information on computer readable medium, using any such methods as known in the art. Any convenient data storage structure can be chosen, based on the means used to access the stored information. A variety of data processor programs and formats can be used for storage, *e.g.* word processing text file, database format, *etc.* In addition to the sequence information, electronic versions of the libraries of the invention can be provided in conjunction or connection with other computer-readable information and/or other types of

WO 99/33982

PCT/US98/27610

computer-readable files (e.g., searchable files, executable files, *etc.*, including, but not limited to, for example, search program software, *etc.*).

By providing the nucleotide sequence in computer readable form, the information can be accessed for a variety of purposes. Computer software to access sequence information is publicly available. For example, the BLAST (Altschul *et al.*, *supra.*) and BLAZE (Brutlag *et al. Comp. Chem.* (1993) 17:203) search algorithms on a Sybase system can be used to identify open reading frames (ORFs) within the genome that contain homology to ORFs from other organisms.

As used herein, "a computer-based system" refers to the hardware means, software means, and data storage means used to analyze the nucleotide sequence information of the present invention. The minimum hardware of the computer-based systems of the present invention comprises a central processing unit (CPU), input means, output means, and data storage means. A skilled artisan can readily appreciate that any one of the currently available computer-based systems are suitable for use in the present invention. The data storage means can comprise any manufacture comprising a recording of the present sequence information as described above, or a memory access means that can access such a manufacture.

"Search means" refers to one or more programs implemented on the computer-based system, to compare a target sequence or target structural motif with the stored sequence information. Search means are used to identify fragments or regions of the genome that match a particular target sequence or target motif. A variety of known algorithms are publicly known and commercially available, e.g. MacPattern (EMBL), BLASTN and BLASTX (NCBI). A "target sequence" can be any DNA or amino acid sequence of six or more nucleotides or two or more amino acids, preferably from about 10 to 100 amino acids or from about 30 to 300 nucleotide residues.

A "target structural motif," or "target motif," refers to any rationally selected sequence or combination of sequences in which the sequence(s) are chosen based on a three-dimensional configuration that is formed upon the folding of the target motif, or on consensus sequences of regulatory or active sites. There are a variety of target motifs known in the art. Protein target motifs include, but are not limited to, enzyme active sites and signal sequences. Nucleic acid target motifs include, but are not limited to, hairpin structures,

WO 99/33982

PCT/US98/27610

promoter sequences and other expression elements such as binding sites for transcription factors.

A variety of structural formats for the input and output means can be used to input and output the information in the computer-based systems of the present invention. One format for an output means ranks fragments of the genome possessing varying degrees of homology to a target sequence or target motif. Such presentation provides a skilled artisan with a ranking of sequences and identifies the degree of sequence similarity contained in the identified fragment.

A variety of comparing means can be used to compare a target sequence or target motif with the data storage means to identify sequence fragments of the genome. A skilled artisan can readily recognize that any one of the publicly available homology search programs can be used as the search means for the computer based systems of the present invention.

As discussed above, the "library" of the invention also encompasses biochemical libraries of the polynucleotides of SEQ ID NOS:1-844, *e.g.*, collections of nucleic acids representing the provided polynucleotides. The biochemical libraries can take a variety of forms, *e.g.*, a solution of cDNAs, a pattern of probe nucleic acids stably associated with a surface of a solid support (*i.e.*, an array) and the like. Of particular interest are nucleic acid arrays in which one or more of SEQ ID NOS:1-844 is represented on the array. By array is meant an article of manufacture that has at least a substrate with at least two distinct nucleic acid targets on one of its surfaces, where the number of distinct nucleic acids can be considerably higher, typically being at least 10 nt, usually at least 20 nt and often at least 25 nt. A variety of different array formats have been developed and are known to those of skill in the art, including those described in 5,242,974; 5,384,261; 5,405,783; 5,412,087; 5,424,186; 5,429,807; 5,436,327; 5,445,934; 5,472,672; 5,527,681; 5,529,756; 5,545,531; 5,554,501; 5,556,752; 5,561,071; 5,599,895; 5,624,711; 5,639,603; 5,658,734; WO 93/17126; WO 95/11995; WO 95/35505; EP 742287; and EP 799897. The arrays of the subject invention find use in a variety of applications, including gene expression analysis, drug screening, mutation analysis and the like, as disclosed in the above-listed exemplary patent documents.

WO 99/33982

PCT/US98/27610

In addition to the above nucleic acid libraries, analogous libraries of polypeptides are also provided, where the where the polypeptides of the library will represent at least a portion of the polypeptides encoded by SEQ ID NOS:1-844.

5 VII. Utilities

A. Use of Polynucleotide Probes in Mapping, and in Tissue Profiling

Polynucleotide probes, generally comprising at least 12 contiguous nucleotides of a polynucleotide as shown in the Sequence Listing, are used for a variety of purposes, such as chromosome mapping of the polynucleotide and detection of transcription levels. Additional
10 disclosure about preferred regions of the disclosed polynucleotide sequences is found in the Examples. A probe that hybridizes specifically to a polynucleotide disclosed herein should provide a detection signal at least 5-, 10-, or 20-fold higher than the background hybridization provided with other unrelated sequences.

Probes in Detection of Expression Levels. Nucleotide probes are used to detect
15 expression of a gene corresponding to the provided polynucleotide. The references describe an example of a sandwich nucleotide hybridization assay. For example, in Northern blots, mRNA is separated electrophoretically and contacted with a probe. A probe is detected as hybridizing to an mRNA species of a particular size. The amount of hybridization is quantitated to determine relative amounts of expression, for example under a particular
20 condition. Probes are also used to detect products of amplification by polymerase chain reaction. The products of the reaction are hybridized to the probe and hybrids are detected. Probes are used for in situ hybridization to cells to detect expression. Probes can also be used *in vivo* for diagnostic detection of hybridizing sequences. Probes are typically labeled with a radioactive isotope. Other types of detectable labels can be used such as
25 chromophores, fluors, and enzymes. Other examples of nucleotide hybridization assays are described in WO92/02526 and U.S. Patent No. 5,124,246.

Alternatively, the Polymerase Chain Reaction (PCR) is another means for detecting small amounts of target nucleic acids (see, e.g., Mullis *et al.*, *Meth. Enzymol.* (1987) 155:335; U.S. Patent No. 4,683,195; and U.S. Patent No. 4,683,202). Two primer
30 polynucleotides nucleotides hybridize with the target nucleic acids and are used to prime the reaction. The primers can be composed of sequence within or 3' and 5' to the polynucleotides of the Sequence Listing. Alternatively, if the primers are 3' and 5' to these

WO 99/33982

PCT/US98/27610

polynucleotides, they need not hybridize to them or the complements. A thermostable polymerase creates copies of target nucleic acids from the primers using the original target nucleic acids as a template. After a large amount of target nucleic acids is generated by the polymerase, it is detected by methods such as Southern blots. When using the Southern blot method, the labeled probe will hybridize to a polynucleotide of the Sequence Listing or complement.

Furthermore, mRNA or cDNA can be detected by traditional blotting techniques described in Sambrook *et al.*, "Molecular Cloning: A Laboratory Manual" (New York, Cold Spring Harbor Laboratory, 1989). mRNA or cDNA generated from mRNA using a polymerase enzyme can be purified and separated using gel electrophoresis. The nucleic acids on the gel are then blotted onto a solid support, such as nitrocellulose. The solid support is exposed to a labeled probe and then washed to remove any unhybridized probe. Next, the duplexes containing the labeled probe are detected. Typically, the probe is labeled with radioactivity.

Mapping. Polynucleotides of the present invention are used to identify a chromosome on which the corresponding gene resides. Such mapping can be useful in identifying the function of the polynucleotide-related gene by its proximity to other genes with known function. Function can also be assigned to the polynucleotide-related gene when particular syndromes or diseases map to the same chromosome. For example, use of polynucleotide probes in identification and quantification of nucleic acid sequence aberrations is described in U.S. Patent No. 5,783,387.

For example, fluorescence in situ hybridization (FISH) on normal metaphase spreads facilitates comparative genomic hybridization to allow total genome assessment of changes in relative copy number of DNA sequences. See Schwartz and Samad, *Curr. Opin. Biotechnol.* (1994) 8:70; Kallioniemi *et al.*, *Sem. Cancer Biol.* (1993) 4:41; Valdes *et al.*, *Methods in Molecular Biology* (1997) 68:1, Boultonwood, ed., Human Press, Totowa, NJ. Preparations of human metaphase chromosomes are prepared using standard cytogenetic techniques from human primary tissues or cell lines. Nucleotide probes comprising at least 12 contiguous nucleotides selected from the nucleotide sequence shown in the Sequence Listing are used to identify the corresponding chromosome. The nucleotide probes are labeled, for example, with a radioactive, fluorescent, biotinylated, or chemiluminescent label,

WO 99/33982

PCT/US98/27610

and detected by well known methods appropriate for the particular label selected. Protocols for hybridizing nucleotide probes to preparations of metaphase chromosomes are also well known in the art. A nucleotide probe will hybridize specifically to nucleotide sequences in the chromosome preparations that are complementary to the nucleotide sequence of the probe.

Polynucleotides are mapped to particular chromosomes using, for example, radiation hybrids or chromosome-specific hybrid panels. See Leach *et al.*, *Advances in Genetics*, (1995) 33:63-99; Walter *et al.*, *Nature Genetics* (1994) 7:22; Walter and Goodfellow, *Trends in Genetics* (1992) 9:352. Panels for radiation hybrid mapping are available from Research Genetics, Inc., Huntsville, Alabama, USA. Databases for markers using various panels are available via the world wide web at <http://F/shgc-www.stanford.edu>; and <http://www-genome.wi.mit.edu/cgi-bin/contig/rhmapper.pl>. The statistical program RHMAP can be used to construct a map based on the data from radiation hybridization with a measure of the relative likelihood of one order versus another. RHMAP is available via the world wide web at <http://www.sph.umich.edu/group/statgen/software>.

In addition, commercial programs are available for identifying regions of chromosomes commonly associated with disease, such as cancer. Polynucleotides based on the polynucleotides of the invention can be used to probe these regions. For example, if through profile searching a provided polynucleotide is identified as corresponding to a gene encoding a kinase, its ability to bind to a cancer-related chromosomal region will suggest its role as a kinase in one or more stages of tumor cell development/growth. Although some experimentation would be required to elucidate the role, the polynucleotide constitutes a new material for isolating a specific protein that has potential for developing a cancer diagnostic or therapeutic.

Tissue Typing or Profiling. Expression of specific mRNA corresponding to the provided polynucleotides can vary in different cell types and can be tissue-specific. This variation of mRNA levels in different cell types can be exploited with nucleic acid probe assays to determine tissue types. For example, PCR, branched DNA probe assays, or blotting techniques utilizing nucleic acid probes substantially identical or complementary to polynucleotides listed in the Sequence Listing can determine the presence or absence of the corresponding cDNA or mRNA.

WO 99/33982

PCT/US98/27610

For example, a metastatic lesion is identified by its developmental organ or tissue source by identifying the expression of a particular marker of that organ or tissue. If a polynucleotide is expressed only in a specific tissue type, and a metastatic lesion is found to express that polynucleotide, then the developmental source of the lesion has been identified.

- 5 Expression of a particular polynucleotide is assayed by detection of either the corresponding mRNA or the protein product. Immunological methods, such as antibody staining, are used to detect a particular protein product. Hybridization methods can be used to detect particular mRNA species, including but not limited to in situ hybridization and Northern blotting.

- Use of Polymorphisms. A polynucleotide of the invention will be useful in forensics, genetic analysis, mapping, and diagnostic applications if the corresponding region of a gene is polymorphic in the human population. Particular polymorphic forms of the provided polynucleotides can be used to either identify a sample as deriving from a suspect or rule out the possibility that the sample derives from the suspect. Any means for detecting a polymorphism in a gene are used, including but not limited to electrophoresis of protein polymorphic variants, differential sensitivity to restriction enzyme cleavage, and hybridization to allele-specific probes.

B. Antibody Production

- Expression products of a polynucleotide of the invention, the corresponding mRNA or cDNA, or the corresponding complete gene are prepared and used for raising antibodies for experimental, diagnostic, and therapeutic purposes. For polynucleotides to which a corresponding gene has not been assigned, this provides an additional method of identifying the corresponding gene. The polynucleotide or related cDNA is expressed as described above, and antibodies are prepared. These antibodies are specific to an epitope on the polypeptide encoded by the polynucleotide, and can precipitate or bind to the corresponding native protein in a cell or tissue preparation or in a cell-free extract of an in vitro expression system.

- Immunogens for raising antibodies are prepared by mixing the polypeptides encoded by the polynucleotides of the present invention with adjuvants. Alternatively, polypeptides are made as fusion proteins to larger immunogenic proteins. Polypeptides are also covalently linked to other larger immunogenic proteins, such as keyhole limpet hemocyanin. Immunogens are typically administered intradermally, subcutaneously, or intramuscularly.

WO 99/33982

PCT/US98/27610

Immunogens are administered to experimental animals such as rabbits, sheep, and mice, to generate antibodies. Optionally, the animal spleen cells are isolated and fused with myeloma cells to form hybridomas which secrete monoclonal antibodies. Such methods are well known in the art. According to another method known in the art, the selected polynucleotide is administered directly, such as by intramuscular injection, and expressed *in vivo*. The expressed protein generates a variety of protein-specific immune responses, including production of antibodies, comparable to administration of the protein.

Preparations of polyclonal and monoclonal antibodies specific for polypeptides encoded by a selected polynucleotide are made using standard methods known in the art.

The antibodies specifically bind to epitopes present in the polypeptides encoded by polynucleotides disclosed in the Sequence Listing. Typically, at least 6, 8, 10, or 12 contiguous amino acids are required to form an epitope. However, epitopes which involve non-contiguous amino acids may require more, for example at least 15, 25, or 50 amino acids. A short sequence of a polynucleotide may then be unsuitable for use as an epitope to raise antibodies for identifying the corresponding novel protein, because of the potential for cross-reactivity with a known protein. However, the antibodies can be useful for other purposes, particularly if they identify common structural features of a known protein and a novel polypeptide encoded by a polynucleotide of the invention.

Antibodies that specifically bind to human polypeptides encoded by the provided polypeptides should provide a detection signal at least 5-, 10-, or 20-fold higher than a detection signal provided with other proteins when used in Western blots or other immunochemical assays. Preferably, antibodies that specifically polypeptides of the invention do not bind to other proteins in immunochemical assays at detectable levels and can immunoprecipitate the specific polypeptide from solution.

To test for the presence of serum antibodies to the polypeptide of the invention in a human population, human antibodies are purified by methods well known in the art. Preferably, the antibodies are affinity purified by passing antiserum over a column to which the corresponding selected polypeptide or fusion protein is bound. The bound antibodies can then be eluted from the column, for example using a buffer with a high salt concentration.

WO 99/33982

PCT/US98/27610

In addition to the antibodies discussed above, genetically engineered antibody derivatives are made, such as single chain antibodies, according to methods well known in the art.

C. Use of Polynucleotides to Construct Arrays for Diagnostics

5 Polynucleotide arrays provide a high throughput technique that can assay a large number of polynucleotide sequences in a sample. This technology can be used as a diagnostic and as a tool to test for differential expression to determine function of an encoded protein. Arrays can be created by spotting polynucleotide probes onto a substrate (e.g., glass, nitrocellulose, *etc.*) in a two-dimensional matrix or array having bound probes.

10 The probes can be bound to the substrate by either covalent bonds or by non-specific interactions, such as hydrophobic interactions. Samples of polynucleotides can be detectably labeled (e.g., using radioactive or fluorescent labels) and then hybridized to the probes. Double stranded polynucleotides, comprising the labeled sample polynucleotides bound to probe polynucleotides, can be detected once the unbound portion of the sample is washed

15 away. Techniques for constructing arrays and methods of using these arrays are described in EP No. 0 799 897; PCT No. WO 97/29212; PCT No. WO 97/27317; EP No. 0 785 280; PCT No. WO 97/02357; U.S. Pat. No. 5,593,839; U.S. Pat. No. 5,578,832; EP No. 0 728 520; U.S. Pat. No. 5,599,695; EP No. 0 721 016; U.S. Pat. No. 5,556,752; PCT No. WO 95/22058; and U.S. Pat. No. 5,631,734.

20 As discussed in some detail above, arrays can be used to examine differential expression of genes and can be used to determine gene function. For example, arrays of the instant polynucleotide sequences can be used to determine if any of the provided polynucleotides are differentially expressed between a test cell and control cell (e.g., cancer cells and normal cells). For example, high expression of a particular message in a cancer

25 cell, which is not observed in a corresponding normal cell, can indicate a cancer specific protein. Exemplary uses of arrays are further described in, for example, Pappalarado *et al.*, *Sem. Radiation Oncol.* (1998) 8:217; and Ramsay *Nature Biotechnol.* (1998) 16:40.

D. Differential Expression

The polynucleotides of the invention can also be used to detect differences in

30 expression levels between two cells, e.g., as a method to identify abnormal or diseased tissue in a human. For polynucleotides corresponding to profiles of protein families as described

WO 99/33982

PCT/US98/27610

above, the choice of tissue can be selected according to the putative biological function. In general, the expression of a gene corresponding to a specific polynucleotide is compared between a first tissue that is suspected of being diseased and a second, normal tissue of the human. The tissue suspected of being abnormal or diseased can be derived from a different tissue type of the human, but preferably it is derived from the same tissue type; for example an intestinal polyp or other abnormal growth should be compared with normal intestinal tissue. The normal tissue can be the same tissue as that of the test sample, or any normal tissue of the patient, especially those that express the polynucleotide-related gene of interest (e.g., brain, thymus, testis, heart, prostate, placenta, spleen, small intestine, skeletal muscle, pancreas, and the mucosal lining of the colon). A difference between the polynucleotide-related gene, mRNA, or protein in the two tissues which are compared, for example in molecular weight, amino acid or nucleotide sequence, or relative abundance, indicates a change in the gene, or a gene which regulates it, in the tissue of the human that was suspected of being diseased. Examples of detection of differential expression and its use in diagnosis of cancer are described in U.S. Patent Nos. 5,688,641 and 5,677,125.

The polynucleotide-related genes in the two tissues are compared by any means known in the art. For example, the two genes can be sequenced, and the sequence of the gene in the tissue suspected of being diseased compared with the gene sequence in the normal tissue. The genes corresponding to a provided polynucleotide, or portions thereof, in the two tissues are amplified, for example using nucleotide primers based on the nucleotide sequence shown in the Sequence Listing, using the polymerase chain reaction. The amplified genes or portions of genes are hybridized to detectably labeled nucleotide probes selected from a nucleotide sequence shown in the Sequence Listing. A difference in the nucleotide sequence of the isolated gene in the tissue suspected of being diseased compared with the normal nucleotide sequence suggests a role of the gene product encoded by the subject polynucleotide in the disease, and provides guidance for preparing a therapeutic agent.

Alternatively, mRNA corresponding to a provided polynucleotide in the two tissues is compared. PolyA⁺ RNA is isolated from the two tissues as is known in the art. For example, one of skill in the art can readily determine differences in the size or amount of mRNA transcripts between the two tissues using Northern blots and detectably labeled

WO 99/33982

PCT/US98/27610

nucleotide probes selected from the nucleotide sequence shown in the Sequence Listing.

Increased or decreased expression of a given mRNA in a tissue sample suspected of being diseased, compared with the expression of the same mRNA in a normal tissue, suggests that the expressed protein has a role in the disease, and also provides a lead for preparing a

5 therapeutic agent.

The comparison can also be accomplished by analyzing polypeptides between the matched samples. The sizes of the proteins in the two tissues are compared, for example, using antibodies of the present invention to detect polypeptides in Western blots of protein extracts from the two tissues. Other changes, such as expression levels and subcellular

10 localization, can also be detected immunologically, using antibodies to the corresponding protein. A higher or lower level of expression of a given polypeptide in a tissue suspected of being diseased, compared with the same protein expression level in a normal tissue, is indicative that the expressed protein has a role in the disease, and provides guidance for preparing a therapeutic agent.

15 Similarly, comparison of polynucleotide sequences or of gene expression products, *e.g.*, mRNA and protein, between a human tissue that is suspected of being diseased and a normal tissue of a human, are used to follow disease progression or remission in the human. Such comparisons are made as described above. For example, increased or decreased expression of a gene corresponding to an inventive polynucleotide in the tissue suspected of

20 being neoplastic can indicate the presence of neoplastic cells in the tissue. The degree of increased expression of a given gene in the neoplastic tissue relative to expression of the same gene in normal tissue, or differences in the amount of increased expression of a given gene in the neoplastic tissue over time, is used to assess the progression of the neoplasia in that tissue or to monitor the response of the neoplastic tissue to a therapeutic protocol over

25 time.

The expression pattern of any two cell types can be compared, such as low and high metastatic tumor cell lines, malignant or non-malignant cells, or cells from tissue which have and have not been exposed to a therapeutic agent. A genetic predisposition to disease in a human is detected by comparing expression levels of an mRNA or protein corresponding to

30 a polynucleotide of the invention in a fetal tissue with levels associated in normal fetal tissue. Fetal tissues that are used for this purpose include, but are not limited to, amniotic

WO 99/33982

PCT/US98/27610

fluid, chorionic villi, blood, and the blastomere of an in vitro-fertilized embryo. The comparable normal polynucleotide-related gene is obtained from any tissue. The mRNA or protein is obtained from a normal tissue of a human in which the polynucleotide-related gene is expressed. Differences such as alterations in the nucleotide sequence or size of the same product of the fetal polynucleotide-related gene or mRNA, or alterations in the molecular weight, amino acid sequence, or relative abundance of fetal protein, can indicate a germline mutation in the polynucleotide-related gene of the fetus, which indicates a genetic predisposition to disease. Particular diagnostic and prognostic uses of the disclosed polynucleotides are described in more detail below.

10 E. Diagnostic, Prognostic, and Other Uses Based On Differential Expression

In general, diagnostic methods of the invention for involve detection of a level or amount of a gene product, particularly a differentially expressed gene product, in a test sample obtained from a patient suspected of having or being susceptible to a disease (e.g., breast cancer, lung cancer, colon cancer and/or metastatic forms thereof), and comparing the detected levels to those levels found in normal cells (e.g., cells substantially unaffected by cancer) and/or other control cells (e.g., to differentiate a cancerous cell from a cell affected by dysplasia). Furthermore, the severity of the disease can be assessed by comparing the detected levels of a differentially expressed gene product with those levels detected in samples representing the levels of differentially gene product associated with varying degrees of severity of disease.

The term "differentially expressed gene" is intended to encompass a polynucleotide that can, for example, include an open reading frame encoding a gene product (e.g., a polypeptide), and/or introns of such genes and adjacent 5' and 3' non-coding nucleotide sequences involved in the regulation of expression, up to about 20 kb beyond the coding region, but possibly further in either direction. The gene can be introduced into an appropriate vector for extrachromosomal maintenance or for integration into a host genome. In general, a difference in expression level associated with a decrease in expression level of at least about 25%, usually at least about 50% to 75%, more usually at least about 90% or more is indicative of a differentially expressed gene of interest, i.e., a gene that is underexpressed or down-regulated in the test sample relative to a control sample. Furthermore, a difference in expression level associated with an increase in expression of at

WO 99/33982

PCT/US98/27610

least about 25%, usually at least about 50% to 75%, more usually at least about 90% and can be at least about 1 ½-fold, usually at least about 2-fold to about 10-fold, and can be about 100-fold to about 1,000-fold increase relative to a control sample is indicative of a differentially expressed gene of interest, *i.e.*, an overexpressed or up-regulated gene.

5 "Differentially expressed polynucleotide" as used herein means a nucleic acid molecule (RNA or DNA) having a sequence that represents a differentially expressed gene, *e.g.*, the differentially expressed polynucleotide comprises a sequence (*e.g.*, an open reading frame encoding a gene product) that uniquely identifies a differentially expressed gene so that detection of the differentially expressed polynucleotide in a sample is correlated with the

10 presence of a differentially expressed gene in a sample. "Differentially expressed polynucleotides" is also meant to encompass fragments of the disclosed polynucleotides, *e.g.*, fragments retaining biological activity, as well as nucleic acids homologous, substantially similar, or substantially identical (*e.g.*, having about 90% sequence identity) to the disclosed polynucleotides.

15 Methods of the subject invention useful in diagnosis or prognosis typically involve comparison of the abundance of a selected differentially expressed gene product in a sample of interest with that of a control to determine any relative differences in the expression of the gene product, where the difference can be measured qualitatively and/or quantitatively. Quantitation can be accomplished, for example, by comparing the level of expression

20 product detected in the sample with the amounts of product present in a standard curve. A comparison can be made visually; by using a technique such as densitometry, with or without computerized assistance; by preparing a representative library of cDNA clones of mRNA isolated from a test sample, sequencing the clones in the library to determine that number of cDNA clones corresponding to the same gene product, and analyzing the number

25 of clones corresponding to that same gene product relative to the number of clones of the same gene product in a control sample; or by using an array to detect relative levels of hybridization to a selected sequence or set of sequences, and comparing the hybridization pattern to that of a control. The differences in expression are then correlated with the presence or absence of an abnormal expression pattern. A variety of different methods for

30 determining the nucleic acid abundance in a sample are known to those of skill in the art, where particular methods of interest include those described in: Pietu *et al. Genome Res.*

WO 99/33982

PCT/US98/27610

(1996) 6:492; Zhao *et al.*, *Gene* (1995) 156:207; Soares, *Curr. Opin. Biotechnol.* (1977) 8: 542; Raval, *J. Pharmacol Toxicol Methods* (1994) 32:125; Chalifour *et al.*, *Anal. Biochem* (1994) 216:299; Stolz *et al.*, *Mol. Biotechnol.* (1996) 6:225; Hong *et al.*, *Biosci. Reports* (1982) 2:907; and McGraw, *Anal. Biochem.* (1984) 143:298. Also of interest are the methods disclosed in WO 97/27317, the disclosure of which is herein incorporated by reference.

In general, diagnostic assays of the invention involve detection of a gene product of a the polynucleotide sequence (*e.g.*, mRNA or polypeptide) that corresponds to a sequence of SEQ ID NOS:1-844. The patient from whom the sample is obtained can be apparently healthy, susceptible to disease (*e.g.*, as determined by family history or exposure to certain environmental factors), or can already be identified as having a condition in which altered expression of a gene product of the invention is implicated.

In the assays of the invention, the diagnosis can be determined based on detected gene product expression levels of a gene product encoded by at least one, preferably at least two or more, at least 3 or more, or at least 4 or more of the polynucleotides having a sequence set forth in SEQ ID NOS:1-844, and can involve detection of expression of genes corresponding to all of SEQ ID NOS:1-844 and/or additional sequences that can serve as additional diagnostic markers and/or reference sequences. Where the diagnostic method is designed to detect the presence or susceptibility of a patient to cancer, the assay preferably involves detection of a gene product encoded by a gene corresponding to a polynucleotide that is differentially expressed in cancer. For example, a higher level of expression of a polynucleotide corresponding to SEQ ID NO:52 relative to a level associated with a normal sample can indicate the presence of cancer in the patient from whom the sample is derived. In another example, detection of a lower level of a polynucleotide corresponding to SEQ ID NO:39 relative to a normal level is indicative of the presence of cancer in the patient. Further examples of such differentially expressed polynucleotides are described in the Examples below. Given the provided polynucleotides and information regarding their relative expression levels provided herein, assays using such polynucleotides and detection of their expression levels in diagnosis and prognosis will be readily apparent to the ordinarily skilled artisan.

WO 99/33982

PCT/US98/27610

- Any of a variety of detectable labels can be used in connection with the various embodiments of the diagnostic methods of the invention. Suitable detectable labels include fluorochromes, (e.g. fluorescein isothiocyanate (FITC), rhodamine, Texas Red, phycoerythrin, allophycocyanin, 6-carboxyfluorescein (6-FAM), 2',7'-dimethoxy-4',5'-dichloro-6-carboxyfluorescein (JOE), 6-carboxy-X-rhodamine (ROX), 6-carboxy-2',4',7',4,7-hexachlorofluorescein (HEX), 5-carboxyfluorescein (5-FAM) or N,N,N',N'-tetramethyl-6-carboxyrhodamine (TAMRA)), radioactive labels, (e.g. ^{32}P , ^{35}S , ^3H , etc.), and the like. The detectable label can involve a two stage systems (e.g., biotin-avidin, hapten-anti-hapten antibody, etc.)
- Reagents specific for the polynucleotides and polypeptides of the invention, such as antibodies and nucleotide probes, can be supplied in a kit for detecting the presence of an expression product in a biological sample. The kit can also contain buffers or labeling components, as well as instructions for using the reagents to detect and quantify expression products in the biological sample. Exemplary embodiments of the diagnostic methods of the invention are described below in more detail.

- Polypeptide detection in diagnosis. In one embodiment, the test sample is assayed for the level of a differentially expressed polypeptide. Diagnosis can be accomplished using any of a number of methods to determine the absence or presence or altered amounts of the differentially expressed polypeptide in the test sample. For example, detection can utilize staining of cells or histological sections with labeled antibodies, performed in accordance with conventional methods. Cells can be permeabilized to stain cytoplasmic molecules. In general, antibodies that specifically bind a differentially expressed polypeptide of the invention are added to a sample, and incubated for a period of time sufficient to allow binding to the epitope, usually at least about 10 minutes. The antibody can be detectably labeled for direct detection (e.g., using radioisotopes, enzymes, fluorescers, chemilumescers, and the like), or can be used in conjunction with a second stage antibody or reagent to detect binding (e.g., biotin with horseradish peroxidase-conjugated avidin, a secondary antibody conjugated to a fluorescent compound, e.g. fluorescein, rhodamine, Texas red, etc.). The absence or presence of antibody binding can be determined by various methods, including flow cytometry of dissociated cells, microscopy, radiography, scintillation counting, etc. Any suitable alternative methods can of qualitative or quantitative

WO 99/33982

PCT/US98/27610

detection of levels or amounts of differentially expressed polypeptide can be used, for example ELISA, western blot, immunoprecipitation, radioimmunoassay, etc.

In general, the detected level of differentially expressed polypeptide in the test sample is compared to a level of the differentially expressed gene product in a reference or control sample, *e.g.*, in a normal cell (negative control) or in a cell having a known disease state (positive control). For example, a higher level of expression of a polypeptide encoded by SEQ ID NO:52 relative to a level associated with a normal sample can indicate the presence of cancer in the patient from whom the sample is derived. In another example, detection of a lower level of the polypeptide encoded by SEQ ID NO:39 relative to a normal level is indicative of the presence of cancer in the patient.

mRNA detection. The diagnostic methods of the invention can also or alternatively involve detection of mRNA encoded by a gene corresponding to a differentially expressed polynucleotides of the invention. Any suitable qualitative or quantitative methods known in the art for detecting specific mRNAs can be used. mRNA can be detected by, for example, *in situ* hybridization in tissue sections, by reverse transcriptase-PCR, or in Northern blots containing poly A+ mRNA. One of skill in the art can readily use these methods to determine differences in the size or amount of mRNA transcripts between two samples. For example, the level of mRNA of the invention in a tissue sample suspected of being cancerous or dysplastic is compared with the expression of the mRNA in a reference sample, *e.g.*, a positive or negative control sample (*e.g.*, normal tissue, cancerous tissue, *etc.*). In a specific non-limiting example, a higher level of mRNA corresponding to SEQ ID NO:52 relative to a level associated with a normal sample can indicate the presence of cancer in the patient from whom the sample is derived. In another example, detection of a lower level of mRNA corresponding to SEQ ID NO:39 relative to a normal level is indicative of the presence of cancer in the patient.

Any suitable method for detecting and comparing mRNA expression levels in a sample can be used in connection with the diagnostic methods of the invention (*see, e.g.*, U.S. 5,804,382). For example, mRNA expression levels in a sample can be determined by generation of a library of expressed sequence tags (ESTs) from the sample, where the EST library is representative of sequences present in the sample (Adams, et al., (1991) *Science* 252:1651). Enumeration of the relative representation of ESTs within the library can be used

WO 99/33982

PCT/US98/27610

to approximate the relative representation of the gene transcript within the starting sample. The results of EST analysis of a test sample can then be compared to EST analysis of a reference sample to determine the relative expression levels of a selected polynucleotide, particularly a polynucleotide corresponding to one or more of the differentially expressed genes described herein.

Alternatively, gene expression in a test sample can be performed using serial analysis of gene expression (SAGE) methodology (Velculescu et al., *Science* (1995) 270:484). In short, SAGE involves the isolation of short unique sequence tags from a specific location within each transcript (e.g., a sequence of any one of SEQ ID NOS:1-6). The sequence tags are concatenated, cloned, and sequenced. The frequency of particular transcripts within the starting sample is reflected by the number of times the associated sequence tag is encountered with the sequence population.

Gene expression in a test sample can also be analyzed using differential display (DD) methodology. In DD, fragments defined by specific sequence delimiters (e.g., restriction enzyme sites) are used as unique identifiers of genes, coupled with information about fragment length or fragment location within the expressed gene. The relative representation of an expressed gene with a sample can then be estimated based on the relative representation of the fragment associated with that gene within the pool of all possible fragments. Methods and compositions for carrying out DD are well known in the art, see, e.g., U.S. 5,776,683; and U.S. 5,807,680.

Alternatively, gene expression in a sample using hybridization analysis, which is based on the specificity of nucleotide interactions. Oligonucleotides or cDNA can be used to selectively identify or capture DNA or RNA of specific sequence composition, and the amount of RNA or cDNA hybridized to a known capture sequence determined qualitatively or quantitatively, to provide information about the relative representation of a particular message within the pool of cellular messages in a sample. Hybridization analysis can be designed to allow for concurrent screening of the relative expression of hundreds to thousands of genes by using, for example, array-based technologies having high density formats, including filters, microscope slides, or microchips, or solution-based technologies that use spectroscopic analysis (e.g., mass spectrometry). One exemplary use of arrays in the diagnostic methods of the invention is described below in more detail.

WO 99/33982

PCT/US98/27610

Use of a single gene in diagnostic applications. The diagnostic methods of the invention can focus on the expression of a single differentially expressed gene. For example, the diagnostic method can involve detecting a differentially expressed gene, or a polymorphism of such a gene (*e.g.*, a polymorphism in an coding region or control region), that is associated with disease. Disease-associated polymorphisms can include deletion or truncation of the gene, mutations that alter expression level and/or affect activity of the encoded protein, *etc.*

Changes in the promoter or enhancer sequence that affect expression levels of an differentially gene can be compared to expression levels of the normal allele by various methods known in the art. Methods for determining promoter or enhancer strength include quantitation of the expressed natural protein; insertion of the variant control element into a vector with a reporter gene such as β -galactosidase, luciferase, chloramphenicol acetyltransferase, *etc.* that provides for convenient quantitation; and the like.

A number of methods are available for analyzing nucleic acids for the presence of a specific sequence, *e.g.* a disease associated polymorphism. Where large amounts of DNA are available, genomic DNA is used directly. Alternatively, the region of interest is cloned into a suitable vector and grown in sufficient quantity for analysis. Cells that express a differentially expressed gene can be used as a source of mRNA, which can be assayed directly or reverse transcribed into cDNA for analysis. The nucleic acid can be amplified by conventional techniques, such as the polymerase chain reaction (PCR), to provide sufficient amounts for analysis, and a detectable label can be included in the amplification reaction (*e.g.*, using a detectably labeled primer or detectably labeled oligonucleotides) to facilitate detection. The use of the polymerase chain reaction is described in Saiki, *et al.*, *Science* (1985) 239:487, and a review of techniques can be found in Sambrook, *et al.*, *Molecular Cloning: A Laboratory Manual*, (1989) pp. 14.2. Alternatively, various methods are known in the art that utilize oligonucleotide ligation as a means of detecting polymorphisms, for examples see Riley *et al.*, *Nucl. Acids Res.* (1990) 18:2887; and Delahunty *et al.*, *Am. J. Hum. Genet.* (1996) 58:1239.

The sample nucleic acid, *e.g.* amplified or cloned fragment, is analyzed by one of a number of methods known in the art. The nucleic acid can be sequenced by dideoxy or other methods, and the sequence of bases compared to a selected sequence, *e.g.*, to a wild-type

WO 99/33982

PCT/US98/27610

sequence. Hybridization with the polymorphic or variant sequence can also be used to determine its presence in a sample (*e.g.*, by Southern blot, dot blot, *etc.*). The hybridization pattern of a polymorphic or variant sequence and a control sequence to an array of oligonucleotide probes immobilized on a solid support, as described in US 5,445,934, or in WO 95/35505, can also be used as a means of identifying polymorphic or variant sequences associated with disease. Single strand conformational polymorphism (SSCP) analysis, denaturing gradient gel electrophoresis (DGGE), and heteroduplex analysis in gel matrices are used to detect conformational changes created by DNA sequence variation as alterations in electrophoretic mobility. Alternatively, where a polymorphism creates or destroys a recognition site for a restriction endonuclease, the sample is digested with that endonuclease, and the products size fractionated to determine whether the fragment was digested. Fractionation is performed by gel or capillary electrophoresis, particularly acrylamide or agarose gels.

Screening for mutations in an differentially expressed gene can be based on the functional or antigenic characteristics of the protein. Protein truncation assays are useful in detecting deletions that can affect the biological activity of the protein. Various immunoassays designed to detect polymorphisms in proteins can be used in screening. Where many diverse genetic mutations lead to a particular disease phenotype, functional protein assays have proven to be effective screening tools. The activity of the encoded protein can be determined by comparison with the wild-type protein.

Pattern matching in diagnosis using arrays. In another embodiment, the diagnostic and/or prognostic methods of the invention involve detection of expression of a selected set of genes in a test sample to produce a test expression pattern (TEP). The TEP is compared to a reference expression pattern (REP), which is generated by detection of expression of the selected set of genes in a reference sample (*e.g.*, a positive or negative control sample). The selected set of genes includes at least one of the genes of the invention, which genes correspond to the polynucleotide sequences of SEQ ID NOS:1-844. Of particular interest is a selected set of genes that includes gene differentially expressed in the disease for which the test sample is to be screened.

"Reference sequences" or "reference polynucleotides" as used herein in the context of differential gene expression analysis and diagnosis/prognosis refers to a selected set of

WO 99/33982

PCT/US98/27610

polynucleotides, which selected set includes at least one or more of the differentially expressed polynucleotides described herein. A plurality of reference sequences, preferably comprising positive and negative control sequences, can be included as reference sequences. Additional suitable reference sequences are found in Genbank, Unigene, and other nucleotide sequence databases (including, *e.g.*, expressed sequence tag (EST), partial, and full-length sequences).

"Reference array" means an array having reference sequences for use in hybridization with a sample, where the reference sequences include all, at least one of, or any subset of the differentially expressed polynucleotides described herein. Usually such an array will include at least 3 different reference sequences, and can include any one or all of the provided differentially expressed sequences. Arrays of interest can further comprise sequences, including polymorphisms, of other genetic sequences, particularly other sequences of interest for screening for a disease or disorder (*e.g.*, cancer, dysplasia, or other related or unrelated diseases, disorders, or conditions). The oligonucleotide sequence on the array will usually be at least about 12 nt in length, and can be of about the length of the provided sequences, or can extend into the flanking regions to generate fragments of 100 nt to 200 nt in length or more.

A "reference expression pattern" or "REP" as used herein refers to the relative levels of expression of a selected set of genes, particularly of differentially expressed genes, that is associated with a selected cell type, *e.g.*, a normal cell, a cancerous cell, a cell exposed to an environmental stimulus, and the like. A "test expression pattern" or "TEP" refers to relative levels of expression of a selected set of genes, particularly of differentially expressed genes, in a test sample (*e.g.*, a cell of unknown or suspected disease state, from which mRNA is isolated).

"Diagnosis" as used herein generally includes determination of a subject's susceptibility to a disease or disorder, determination as to whether a subject is presently affected by a disease or disorder, as well as to the prognosis of a subject affected by a disease or disorder (*e.g.*, identification of pre-metastatic or metastatic cancerous states, stages of cancer, or responsiveness of cancer to therapy). The present invention particularly encompasses diagnosis of subjects in the context of breast cancer (*e.g.*, carcinoma in situ (*e.g.*, ductal carcinoma in situ), estrogen receptor (ER)-positive breast cancer, ER-negative

WO 99/33982

PCT/US98/27610

breast cancer, or other forms and/or stages of breast cancer), lung cancer (e.g., small cell carcinoma, non-small cell carcinoma, mesothelioma, and other forms and/or stages of lung cancer), and colon cancer (e.g., adenomatous polyp, colorectal carcinoma, and other forms and/or stages of colon cancer).

- 5 "Sample" or "biological sample" as used throughout here are generally meant to refer to samples of biological fluids or tissues, particularly samples obtained from tissues, especially from cells of the type associated with the disease for which the diagnostic application is designed (e.g., ductal adenocarcinoma), and the like. "Samples" is also meant to encompass derivatives and fractions of such samples (e.g., cell lysates). Where the sample
10 is solid tissue, the cells of the tissue can be dissociated or tissue sections can be analyzed.

- REPs can be generated in a variety of ways according to methods well known in the art. For example, REPs can be generated by hybridizing a control sample to an array having a selected set of polynucleotides (particularly a selected set of differentially expressed polynucleotides), acquiring the hybridization data from the array, and storing the data in a
15 format that allows for ready comparison of the REP with a TEP. Alternatively, all expressed sequences in a control sample can be isolated and sequenced, e.g., by isolating mRNA from a control sample, converting the mRNA into cDNA, and sequencing the cDNA. The resulting sequence information roughly or precisely reflects the identity and relative number of expressed sequences in the sample. The sequence information can then be stored in a
20 format (e.g., a computer-readable format) that allows for ready comparison of the REP with a TEP. The REP can be normalized prior to or after data storage, and/or can be processed to selectively remove sequences of expressed genes that are of less interest or that might complicate analysis (e.g., some or all of the sequences associated with housekeeping genes can be eliminated from REP data).

- 25 TEPs can be generated in a manner similar to REPs, e.g., by hybridizing a test sample to an array having a selected set of polynucleotides, particularly a selected set of differentially expressed polynucleotides, acquiring the hybridization data from the array, and storing the data in a format that allows for ready comparison of the TEP with a REP. The REP and TEP to be used in a comparison can be generated simultaneously, or the TEP can
30 be compared to previously generated and stored REPs.

WO 99/33982

PCT/US98/27610

In one embodiment of the invention, comparison of a TEP with a REP involves hybridizing a test sample with a reference array, where the reference array has one or more reference sequences for use in hybridization with a sample. The reference sequences include all, at least one of, or any subset of the differentially expressed polynucleotides described herein. Hybridization data for the test sample is acquired, the data normalized, and the produced TEP compared with a REP generated using an array having the same or similar selected set of differentially expressed polynucleotides. Probes that correspond to sequences differentially expressed between the two samples will show decreased or increased hybridization efficiency for one of the samples relative to the other.

Reference arrays can be produced according to any suitable methods known in the art. For example, methods of producing large arrays of oligonucleotides are described in U.S. 5,134,854, and U.S. 5,445,934 using light-directed synthesis techniques. Using a computer controlled system, a heterogeneous array of monomers is converted, through simultaneous coupling at a number of reaction sites, into a heterogeneous array of polymers.

Alternatively, microarrays are generated by deposition of pre-synthesized oligonucleotides onto a solid substrate, for example as described in PCT published application no. WO 95/35505.

Methods for collection of data from hybridization of samples with a reference arrays are also well known in the art. For example, the polynucleotides of the reference and test samples can be generated using a detectable fluorescent label, and hybridization of the polynucleotides in the samples detected by scanning the microarrays for the presence of the detectable label. Methods and devices for detecting fluorescently marked targets on devices are known in the art. Generally, such detection devices include a microscope and light source for directing light at a substrate. A photon counter detects fluorescence from the substrate, while an x-y translation stage varies the location of the substrate. A confocal detection device that can be used in the subject methods is described in U.S. Patent no.

5,631,734. A scanning laser microscope is described in Shalon et al., *Genome Res.* (1996) 6:639. A scan, using the appropriate excitation line, is performed for each fluorophore used. The digital images generated from the scan are then combined for subsequent analysis. For any particular array element, the ratio of the fluorescent signal from one sample (e.g., a test

WO 99/33982

PCT/US98/27610

sample) is compared to the fluorescent signal from another sample (e.g., a reference sample), and the relative signal intensity determined.

Methods for analyzing the data collected from hybridization to arrays are well known in the art. For example, where detection of hybridization involves a fluorescent label, data analysis can include the steps of determining fluorescent intensity as a function of substrate position from the data collected, removing outliers, *i.e.* data deviating from a predetermined statistical distribution, and calculating the relative binding affinity of the targets from the remaining data. The resulting data can be displayed as an image with the intensity in each region varying according to the binding affinity between targets and probes.

In general, the test sample is classified as having a gene expression profile corresponding to that associated with a disease or non-disease state by comparing the TEP generated from the test sample to one or more REPs generated from reference samples (e.g., from samples associated with cancer or specific stages of cancer, dysplasia, samples affected by a disease other than cancer, normal samples, *etc.*). The criteria for a match or a substantial match between a TEP and a REP include expression of the same or substantially the same set of reference genes, as well as expression of these reference genes at substantially the same levels (e.g., no significant difference between the samples for a signal associated with a selected reference sequence after normalization of the samples, or at least no greater than about 25% to about 40% difference in signal strength for a given reference sequence. In general, a pattern match between a TEP and a REP includes a match in expression, preferably a match in qualitative or quantitative expression level, of at least one of, all or any subset of the differentially expressed genes of the invention.

Pattern matching can be performed manually, or can be performed using a computer program. Methods for preparation of substrate matrices (e.g., arrays), design of oligonucleotides for use with such matrices, labeling of probes, hybridization conditions, scanning of hybridized matrices, and analysis of patterns generated, including comparison analysis, are described in, for example, U.S. 5,800,992.

F. Use of the Polynucleotides of the Invention in Cancer

Oncogenesis involves the unbridled growth, dedifferentiation and abnormal migration of cells. Cancerous cells can have the ability to compress, invade, and destroy normal tissue. Cancerous cells may also metastasize to other parts of the body via the

WO 99/33982

PCT/US98/27610

bloodstream or the lymph system and colonize in these other areas. Different cancers are classified by the cell from which the cancerous cell is derived and from its cellular morphology and/or state of differentiation.

- Somatic genetic abnormalities cause cancer initiation and progression. Cancer generally is clonally formed, *i.e.* gain of function of oncogenes and loss of function of tumor suppressor genes within a single cell transform the cell to be cancerous, and that single cell grows and divides to form a cancerous lesion. The genes known to be involved in cancer initiation and progression are involved in numerous cellular functions, including developmental differentiation, cell cycle regulation, cell signaling, immunological response, DNA replication, and DNA repair.

- The identification and characterization of genetic or biochemical markers in blood or tissues that will detect the earliest changes along the carcinogenesis pathway and monitor the efficacy of various therapies and preventive interventions is a major goal of cancer research. Scientists have identified genetic changes in stool specimens that indicate the stages of colon cancer, and other biomarkers such as gene mutations, hormone receptors, proteins that inhibit metastasis, and enzymes that metabolize drugs are all being used to determine the severity and predict the course of breast, prostate, lung, and other cancers.

- Recent advances in the pathogenesis of certain cancers has been helpful in determining patient treatment. The level of expression of certain polynucleotides can be indicative of a poorer prognosis, and therefore warrant more aggressive chemo- or radio-therapy for a patient. The correlation of novel surrogate tumor specific features with response to treatment and outcome in patients has defined certain prognostic indicators that allow the design of tailored therapy based on the molecular profile of the tumor. These therapies include antibody targeting and gene therapy. Moreover, a promising level of one or more marker polynucleotides can provide impetus for not aggressively treating a particular patient, thus sparing the patient the deleterious side effects of aggressive therapy. Determining expression of certain polynucleotides and comparison of a patient's profile with known expression in normal tissue and variants of the disease allows a determination of the best possible treatment for a patient, both in terms of specificity of treatment and in terms of comfort level of the patient.

WO 99/33982

PCT/US98/27610

Surrogate tumor markers, such as polynucleotide expression, can also be used to better classify, and thus diagnose and treat, different forms and disease states of cancer. Two classifications widely used in oncology that can benefit from identification of the expression levels of the polynucleotides of the invention are staging of the cancerous disorder, and grading the nature of the cancerous tissue.

Staging. Staging is a process used by physicians to describe how advanced the cancerous state is in a patient. Staging assists the physician in determining a prognosis, planning treatment and evaluating the results of such treatment. Different staging systems are used for different types of cancer, but each generally involves the following determinations: the type of tumor, indicated by T; whether the cancer has metastasized to nearby lymph nodes, indicated by N; and whether the cancer has metastasized to more distant parts of the body, indicated by M. This system of staging is called the TNM system. Generally, if a cancer is only detectable in the area of the primary lesion without having spread to any lymph nodes it is called Stage I. If it has spread only to the closest lymph nodes, it is called Stage II. In Stage III, the cancer has generally spread to the lymph nodes in near proximity to the site of the primary lesion. Cancers that have spread to a distant part of the body, such as the liver, bone, brain or another site, are called Stage IV, the most advanced stage.

Currently, the determination of staging is done using pathological techniques and is based more on the presence or absence of malignant tissue rather than the characteristics of the tumor type. Presence or absence of malignant tissue is based primarily on the gross morphology of the cells in the areas biopsied. The polynucleotides of the invention can facilitate fine-tuning of the staging process by identifying markers for the aggressivity of a cancer, e.g. the metastatic potential, as well as the presence in different areas of the body. Thus, a Stage II cancer with a polynucleotide signifying a high metastatic potential cancer can be used to change a borderline Stage II tumor to a Stage III tumor, justifying more aggressive therapy. Conversely, the presence of a polynucleotide signifying a lower metastatic potential allows more conservative staging of a tumor.

Grading of cancers. Grade is a term used to describe how closely a tumor resembles normal tissue of its same type. Based on the microscopic appearance of a tumor, pathologists will identify the grade of a tumor based on parameters such as cell morphology,

WO 99/33982

PCT/US98/27610

cellular organization, and other markers of differentiation. As a general rule, the grade of a tumor corresponds to its rate of growth or aggressiveness. That is, undifferentiated or high-grade tumors grow more quickly than well differentiated or low-grade tumors. Information about tumor grade is useful in planning treatment and predicting prognosis.

5 The American Joint Commission on Cancer has recommended the following guidelines for grading tumors: 1) GX Grade cannot be assessed; 2) G1 Well differentiated; G2 Moderately well differentiated; 3) G3 Poorly differentiated; 4) G4 Undifferentiated. Although grading is used by pathologists to describe most cancers, it plays a more important role in treatment planning for certain types than for others. An example is the Gleason

10 system that is specific for prostate cancer, which uses grade numbers to describe the degree of differentiation. Lower Gleason scores indicate well-differentiated cells. Intermediate scores denote tumors with moderately differentiated cells. Higher scores describe poorly differentiated cells. Grade is also important in some types of brain tumors and soft tissue sarcomas.

15 The polynucleotides of the invention can be especially valuable in determining the grade of the tumor, as they not only can aid in determining the differentiation status of the cells of a tumor, they can also identify factors other than differentiation that are valuable in determining the aggressivity of a tumor, such as metastatic potential.

Familial Cancer Genes. A number of cancer syndromes are linked to Mendelian

20 inheritance of a predisposition to develop particular cancers. The following table contains a list of cancer types that can be inherited, and for which the gene or genes responsible have been identified. Most of the cancer types listed can occur as part of several different genetic conditions, each caused by alterations in a different gene.

Cancer Type	Genetic Condition	Gene
Brain	Li-Fraumeni syndrome	TP53
	Neurofibromatosis 1	NF1
	Neurofibromatosis 2	NF2
	von Hippel-Lindau syndrome	VHL
	Tuberous sclerosis 2	TSC2
Breast	Hereditary breast/ovarian cancer 1	BRCA1
	Hereditary breast/ovarian cancer 2	BRCA2
	Li-Fraumeni syndrome	TP53
	Ataxia telangiectasia	ATM
Colon	Familial adenomatous polyposis (FAP)	APC
	Hereditary non-polyposis colon cancer (HNPCC) 1	HMSH2
	Hereditary non-polyposis colon cancer (HNPCC) 2	hMLH1

WO 99/33982

PCT/US98/27610

Cancer Type	Genetic Condition	Gene
	Hereditary non-polyposis colon cancer (HNPCC) 3	hPMS1
Endocrine (parathyroid, pituitary, GI endocrine)	Hereditary non-polyposis colon cancer (HNPCC) 4	hPMS2
	Multiple endocrine neoplasia 1 (MEN1)	MEN1
Endocrine (pheochromocytoma, medullary thyroid)	Multiple endocrine neoplasia 2 (MEN2)	RET
Endometrial	Hereditary non-polyposis colon cancer (HNPCC) 1	hMSH2
	Hereditary non-polyposis colon cancer (HNPCC) 2	hMLH1
	Hereditary non-polyposis colon cancer (HNPCC) 3	hPMS1
	Hereditary non-polyposis colon cancer (HNPCC) 4	hPMS2
Eye	Hereditary retinoblastoma	RB1
Hematologic (lymphomas and leukemia)	Li-Fraumeni syndrome	TP53
	Ataxia telangiectasia	ATM
Kidney	Hereditary Wilms' tumor	WT1
	von Hippel-Lindau syndrome	VHL
	Tuberous sclerosis 2	TSC2
Ovary	Hereditary breast/ovarian cancer 1	BRCA1
	Hereditary breast/ovarian cancer 2	BRCA2
Sarcoma	Hereditary retinoblastoma	RB1
	Li-Fraumeni syndrome	TP53
	Neurofibromatosis 1	NF1
Skin	Hereditary melanoma 1	CDKN2
	Hereditary melanoma 2	CDK4
	Basal cell naevus (Gorlin) syndrome	PTCH
Stomach	Hereditary non-polyposis colon cancer (HNPCC) 1	hMSH2
	Hereditary non-polyposis colon cancer (HNPCC) 2	hMLH1
	Hereditary non-polyposis colon cancer (HNPCC) 3	hPMS1
	Hereditary non-polyposis colon cancer (HNPCC) 4	hPMS2

The polynucleotides of the invention can be especially useful to monitor patients having any of the above syndromes to detect potentially malignant events at a molecular level before they are detectable at a gross morphological level. As can be seen from the table, a number of genes are involved in multiple forms of cancer. Thus, a polynucleotide of the invention identified as important for metastatic colon cancer can also have clinical implications for a patient diagnosed with stomach cancer or endometrial cancer.

Lung Cancer. Lung cancer is one of the most common cancers in the United States, accounting for about 15 percent of all cancer cases, or 170,000 new cases each year. At this time, over half of the lung cancer cases in the United States are in men, but the number found in women is increasing and will soon equal that in men. Today more women die of lung cancer than of breast cancer. Lung cancer is especially difficult to diagnose and treat because of the large size of the lungs, which allows cancer to develop for years undetected.

WO 99/33982

PCT/US98/27610

In fact, lung cancer can spread outside the lungs without causing any symptoms. Adding to the confusion, the most common symptom of lung cancer, a persistent cough, can often be mistaken for a cold or bronchitis.

- Although there are more than a dozen different kinds of lung cancer, the two main types of lung cancer are small cell and nonsmall cell, which encompass about 90% of all lung cancer cases. Small cell carcinoma (also called oat cell carcinoma), which usually starts in one of the larger bronchial tubes, grows fairly rapidly, and is likely to be large by the time of diagnosis. Nonsmall cell lung cancer (NSCLC) is made up of three general subtypes of lung cancer. Epidermoid carcinoma (also called squamous cell carcinoma) usually starts in one of the larger bronchial tubes and grows relatively slowly. The size of these tumors can range from very small to quite large. Adenocarcinoma starts growing near the outside surface of the lung and can vary in both size and growth rate. Some slowly growing adenocarcinomas are described as alveolar cell cancer. Large cell carcinoma starts near the surface of the lung, grows rapidly, and the growth is usually fairly large when diagnosed. Other less common forms of lung cancer are carcinoid, cylindroma, mucoepidermoid, and malignant mesothelioma.

- Currently, CT scans, MRIs, X-rays, sputum cytology, and biopsies are used to diagnose nonsmall cell lung cancer. The form and cellular origin of the lung cancer is diagnosed primarily through biopsy from either a surgical biopsy or a needle aspiration of lung tissue, and usually the biopsy is prompted from an abnormality identified on an X-ray. In some cases, sputum cytology can reveal lung cancers in patients with normal X-rays or can determine the type of lung cancer, but because it cannot pinpoint the tumor's location, a positive sputum cytology test is usually followed by further tests. Since these tests are based in large part on gross morphology of the tissue, the diagnosis of a particular kind of tumor is largely subjective, and the diagnosis can vary significantly between clinicians.

- The polynucleotides of the invention can be used to distinguish types of lung cancer as well as identifying traits specific to a certain patient's cancer. For example, if the patient's biopsy expresses a polynucleotide that is associated with a low metastatic potential, it may justify leaving a larger portion of the patient's lung in surgery to remove the lesion. Alternatively, a smaller lesion with expression of a polynucleotide that is associated with high metastatic potential may justify a more radical removal of lung tissue and/or the

WO 99/33982

PCT/US98/27610

surrounding lymph nodes, even if no metastasis can be identified through pathological examination.

Similarly, the expression of polynucleotides of the invention can be used in the diagnosis, prognosis and management of colorectal cancer. The differential expression of a polynucleotide in hyperplasia can be used as a diagnostic marker for metastatic lung cancer. The polynucleotides of the invention that would be especially useful for this purpose are those that exhibit differential expression between high metastatic versus low metastatic lung cancer, *i.e.* SEQ ID NOS: 9, 34, 42, 62, 74, 106, 119, 135, 154, 160, 260, 308, 323, 349, 361, 369, 371, 381, 395, and 400. Detection of malignant lung cancer with a higher metastatic potential can be determined using expression levels of any of these sequences alone or in combination with the levels of expression of other known genes.

Breast Cancer. The National Cancer Institute (NCI) estimates that about 1 in 8 women in the United States will develop breast cancer during her lifetime. Clinical breast examination and mammography are recommended as combined modalities for breast cancer screening, and the nature of the cancer will often depend upon the location of the tumor and the cell type from which the tumor is derived. The majority of breast cancers are adenocarcinomas subtypes, which can be summarized as follows:

Ductal carcinoma in situ (DCIS): Ductal carcinoma in situ is the most common type of noninvasive breast cancer. In DCIS, the malignant cells have not metastasized through the walls of the ducts into the fatty tissue of the breast. Comedocarcinoma is a type of DCIS that is more likely than other types of DCIS to come back in the same area after lumpectomy. It is more closely linked to eventual development of invasive ductal carcinoma than other forms of DCIS.

Infiltrating (or invasive) ductal carcinoma (IDC): this type of cancer has metastasized through the wall of the duct and invaded the fatty tissue of the breast. At this point, it has the potential to use the lymphatic system and bloodstream for metastasis to more distant parts of the body. Infiltrating ductal carcinoma accounts for about 80% of breast cancers.

Lobular carcinoma in situ (LCIS): While not a true cancer, LCIS (also called lobular neoplasia) is sometimes classified as a type of noninvasive breast cancer. It does not penetrate through the wall of the lobules. Although it does not itself usually become an

WO 99/33982

PCT/US98/27610

invasive cancer, women with this condition have a higher risk of developing an invasive breast cancer in the same breast, or in the opposite breast.

Infiltrating (or invasive) lobular carcinoma (ILC): ILC is similar to IDC, in that it has the potential metastasize elsewhere in the body. About 10% to 15% of invasive breast

5 cancers are invasive lobular carcinomas. ILC can be more difficult to detect by mammogram than IDC.

Inflammatory breast cancer: This rare type of invasive breast cancer accounts for about 1% of all breast cancers and is extremely aggressive. Multiple skin symptoms associated with this cancer are caused by cancer cells blocking lymph vessels or channels in
10 the skin over the breast.

Medullary carcinoma: This special type of infiltrating breast cancer has a relatively well defined, distinct boundary between tumor tissue and normal tissue. It accounts for about 5% of breast cancers. The prognosis for this kind of breast cancer is better than for other types of invasive breast cancer.

15 Mucinous carcinoma: This rare type of invasive breast cancer originates from mucus-producing cells. The prognosis for mucinous carcinoma is better than for the more common types of invasive breast cancer.

Paget's disease of the nipple: This type of breast cancer starts in the ducts and spreads to the skin of the nipple and the areola. It is a rare type of breast cancer, occurring in only
20 1% of all cases. Paget's disease can be associated with in situ carcinoma, or with infiltrating breast carcinoma. If no lump can be felt in the breast tissue, and the biopsy shows DCIS but no invasive cancer, the prognosis is excellent.

Phyllodes tumor: This very rare type of breast tumor forms from the stroma of the breast, in contrast to carcinomas which develop in the ducts or lobules. Phyllodes (also
25 spelled phylloides) tumors are usually benign, but are malignant on rare occasions. Nevertheless, malignant phyllodes tumors are very rare and less than 10 women per year in the US die of this disease. Benign phyllodes tumors are successfully treated by removing the mass and a narrow margin of normal breast tissue.

Tubular carcinoma: Accounting for about 2% of all breast cancers, tubular
30 carcinomas are a special type of infiltrating breast carcinoma. They have a better prognosis than usual infiltrating ductal or lobular carcinomas.

WO 99/33982

PCT/US98/27610

High-quality mammography combined with clinical breast exam remains the only screening method clearly tied to reduction in breast cancer mortality. Lower dose x-rays, digitized computer rather than film images, and the use of computer programs to assist diagnosis, are almost ready for widespread dissemination. Other technologies also are being developed, including magnetic resonance imaging and ultrasound. In addition, a very low radiation exposure technique, positron emission tomography has the potential for detecting early breast cancer.

It is also possible to differentiate between non-cancerous breast tissue and malignant breast tissue by analyzing differential gene expression between tissues. In addition, there may be several possible alterations that lead to the various possible types of breast cancer. The different types of breast tumors (e.g., invasive vs. non-invasive, ductal vs. axillary lymph node) can be differentiable from one another by the identification of the differences in genes expressed by different types of breast tumor tissues (Porter-Jordan *et al.*, *Hematol Oncol Clin North Am* (1994) 8:73). Breast cancer can thus be generally diagnosed by detection of expression of a gene or genes associated with breast tumors. Where enough information is available about the differential gene expression between various types of breast tumor tissues, the specific type of breast tumor can also be diagnosed.

For example, increased estrogen receptor (ER) expression in normal breast epithelium, while not itself indicative of malignant tissue, is a known risk marker for development of breast cancer. Khan SA *et al.*, *Cancer Res* (1994) 54:993. Malignant breast cancer is often divided into two groups, ER-positive and ER-negative, based on the estrogen receptor status of the tissue. The ER status represents different survival length and response to hormone therapy, and is thought to represent either: 1) an indicator of different stages of the disease, or 2) an indicator that allows differentiation between two similar but distinct diseases. K. Zhu *et al.*, *Med. Hypoth.* (1997) 49:69. A number of other genes are known to vary expression between either different stages of cancer or different types of similar breast cancer.

Similarly, the expression of polynucleotides of the invention can be used in the diagnosis and management of breast cancer. The differential expression of a polynucleotide in human breast tumor tissue can be used as a diagnostic marker for human breast cancer. The polynucleotides of the invention that would be especially useful for this purpose are

WO 99/33982

PCT/US98/27610

those that exhibit differential expression between breast cancer tissue with a high metastatic potential and a low metastatic potential, *i.e.* SEQ ID NOS: 9, 42, 52, 62, 65, 66, 68, 114, 123, 144, 172, 178, 214, 219, 223, 258, 317, and 379. Detection of breast cancer can be determined using expression levels of any of these sequences alone or in combination.

- 5 Determination of the aggressive nature and/or the metastatic potential of a breast cancer can also be determined by comparing levels of one or more polynucleotides of the invention and comparing levels of another sequence known to vary in cancerous tissue, *e.g.* ER expression. In addition, development of breast cancer can be detected by examining the ratio of SEQ ID NO: to the levels of steroid hormones (*e.g.*, testosterone or estrogen) or to other hormones
- 10 (*e.g.*, growth hormone, insulin). Thus expression of specific marker polynucleotides can be used to discriminate between normal and cancerous breast tissue, to discriminate between breast cancers with different cells of origin, to discriminate between breast cancers with different potential metastatic rates, etc.

- Diagnosis of breast cancer can also involve comparing the expression of a
- 15 polynucleotide of the invention with the expression of other sequences in non-malignant breast tissue samples in comparison to one or more forms of the diseased tissue. A comparison of expression of one or more polynucleotides of the invention between the samples provides information on relative levels of these polynucleotides as well as the ratio of these polynucleotides to the expression of other sequences in the tissue of interest
- 20 compared to normal.

- This risk of breast cancer is elevated significantly by the presence of an inherited risk for breast cancer, such as a mutation in BRCA-1 or BRCA-2. New diagnostic tools are being developed to address the needs of higher risk patients to complement mammography and physical examinations for early detection of breast cancer, particularly among younger
- 25 women. The presence of antigen or expression markers in nipple aspirate fluid (NAF) samples collected from one or both breasts can be useful for useful for risk assessment or early cancer detection. Breast cytology and biomarkers obtained by random fine needle aspiration have been used to identify hyperplasia with atypia and overexpression of p53 and EGFR. The polynucleotides of the invention can be used in multivariate analysis with
- 30 expression studies with genes such as p53 and EGFR as risk predictors and as surrogate endpoint biomarkers for breast cancer.

WO 99/33982

PCT/US98/27610

As well as being used for diagnosis and risk assessment, the expression of certain genes can also be correlated to prognosis of a disease state. The expression of particular gene have been used as prognostic indicators for breast cancer including increased expression of *c-erbB-2*, pS2, ER, progesterone receptor, epidermal growth factor receptor (EGFR), *neu*,
5 *myc*, *bcl-2*, *int2*, cytosolic tyrosine kinase, cyclin E, *prad-1*, *hst*, uPA, PAI-1, PAI-2, cathepsin D, as well as the presence of a number of cancer-specific antigens, e.g. CEA, CA M26, CA M29 and CA 15.3. Davis, *Br. J. Biomed Sci.* (1996) 53:157. Poor prognosis has also been linked to a decrease in expression of certain genes, such as *p53*, *Rb*, *nm23*. The expression of the polynucleotides of the invention can be of prognostic value for determining
10 the metastatic potential of a malignant breast cancer, as this molecules are differentially expressed between high and low metastatic potential tissues tumors. The levels of these polynucleotides in patients with malignant breast cancer can be compared to normal tissue, malignant tissue with a known high potential metastatic level, and malignant tissue with a known lower level of metastatic potential to provide a prognosis for a particular patient.
15 Such a prognosis is predictive of the extent and nature of the cancer. The determined prognosis is useful in determining the prognosis of a patient with breast cancer, both for initial treatment of the disease and for longer-term monitoring of the same patient. If samples are taken from the same individual over a period of time, differences in polynucleotide expression that are specific to that patient can be identified and closely
20 watched.

Colon Cancer. Colorectal cancer is one of the most common neoplasms in humans and perhaps the most frequent form of hereditary neoplasia. Prevention and early detection are key factors in controlling and curing colorectal cancer. Indeed, colorectal cancer is the second most preventable cancer, after lung cancer. Colorectal cancer begins as polyps,
25 which are small, benign growths of cells that form on the inner lining of the colon. Over a period of several years, some of these polyps accumulate additional mutations and become cancerous. About 20 percent of all cases of colon cancer are thought to be related to heredity. Currently, multiple familial colorectal cancer disorders have been identified, which are summarized as follows:

30 Familial adenomatous polyposis (FAP): This condition results in a person having hundreds or even thousands of polyps in the colon and rectum that usually first appear during

WO 99/33982

PCT/US98/27610

the teenage years. Cancer nearly always develops in one or more of these polyps between the ages of 30 and 50.

Gardner's syndrome: Like FAP, Gardner's syndrome results in polyps and colorectal cancers that develop at a young age. It can also cause benign tumors of the skin, soft

5 connective tissue and bones.

Hereditary nonpolyposis colon cancer (HNPCC): People with this condition tend to develop colorectal cancer at a young age, without first having many polyps. HNPCC has an autosomal dominant pattern of inheritance with variable but high penetrance estimated to be about 90%. HNPCC underlies 0.5%-10% of all cases of colorectal cancer. An understanding
10 of the mechanisms behind the development of HNPCC is emerging, and genetic presymptomatic testing, now being conducted in research settings, soon will be available on a widespread basis for individuals identified at risk for this disease.

Familial colorectal cancer in Ashkenazi Jews: Recent research has found an inherited tendency to developing colorectal cancer among some Jews of Eastern European descent.

15 Like people with FAP, Gardner's syndrome, and HNPCC, their increased risk is due to an inherited mutation present in about 6% of American Jews.

Several tests are currently used to screen for colorectal cancer, including digital rectal examination, fecal occult blood test, sigmoidoscopy, colonoscopy, virtual colonoscopy and MRI. Each of these tests identifies potential colorectal cancer lesions, or a risk of
20 development of these lesions, at a fairly gross morphological level.

The sequential alteration of a number of genes is associated with malignant adenocarcinoma, including the genes DCC, p53, ras, and FAP. For a review, see *e.g.* Fearon ER, *et al.*, *Cell* (1990) 61(5):759; Hamilton SR *et al.*, *Cancer* (1993) 72:957; Bodmer W, *et al.*, *Nat Genet.* (1994) 4(3):217; Fearon ER, *Ann N Y Acad Sci.* (1995) 768:101. Molecular
25 genetic alterations are thus promising as potential diagnostic and prognostic indicators in colorectal carcinoma and molecular genetics of colorectal carcinoma since it is possible to differentiate between different types of colorectal neoplasias using molecular markers. Colorectal cancer can thus be generally diagnosed by detection of expression of a gene or genes associated with colorectal tumors.

30 Similarly, the expression of polynucleotides of the invention can be used in the diagnosis, prognosis and management of colorectal cancer. The differential expression of a

WO 99/33982

PCT/US98/27610

polynucleotide in hyperplasia can be used as a diagnostic marker for colon cancer. The polynucleotides of the invention that would be especially useful for this purpose are those that exhibit differential expression between malignant metastatic colon cancer and normal patient tissue, *i.e.* SEQ ID NOS: 52, 119, 172, 288. Detection of malignant colon cancer can be determined using expression levels of any of these sequences alone or in combination with the levels of expression.

Determination of the aggressive nature and/or the metastatic potential of a colon cancer can also be determined by comparing levels of one or more polynucleotides of the invention and comparing total levels of another sequence known to vary in cancerous tissue, *e.g.* p53 expression. In addition, development of colon cancer can be detected by examining the ratio of any of the polynucleotides of the invention to the levels of oncogenes (*e.g.* ras) or tumor suppressor genes (*e.g.* FAP or p53). Thus expression of specific marker polynucleotides can be used to discriminate between normal and cancerous breast tissue, to discriminate between breast cancers with different cells of origin, to discriminate between breast cancers with different potential metastatic rates, etc.

G. Use of Polynucleotides to Screen for Peptide Analogs and Antagonists

Polypeptides encoded by the instant polynucleotides and corresponding full length genes can be used to screen peptide libraries to identify binding partners, such as receptors, from among the encoded polypeptides.

A library of peptides can be synthesized following the methods disclosed in U.S. Pat. No. 5,010,175 ('175), and in WO 91/17823. As described below in brief, one prepares a mixture of peptides, which is then screened to identify the peptides exhibiting the desired signal transduction and receptor binding activity. In the '175 method, a suitable peptide synthesis support (*e.g.*, a resin) is coupled to a mixture of appropriately protected, activated amino acids. The concentration of each amino acid in the reaction mixture is balanced or adjusted in inverse proportion to its coupling reaction rate so that the product is an equimolar mixture of amino acids coupled to the starting resin. The bound amino acids are then deprotected, and reacted with another balanced amino acid mixture to form an equimolar mixture of all possible dipeptides. This process is repeated until a mixture of peptides of the desired length (*e.g.*, hexamers) is formed. Note that one need not include all amino acids in each step: one can include only one or two amino acids in some steps (*e.g.*, where it is

WO 99/33982

PCT/US98/27610

known that a particular amino acid is essential in a given position), thus reducing the complexity of the mixture. After the synthesis of the peptide library is completed, the mixture of peptides is screened for binding to the selected polypeptide. The peptides are then tested for their ability to inhibit or enhance activity. Peptides exhibiting the desired activity are then isolated and sequenced.

The method described in WO 91/17823 is similar. However, instead of reacting the synthesis resin with a mixture of activated amino acids, the resin is divided into twenty equal portions (or into a number of portions corresponding to the number of different amino acids to be added in that step), and each amino acid is coupled individually to its portion of resin.

The resin portions are then combined, mixed, and again divided into a number of equal portions for reaction with the second amino acid. In this manner, each reaction can be easily driven to completion. Additionally, one can maintain separate "subpools" by treating portions in parallel, rather than combining all resins at each step. This simplifies the process of determining which peptides are responsible for any observed receptor binding or signal transduction activity.

In such cases, the subpools containing, *e.g.*, 1-2,000 candidates each are exposed to one or more polypeptides of the invention. Each subpool that produces a positive result is then resynthesized as a group of smaller subpools (sub-subpools) containing, *e.g.*, 20-100 candidates, and reassayed. Positive sub-subpools can be resynthesized as individual compounds, and assayed finally to determine the peptides that exhibit a high binding constant. These peptides can be tested for their ability to inhibit or enhance the native activity. The methods described in WO 91/7823 and U.S. Patent No. 5,194,392 (herein incorporated by reference) enable the preparation of such pools and subpools by automated techniques in parallel, such that all synthesis and resynthesis can be performed in a matter of days.

Peptide agonists or antagonists are screened using any available method, such as signal transduction, antibody binding, receptor binding, mitogenic assays, chemotaxis assays, etc. The methods described herein are presently preferred. The assay conditions ideally should resemble the conditions under which the native activity is exhibited *in vivo*, that is, under physiologic pH, temperature, and ionic strength. Suitable agonists or antagonists will exhibit strong inhibition or enhancement of the native activity at

WO 99/33982

PCT/US98/27610

concentrations that do not cause toxic side effects in the subject. Agonists or antagonists that compete for binding to the native polypeptide can require concentrations equal to or greater than the native concentration, while inhibitors capable of binding irreversibly to the polypeptide can be added in concentrations on the order of the native concentration.

5 The end results of such screening and experimentation will be at least one novel polypeptide binding partner, such as a receptor, encoded by a gene or a cDNA corresponding to a polynucleotide of the invention, and at least one peptide agonist or antagonist of the novel binding partner. Such agonists and antagonists can be used to modulate, enhance, or inhibit receptor function in cells to which the receptor is native, or in cells that possess the
10 receptor as a result of genetic engineering. Further, if the novel receptor shares biologically important characteristics with a known receptor, information about agonist/antagonist binding can facilitate development of improved agonists/antagonists of the known receptor.

H. Pharmaceutical Compositions and Therapeutic Uses

Pharmaceutical compositions can comprise polypeptides, antibodies, or
15 polynucleotides of the claimed invention. The pharmaceutical compositions will comprise a therapeutically effective amount of either polypeptides, antibodies, or polynucleotides of the claimed invention.

The term "therapeutically effective amount" as used herein refers to an amount of a therapeutic agent to treat, ameliorate, or prevent a desired disease or condition, or to exhibit a
20 detectable therapeutic or preventative effect. The effect can be detected by, for example, chemical markers or antigen levels. Therapeutic effects also include reduction in physical symptoms, such as decreased body temperature. The precise effective amount for a subject will depend upon the subject's size and health, the nature and extent of the condition, and the therapeutics or combination of therapeutics selected for administration. Thus, it is not useful
25 to specify an exact effective amount in advance. However, the effective amount for a given situation is determined by routine experimentation and is within the judgment of the clinician. For purposes of the present invention, an effective dose will generally be from about 0.01 mg/kg to 50 mg/kg or 0.05 mg/kg to about 10 mg/kg of the DNA constructs in the individual to which it is administered.

30 A pharmaceutical composition can also contain a pharmaceutically acceptable carrier. The term "pharmaceutically acceptable carrier" refers to a carrier for administration of a

WO 99/33982

PCT/US98/27610

therapeutic agent, such as antibodies or a polypeptide, genes, and other therapeutic agents.

The term refers to any pharmaceutical carrier that does not itself induce the production of antibodies harmful to the individual receiving the composition, and which can be administered without undue toxicity. Suitable carriers can be large, slowly metabolized macromolecules such as proteins, polysaccharides, polylactic acids, polyglycolic acids, polymeric amino acids, amino acid copolymers, and inactive virus particles. Such carriers are well known to those of ordinary skill in the art.

Pharmaceutically acceptable salts can be used therein, for example, mineral acid salts such as hydrochlorides, hydrobromides, phosphates, sulfates, and the like; and the salts of organic acids such as acetates, propionates, malonates, benzoates, and the like. A thorough discussion of pharmaceutically acceptable excipients is available in *Remington's Pharmaceutical Sciences* (Mack Pub. Co., N.J. 1991).

Pharmaceutically acceptable carriers in therapeutic compositions can include liquids such as water, saline, glycerol and ethanol. Auxiliary substances, such as wetting or emulsifying agents, pH buffering substances, and the like, can also be present in such vehicles. Typically, the therapeutic compositions are prepared as injectables, either as liquid solutions or suspensions; solid forms suitable for solution in, or suspension in, liquid vehicles prior to injection can also be prepared. Liposomes are included within the definition of a pharmaceutically acceptable carrier.

Delivery Methods. Once formulated, the compositions of the invention can be (1) administered directly to the subject (*e.g.*, as polynucleotide or polypeptides); (2) delivered *ex vivo*, to cells derived from the subject (*e.g.*, as in *ex vivo* gene therapy); or (3) delivered *in vitro* for expression of recombinant proteins (*e.g.*, polynucleotides). Direct delivery of the compositions will generally be accomplished by injection, either subcutaneously, intraperitoneally, intravenously or intramuscularly, or delivered to the interstitial space of a tissue. The compositions can also be administered into a tumor or lesion. Other modes of administration include oral and pulmonary administration, suppositories, and transdermal applications, needles, and gene guns or hypodermic sprays. Dosage treatment can be a single dose schedule or a multiple dose schedule.

Methods for the *ex vivo* delivery and reimplantation of transformed cells into a subject are known in the art and described in *e.g.*, International Publication No. WO

WO 99/33982

PCT/US98/27610

93/14778. Examples of cells useful in ex vivo applications include, for example, stem cells, particularly hematopoietic, lymph cells, macrophages, dendritic cells, or tumor cells. Generally, delivery of nucleic acids for both ex vivo and in vitro applications can be accomplished by, for example, dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei, all well known in the art.

Once a gene corresponding to a polynucleotide of the invention has been found to correlate with a proliferative disorder, such as neoplasia, dysplasia, and hyperplasia, the disorder can be amenable to treatment by administration of a therapeutic agent based on the provided polynucleotide or corresponding polypeptide.

Preparation of antisense polynucleotides is discussed above. Neoplasias that are treated with the antisense composition include, but are not limited to, cervical cancers, melanomas, colorectal adenocarcinomas, Wilms' tumor, retinoblastoma, sarcomas, myosarcomas, lung carcinomas, leukemias, such as chronic myelogenous leukemia, promyelocytic leukemia, monocytic leukemia, and myeloid leukemia, and lymphomas, such as histiocytic lymphoma. Proliferative disorders that are treated with the therapeutic composition include disorders such as anhydric hereditary ectodermal dysplasia, congenital alveolar dysplasia, epithelial dysplasia of the cervix, fibrous dysplasia of bone, and mammary dysplasia. Hyperplasias, for example, endometrial, adrenal, breast, prostate, or thyroid hyperplasias or pseudoepitheliomatous hyperplasia of the skin, are treated with antisense therapeutic compositions based upon a polynucleotide of the invention. Even in disorders in which mutations in the corresponding gene are not implicated, downregulation or inhibition of expression of a gene corresponding to a polynucleotide of the invention can have therapeutic application. For example, decreasing gene expression can help to suppress tumors in which enhanced expression of the gene is implicated.

Both the dose of the antisense composition and the means of administration are determined based on the specific qualities of the therapeutic composition, the condition, age, and weight of the patient, the progression of the disease, and other relevant factors.

Administration of the therapeutic antisense agents of the invention includes local or systemic administration, including injection, oral administration, particle gun or catheterized

WO 99/33982

PCT/US98/27610

administration, and topical administration. Preferably, the therapeutic antisense composition contains an expression construct comprising a promoter and a polynucleotide segment of at least 12, 22, 25, 30, or 35 contiguous nucleotides of the antisense strand of a polynucleotide disclosed herein. Within the expression construct, the polynucleotide segment is located downstream from the promoter, and transcription of the polynucleotide segment initiates at the promoter.

Various methods are used to administer the therapeutic composition directly to a specific site in the body. For example, a small metastatic lesion is located and the therapeutic composition injected several times in several different locations within the body of tumor. Alternatively, arteries which serve a tumor are identified, and the therapeutic composition injected into such an artery, in order to deliver the composition directly into the tumor. A tumor that has a necrotic center is aspirated and the composition injected directly into the now empty center of the tumor. The antisense composition is directly administered to the surface of the tumor, for example, by topical application of the composition. X-ray imaging is used to assist in certain of the above delivery methods.

Receptor-mediated targeted delivery of therapeutic compositions containing an antisense polynucleotide, subgenomic polynucleotides, or antibodies to specific tissues is also used. Receptor-mediated DNA delivery techniques are described in, for example, Findeis *et al.*, *Trends Biotechnol.* (1993) 11:202; Chiou *et al.*, *Gene Therapeutics: Methods And Applications Of Direct Gene Transfer* (J.A. Wolff, ed.) (1994); Wu *et al.*, *J. Biol. Chem.* (1988) 263:621; Wu *et al.*, *J. Biol. Chem.* (1994) 269:542; Zenke *et al.*, *Proc. Natl. Acad. Sci. (USA)* (1990) 87:3655; Wu *et al.*, *J. Biol. Chem.* (1991) 266:338. Preferably, receptor-mediated targeted delivery of therapeutic compositions containing antibodies of the invention is used to deliver the antibodies to specific tissue.

Therapeutic compositions containing antisense subgenomic polynucleotides are administered in a range of about 100 ng to about 200 mg of DNA for local administration in a gene therapy protocol. Concentration ranges of about 500 ng to about 50 mg, about 1 μ g to about 2 mg, about 5 μ g to about 500 μ g, and about 20 μ g to about 100 μ g of DNA can also be used during a gene therapy protocol. Factors such as method of action and efficacy of transformation and expression are considerations which will affect the dosage required for ultimate efficacy of the antisense subgenomic polynucleotides. Where greater expression is

WO 99/33982

PCT/US98/27610

desired over a larger area of tissue, larger amounts of antisense subgenomic polynucleotides or the same amounts readministered in a successive protocol of administrations, or several administrations to different adjacent or close tissue portions of, for example, a tumor site, may be required to effect a positive therapeutic outcome. In all cases, routine

- 5 experimentation in clinical trials will determine specific ranges for optimal therapeutic effect. A more complete description of gene therapy vectors, especially retroviral vectors, is contained in U.S. Serial No. 08/869,309, which is expressly incorporated herein, and in section G below.

- For polynucleotide-related genes encoding polypeptides or proteins with anti-inflammatory activity, suitable use, doses, and administration are described in U.S. Patent 10 No. 5,654,173. Therapeutic agents also include antibodies to proteins and polypeptides encoded by the polynucleotides of the invention and related genes, as described in U.S. Patent No. 5,654,173.

I. Gene Therapy

- 15 The therapeutic polynucleotides and polypeptides of the present invention can be utilized in gene delivery vehicles. The gene delivery vehicle can be of viral or non-viral origin (see generally, Jolly, *Cancer Gene Therapy* (1994) 1:51; Kimura, *Human Gene Therapy* (1994) 5:845; Connelly, *Human Gene Therapy* (1995) 1:185; and Kaplitt, *Nature Genetics* (1994) 6:148). Gene therapy vehicles for delivery of constructs including a coding 20 sequence of a therapeutic of the invention can be administered either locally or systemically. These constructs can utilize viral or non-viral vector approaches. Expression of such coding sequences can be induced using endogenous mammalian or heterologous promoters. Expression of the coding sequence can be either constitutive or regulated.

- The present invention can employ recombinant retroviruses which are constructed to 25 carry or express a selected nucleic acid molecule of interest. Retrovirus vectors that can be employed include those described in EP 0 415 731; WO 90/07936; WO 94/03622; WO 93/25698; WO 93/25234; U.S. Patent No. 5, 219,740; WO 93/11230; WO 93/10218; Vile and Hart, *Cancer Res.* (1993) 53:3860; Vile *et al.*, *Cancer Res.* (1993) 53:962; Ram *et al.*, *Cancer Res.* (1993) 53:83; Takamiya *et al.*, *J. Neurosci. Res.* (1992) 33:493; Baba *et al.*, *J. Neurosurg.* (1993) 79:729; U.S. Patent No. 4,777,127; GB Patent No. 2,200,651; and EP 0 345 242. Preferred recombinant retroviruses include those described in WO 91/02805.
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WO 99/33982

PCT/US98/27610

Packaging cell lines suitable for use with the above-described retroviral vector constructs can be readily prepared (see, *e.g.*, WO 95/30763 and WO 92/05266), and used to create producer cell lines (also termed vector cell lines) for the production of recombinant vector particles. Within particularly preferred embodiments of the invention, packaging cell lines are made from human (such as HT1080 cells) or mink parent cell lines, thereby allowing production of recombinant retroviruses that can survive inactivation in human serum.

The present invention also employs alphavirus-based vectors that can function as gene delivery vehicles. Such vectors can be constructed from a wide variety of alphaviruses, including, for example, Sindbis virus vectors, Semliki forest virus (ATCC VR-67; ATCC VR-1247), Ross River virus (ATCC VR-373; ATCC VR-1246) and Venezuelan equine encephalitis virus (ATCC VR-923; ATCC VR-1250; ATCC VR 1249; ATCC VR-532). Representative examples of such vector systems include those described in U.S. Patent Nos. 5,091,309; 5,217,879; and 5,185,440; WO 92/10578; WO 94/21792; WO 95/27069; WO 95/27044; and WO 95/07994. Gene delivery vehicles of the present invention can also employ parvovirus such as adeno-associated virus (AAV) vectors. Representative examples include the AAV vectors disclosed by Srivastava in WO 93/09239, Samulski *et al.*, *J. Virol.* (1989) 63:3822; Mendelson *et al.*, *Virol.* (1988) 166:154; and Flotte *et al.*, *PNAS* (1993) 90:10613.

Representative examples of adenoviral vectors include those described by Berkner, *Biotechniques* (1988) 6:616; Rosenfeld *et al.*, *Science* (1991) 252:431; WO 93/19191; Kolls *et al.*, *PNAS* (1994) 91:215; Kass-Eisler *et al.*, *PNAS* (1993) 90:11498; Guzman *et al.*, *Circulation* (1993) 88:2838; Guzman *et al.*, *Cir. Res.* (1993) 73:1202; Zabner *et al.*, *Cell* (1993) 75:207; Li *et al.*, *Hum. Gene Ther.* (1993) 4:403; Cailaud *et al.*, *Eur. J. Neurosci.* (1993) 5:1287; Vincent *et al.*, *Nat. Genet.* (1993) 5:130; Jaffe *et al.*, *Nat. Genet.* (1992) 1:372; and Levrero *et al.*, *Gene* (1991) 101:195. Exemplary adenoviral gene therapy vectors employable in this invention also include those described in WO 94/12649, WO 93/03769; WO 93/19191; WO 94/28938; WO 95/11984 and WO 95/00655. Administration of DNA linked to killed adenovirus as described in Curiel, *Hum. Gene Ther.* (1992) 3:147 can be employed.

WO 99/33982

PCT/US98/27610

Other gene delivery vehicles and methods can be employed, including polycationic condensed DNA linked or unlinked to killed adenovirus alone, for example Curiel. *Hum Gene Ther.* (1992) 3:147; ligand linked DNA, for example see Wu, *J. Biol. Chem.* (1989) 264:16985; eukaryotic cell delivery vehicles cells, for example see U.S. Pat. No. 5,814,482; 5 WO 95/07994; WO 96/17072; WO 95/30763; and WO 97/42338; deposition of photopolymerized hydrogel materials; hand-held gene transfer particle gun, as described in U.S. Patent No. 5,149,655; ionizing radiation as described in U.S. Patent No. 5,206,152 and in WO92/11033; nucleic charge neutralization or fusion with cell membranes. Additional approaches are described in Philip, *Mol. Cell Biol.* (1994) 14:2411, and in Woffendin, *Proc.* 10 *Natl. Acad. Sci.* (1994) 91:1581.

Naked DNA can also be employed. Exemplary naked DNA introduction methods are described in WO 90/11092 and U.S. Patent No. 5,580,859. Uptake efficiency can be improved using biodegradable latex beads. DNA coated latex beads are efficiently transported into cells after endocytosis initiation by the beads. The method can be improved 15 further by treatment of the beads to increase hydrophobicity and thereby facilitate disruption of the endosome and release of the DNA into the cytoplasm. Liposomes that can act as gene delivery vehicles are described in U.S. Patent No. 5,422,120; WO 95/13796; WO 94/23697; WO 91/14445; and EP 0524968.

Further non-viral delivery suitable for use includes mechanical delivery systems such 20 as the approach described in Woffendin *et al.*, *Proc. Natl. Acad. Sci. USA* (1994) 91(24):11581. Moreover, the coding sequence and the product of expression of such can be delivered through deposition of photopolymerized hydrogel materials. Other conventional methods for gene delivery that can be used for delivery of the coding sequence include, for example, use of hand-held gene transfer particle gun, as described in U.S. Patent No. 25 5,149,655; use of ionizing radiation for activating transferred gene, as described in U.S. Patent No. 5,206,152 and WO 92/11033.

The present invention will now be illustrated by reference to the following examples which set forth particularly advantageous embodiments. However, it should be noted that these embodiments are illustrative and are not to be construed as restricting the invention in 30 any way.

EXAMPLES

The present invention is now illustrated by reference to the following examples which set forth particularly advantageous embodiments. However, these embodiments are illustrative and are not meant to be construed as restricting the invention in any way.

5

Example 1: Source of Biological Materials and Overview of Novel Polynucleotides
Expressed by the Biological Materials

Human colon cancer cell line Km12L4-A (Morika, W. A. K. et al., *Cancer Research* (1988) 48:6863) was used to construct a cDNA library from mRNA isolated from the cells.

- 10 As described in the above overview, a total of 4,693 sequences expressed by the Km12L4-A cell line were isolated and analyzed; most sequences were about 275-300 nucleotides in length. The KM12L4-A cell line is derived from the KM12C cell line. The KM12C cell line, which is poorly metastatic (low metastatic) was established in culture from a Dukes' stage B₂ surgical specimen (Morikawa et al. *Cancer Res.* (1988) 48:6863). The KML4-A is
- 15 a highly metastatic subline derived from KM12C (Yeatman et al. *Nucl. Acids. Res.* (1995) 23:4007; Bao-Ling et al. *Proc. Annu. Meet. Am. Assoc. Cancer. Res.* (1995) 21:3269). The KM12C and KM12C-derived cell lines (e.g., KM12L4, KM12L4-A, etc.) are well-recognized in the art as a model cell line for the study of colon cancer (see, e.g., Moriakawa et al., *supra*; Radinsky et al. *Clin. Cancer Res.* (1995) 1:19; Yeatman et al., (1995) *supra*;
- 20 Yeatman et al. *Clin. Exp. Metastasis* (1996) 14:246).

The sequences were first masked to eliminate low complexity sequences using the XBLAST masking program (Claverie "Effective Large-Scale Sequence Similarity Searches," In: Computer Methods for Macromolecular Sequence Analysis, Doolittle, ed., *Meth. Enzymol.* 266:212-227 Academic Press, NY, NY (1996); see particularly Claverie, in "Automated

- 25 DNA Sequencing and Analysis Techniques" Adams et al., eds., Chap. 36, p. 267 Academic Press, San Diego, 1994 and Claverie et al. *Comput. Chem.* (1993) 17:191). Generally, masking does not influence the final search results, except to eliminate of relative little interest due to their low complexity, and to eliminate multiple "hits" based on similarity to repetitive regions common to multiple sequences, e.g., Alu repeats. Masking resulted in the
- 30 elimination of 43 sequences. The remaining sequences were then used in a BLASTN vs. Genbank search with search parameters of greater than 70% overlap, 99% identity, and a p value of less than 1×10^{-40} , which search resulted in the discarding of 1,432 sequences. Sequences from this search also were discarded if the inclusive parameters were met, but the sequence was ribosomal or vector-derived.

WO 99/33982

PCT/US98/27610

The resulting sequences from the previous search were classified into three groups (1, 2 and 3 below) and searched in a BLASTX vs. NRP (non-redundant proteins) database search: (1) unknown (no hits in the Genbank search), (2) weak similarity (greater than 45% identity and p value of less than 1×10^{-5}), and (3) high similarity (greater than 60% overlap, greater than 80% identity, and p value less than 1×10^{-5}). This search resulted in discard of 98 sequences as having greater than 70% overlap, greater than 99% identity, and p value of less than 1×10^{-40} .

The remaining sequences were classified as unknown (no hits), weak similarity, and high similarity (parameters as above). Two searches were performed on these sequences.

First, a BLAST vs. EST database search resulted in discard of 1771 sequences (sequences with greater than 99% overlap, greater than 99% similarity and a p value of less than 1×10^{-40} ; sequences with a p value of less than 1×10^{-65} when compared to a database sequence of human origin were also excluded). Second, a BLASTN vs. Patent GeneSeq database resulted in discard of 15 sequences (greater than 99% identity; p value less than 1×10^{-40} ; greater than 99% overlap).

The remaining sequences were subjected to screening using other rules and redundancies in the dataset. Sequences with a p value of less than 1×10^{-111} in relation to a database sequence of human origin were specifically excluded. The final result provided the 404 sequences listed in the accompanying Sequence Listing. The Sequence Listing is arranged beginning with sequences with no similarity to any sequence in a database searched, and ending with sequences with the greatest similarity. Each identified polynucleotide represents sequence from at least a partial mRNA transcript. Polynucleotides that were determined to be novel were assigned a sequence identification number.

The novel polynucleotides and were assigned sequence identification numbers SEQ ID NOS: 1-404. The DNA sequences corresponding to the novel polynucleotides are provided in the Sequence Listing. The majority of the sequences are presented in the Sequence Listing in the 5' to 3' direction. A small number, 25, are listed in the Sequence Listing in the 5' to 3' direction but the sequence as written is actually 3' to 5'. These sequences are readily identified with the designation "AR" in the Sequence Name in Table 1 (inserted before the claims). The sequences correctly listed in the 5' to 3' direction in the Sequence Listing are designated "AF." The Sequence Listing filed herewith therefore contains 25 sequences listed in the reverse order, namely SEQ ID NOS:47, 97, 137, 171, 173, 179, 182, 194, 200, 202, 213, 227, 258, 264, 275, 302, 313, 324, 329, 330, 331, 338, 358, 379, and 404.

WO 99/33982

PCT/US98/27610

Because the provided polynucleotides represent partial mRNA transcripts, two or more polynucleotides of the invention may represent different regions of the same mRNA transcript and the same gene. Thus, if two or more SEQ ID NOS: are identified as belonging to the same clone, then either sequence can be used to obtain the full-length mRNA or gene.

5 In order to confirm the sequences of SEQ ID NOS:1-404, inserts of the clones corresponding to these polynucleotides were re-sequenced. These "validation" sequences are provided in SEQ ID NOS:405-800. These validation sequences were often longer than the original polynucleotide sequences. They validate, and thus often provide additional sequence information. Validation sequences can be correlated with the original sequences
10 they validate by identifying those sequences of SEQ ID NOS:1-404 and the validation sequences of SEQ ID NOS:405-800 that share the same clone name in Table 1.

Example 2: Results of Public Database Search to Identify Function of Gene Products

SEQ ID NOS:1-404, as well as the validation sequences SEQ ID NOS:405-800, were
15 translated in all three reading frames to determine the best alignment with the individual sequences. These amino acid sequences and nucleotide sequences are referred, generally, as query sequences, which are aligned with the individual sequences. Query and individual sequences were aligned using the BLAST programs, available over the world wide web at <http://www.ncbi.nlm.nih.gov/BLAST/>. Again the sequences were masked to various extents
20 to prevent searching of repetitive sequences or poly-A sequences, using the XBLAST program for masking low complexity as described above in Example 1.

Table 2 (inserted before the claims) shows the results of the alignments. Table 2 refers to each sequence by its SEQ ID NO., the accession numbers and descriptions of nearest neighbors from the Genbank and Non-Redundant Protein searches, and the p values
25 of the search results. Table 1 identifies each SEQ ID NO: by SEQ name, clone ID, and cluster. As discussed above, a single cluster includes polynucleotides representing the same gene or gene family, and generally represents sequences encoding the same gene product.

For each of SEQ ID NOS:1-800, the best alignment to a protein or DNA sequence is included in Table 2. The activity of the polypeptide encoded by SEQ ID NOS:1-800 is the
30 same or similar to the nearest neighbor reported in Table 2. The accession number of the nearest neighbor is reported, providing a reference to the activities exhibited by the nearest neighbor. The search program and database used for the alignment also are indicated as well as a calculation of the p value.

WO 99/33982

PCT/US98/27610

Full length sequences or fragments of the polynucleotide sequences of the nearest neighbors can be used as probes and primers to identify and isolate the full length sequence of SEQ ID NOS:1-800. The nearest neighbors can indicate a tissue or cell type to be used to construct a library for the full-length sequences of SEQ ID NOS:1-800.

- 5 SEQ ID NOS:1-800 and the translations thereof may be human homologs of known genes of other species or novel allelic variants of known human genes. In such cases, these new human sequences are suitable as diagnostics or therapeutics. As diagnostics, the human sequences SEQ ID NOS:1-800 exhibit greater specificity in detecting and differentiating human cell lines and types than homologs of other species. The human polypeptides
- 10 encoded by SEQ ID NOS:1-800 are likely to be less immunogenic when administered to humans than homologs from other species. Further, on administration to humans, the polypeptides encoded by SEQ ID NOS:1-800 can show greater specificity or can be better regulated by other human proteins than are homologs from other species.

15 Example 3: Members of Protein Families

- After conducting a profile search as described in the specification above, several of the polynucleotides of the invention were found to encode polypeptides having characteristics of a polypeptide belonging to a known protein families (and thus represent new members of these protein families) and/or comprising a known functional domain (Table 3). Thus the
- 20 invention encompasses fragments, fusions, and variants of such polynucleotides that retain biological activity associated with the protein family and/or functional domain identified herein.

Table 3 Polynucleotides encoding gene products of a protein family or having a known functional domain(s).

SEQ ID NO:	Biological Activity (Profile hit)	Start	Stop	Dir
24	4 transmembrane segments integral membrane proteins	1218	578	rev
41	4 transmembrane segments integral membrane proteins	1086	413	rev
101	4 transmembrane segments integral membrane proteins	1206	544	rev
157	4 transmembrane segments integral membrane proteins	721	33	rev
341	4 transmembrane segments integral membrane proteins	1253	613	rev
395	4 transmembrane segments integral membrane proteins	530	10	for
395	4 transmembrane segments integral membrane proteins	696	17	for
395	4 transmembrane segments integral membrane proteins	471	39	rev
24	7 transmembrane receptor (Secretin family)	1301	491	rev
41	7 transmembrane receptor (Secretin family)	1309	10	rev
101	7 transmembrane receptor (Secretin family)	1330	296	rev
157	7 transmembrane receptor (Secretin family)	1173	249	rev
291	7 transmembrane receptor (Secretin family)	1400	269	rev

WO 99/33982

PCT/US98/27610

Table 3 Polynucleotides encoding gene products of a protein family or having a known functional domain(s).

SEQ ID NO:	Biological Activity (Profile hit)	Start	Stop	Dir
291	7 transmembrane receptor (Secretin family)	712	130	for
305	7 transmembrane receptor (Secretin family)	926	4	for
305	7 transmembrane receptor (Secretin family)	753	55	rev
315	7 transmembrane receptor (Secretin family)	1058	270	rev
341	7 transmembrane receptor (Secretin family)	1265	534	rev
116	Ank repeat	141	218	for
251	Ank repeat	290	207	for
251	Ank repeat	467	387	for
63	ATPases Associated with Various Cellular Activities	543	60	for
116	ATPases Associated with Various Cellular Activities	802	313	for
134	ATPases Associated with Various Cellular Activities	525	57	rev
136	ATPases Associated with Various Cellular Activities	712	163	for
151	ATPases Associated with Various Cellular Activities	719	73	for
151	ATPases Associated with Various Cellular Activities	386	13	for
384	ATPases Associated with Various Cellular Activities	664	140	for
404	ATPases Associated with Various Cellular Activities	704	52	for
374	basic region plus leucine zipper transcription factors	298	146	for
97	Bromodomain (conserved sequence found in human, Drosophila and yeast proteins.)	230	63	for
136	EF-hand	121	207	for
242	EF-hand	238	155	for
379	EF-hand	212	126	for
308	Eukaryotic aspartyl proteases	1300	461	rev
213	GATA family of transcription factors	720	377	for
367	G-protein alpha subunit	971	467	rev
188	Phorbol esters/diacylglycerol binding	91	177	for
251	Phorbol esters/diacylglycerol binding	133	219	for
202	protein kinase	482	1	rev
202	protein kinase	970	1	rev
315	protein kinase	739	158	for
315	protein kinase	1023	197	for
367	protein kinase	1046	285	rev
397	protein kinase	511	6	for
256	Protein phosphatase 2C	13	90	for
256	Protein phosphatase 2C	163	86	for
382	Protein Tyrosine Phosphatase	261	2	for
306	SH3 Domain	141	296	for
386	SH3 Domain	359	209	for
169	Trypsin	764	164	rev
188	WD domain, G-beta repeats	480	382	for
188	WD domain, G-beta repeats	206	117	for
335	WD domain, G-beta repeats	3	92	for
23	wnt family of developmental signaling proteins	1151	335	rev
291	wnt family of developmental signaling proteins	779	89	rev
291	wnt family of developmental signaling proteins	1347	382	rev
324	wnt family of developmental signaling proteins	1180	499	rev
330	wnt family of developmental signaling proteins	1180	499	rev
341	wnt family of developmental signaling proteins	1399	560	rev

WO 99/33982

PCT/US98/27610

Table 3 Polynucleotides encoding gene products of a protein family or having a known functional domain(s).

SEQ ID NO:	Biological Activity (Profile hit)	Start	Stop	Dir
353	wnt family of developmental signaling proteins	880	49	rev
188	WW/rsp5/WWP domain containing proteins	431	354	for
379	WW/rsp5/WWP domain containing proteins	12	89	for
395	WW/rsp5/WWP domain containing proteins	153	76	for
395	WW/rsp5/WWP domain containing proteins	156	64	for
61	Zinc finger, C2H2 type	254	192	for
306	Zinc finger, C2H2 type	428	367	for
386	Zinc finger, C2H2 type	191	253	for
322	Zinc finger, CCHC class	553	503	for
306	Zinc-binding metalloprotease domain	101	60	rev
395	Zinc-binding metalloprotease domain	28	69	rev

Start and stop indicate the position within the individual sequences that align with the query sequence having the indicated SEQ ID NO. The direction (Dir) indicates the orientation of the query sequence with respect to the individual sequence, where forward (for) indicates that the alignment is in the same direction (left to right) as the sequence provided in the Sequence Listing and reverse (rev) indicates that the alignment is with a sequence complementary to the sequence provided in the Sequence Listing.

Some polynucleotides exhibited multiple profile hits because, for example, the particular sequence contains overlapping profile regions, and/or the sequence contains two different functional domains. These profile hits are described in more detail below.

a) Four Transmembrane Integral Membrane Proteins. SEQ ID NOS: 24, 41, 101,

157, 341, and 395 correspond to a sequence encoding a polypeptide that is a member of the 4 transmembrane segments integral membrane protein family (transmembrane 4 family). The transmembrane 4 family of proteins includes a number of evolutionarily-related eukaryotic cell surface antigens (Levy *et al.*, *J. Biol. Chem.*, (1991) 266:14597; Tomlinson *et al.*, *Eur. J. Immunol.* (1993) 23:136; Barclay *et al.* The leucocyte antigen factbooks. (1993) Academic Press, London/San Diego). The proteins belonging to this family include: 1) Mammalian antigen CD9 (MIC3), which is involved in platelet activation and aggregation; 2)

Mammalian leukocyte antigen CD37, expressed on B lymphocytes; 3) Mammalian leukocyte antigen CD53 (OX-44), which is implicated in growth regulation in hematopoietic cells; 4) Mammalian lysosomal membrane protein CD63 (melanoma-associated antigen ME491; antigen AD1); 5) Mammalian antigen CD81 (cell surface protein TAPA-1), which is implicated in regulation of lymphoma cell growth; 6) Mammalian antigen CD82 (protein

WO 99/33982

PCT/US98/27610

R2; antigen C33; Kangai 1 (KAI1)), which associates with CD4 or CD8 and delivers costimulatory signals for the TCR/CD3 pathway; 7) Mammalian antigen CD151 (SFA-1; platelet-endothelial tetraspan antigen 3 (PETA-3)); 8) Mammalian cell surface glycoprotein A15 (TALLA-1; MXS1); 9) Mammalian novel antigen 2 (NAG-2); 10) Human tumor-associated antigen CO-029; 11) *Schistosoma mansoni* and *japonicum* 23 Kd surface antigen (SM23 / SJ23).

The members of the 4 transmembrane family share several characteristics. First, they all are apparently type III membrane proteins, which are integral membrane proteins containing an N-terminal membrane-anchoring domain which is not cleaved during biosynthesis and which functions both as a translocation signal and as a membrane anchor. The family members also contain three additional transmembrane regions, at least seven conserved cysteines residues, and are of approximately the same size (218 to 284 residues). These proteins are collectively know as the "transmembrane 4 superfamily" (TM4) because they span plasma membrane four times. A schematic diagram of the domain structure of these proteins is as follows:

```

+-+-----+-----+-----+-----+-----+-----+-----+-----+
| | TMa | Extra | TM2| Cyt | TM3 | Extracellular   | TM4 | Cyt|
+-+-----+-----+-----+-----+-----+-----+-----+-----+
                        C-----C-----CC---C---C---+-----C-----+
                        *****

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where Cyt is the cytoplasmic domain, TMa is the transmembrane anchor; TM2 to TM4 represents transmembrane regions 2 to 4, 'C' are conserved cysteines, and '*' indicates the position of the consensus pattern. The consensus pattern spans a conserved region including two cysteines located in a short cytoplasmic loop between two transmembrane domains:
Consensus pattern: G-x(3)-[LIVMF]-x(2)-[GSA]-[LIVMF](2)-G-C-x-[GA]-[STA]- x(2)-[EG]-x(2)-[CWN]-[LIVM](2).

b) Seven Transmembrane Integral Membrane Proteins. SEQ ID NOS: 24, 41, 101, 157, 291, 305, 315, and 341 correspond to a sequence encoding a polypeptide that is a member of the seven transmembrane receptor family. G-protein coupled receptors (Strosberg, *Eur. J. Biochem.* (1991) 196:1; Kerlavage, *Curr. Opin. Struct. Biol.* (1991) 1:394; and Probst *et al.*, *DNA Cell Biol.* (1992) 11:1; and Savarese *et al.*, *Biochem. J.* (1992) 293:1) (also called R7G) are an extensive group of hormones, neurotransmitters, odorants and light receptors which transduce extracellular signals by interaction with guanine nucleotide-binding (G) proteins. The tertiary structure of these receptors is thought to be highly similar. They have seven hydrophobic regions, each of which most probably spans

WO 99/33982

PCT/US98/27610

the membrane. The N-terminus is located on the extracellular side of the membrane and is often glycosylated, while the C-terminus is cytoplasmic and generally phosphorylated. Three extracellular loops alternate with three intracellular loops to link the seven transmembrane regions. Most, but not all of these receptors, lack a signal peptide. The most conserved parts of these proteins are the transmembrane regions and the first two cytoplasmic loops. A conserved acidic-Arg-aromatic triplet is present in the N-terminal extremity of the second cytoplasmic loop (Attwood *et al.*, *Gene* (1991) 98:153) and could be implicated in the interaction with G proteins.

To detect this widespread family of proteins a pattern is used that contains the conserved triplet and that also spans the major part of the third transmembrane helix. Additional information about the seven transmembrane receptor family, and methods for their identification and use, is found in U.S. Patent No. 5,759,804. Due in part to their expression on the cell surface and other attractive characteristics, seven transmembrane protein family members are of particular interest as drug targets, as surface antigen markers, and as drug delivery targets (*e.g.*, using antibody-drug complexes and/or use of anti-seven transmembrane protein antibodies as therapeutics in their own right).

c) Ank Repeats. SEQ ID NOS: 116 and 251 represent polynucleotides encoding Ank repeat-containing proteins. The ankyrin motif is a 33 amino acid sequence named after the protein ankyrin which has 24 tandem 33-amino-acid motifs. Ank repeats were originally identified in the cell-cycle-control protein cdc10 (Breedon *et al.*, *Nature* (1987) 329:651). Proteins containing ankyrin repeats include ankyrin, myotropin, I-kappaB proteins, cell cycle protein cdc10, the Notch receptor (Matsuno *et al.*, *Development* (1997) 124(21):4265); G9a (or BAT8) of the class III region of the major histocompatibility complex (Biochem J. 290:811-818, 1993), FABP, GABP, 53BP2, Lin12, glp-1, SW14, and SW16. The functions of the ankyrin repeats are compatible with a role in protein-protein interactions (Bork, *Proteins* (1993) 17(4):363; Lambert and Bennet, *Eur. J. Biochem.* (1993) 211:1; Kerr *et al.*, *Current Op. Cell Biol.* (1992) 4:496; Bennet *et al.*, *J. Biol. Chem.* (1980) 255:6424).

The 90 kD N-terminal domain of ankyrin contains a series of 24 33-amino-acid ank repeats. (Lux *et al.*, *Nature* (1990) 344:36-42, Lambert *et al.*, *PNAS USA* (1990) 87:1730.) The 24 ank repeats form four folded subdomains of 6 repeats each. These four repeat subdomains mediate interactions with at least 7 different families of membrane proteins. Ankyrin contains two separate binding sites for anion exchanger dimers. One site utilizes repeat subdomain two (repeats 7-12) and the other requires both repeat subdomains 3 and 4 (repeats 13-24). Since the anion exchangers exist in dimers, ankyrin binds 4 anion

WO 99/33982

PCT/US98/27610

exchangers at the same time. (Michaely and Bennett, *J. Biol. Chem.* (1995) 270(37):22050)
 The repeat motifs are involved in ankyrin interaction with tubulin, spectrin, and other
 membrane proteins. (Lux *et al.*, *Nature* (1990) 344:36.)

The Rel/NF-kappaB/Dorsal family of transcription factors have activity that is
 5 controlled by sequestration in the cytoplasm in association with inhibitory proteins referred
 to as I-kappaB. (Gilmore, *Cell* (1990) 62:841; Nolan and Baltimore, *Curr Opin Genet Dev.*
 (1992) 2:211; Baeuerle, *Biochim Biophys Acta* (1991) 1072:63; Schmitz *et al.*, *Trends Cell*
Biol. (1991) 1:130.) I-kappaB proteins contain 5 to 8 copies of 33 amino acid ankyrin
 10 repeats and certain NF-kappaB/rel proteins are also regulated by cis-acting ankyrin repeat
 containing domains including p105NF-kappaB which contains a series of ankyrin repeats
 (Diehl and Hannink, *J. Virol.* (1993) 67(12):7161). The I-kappaBs and Cactus (also
 containing ankyrin repeats) inhibit activators through differential interactions with the Rel-
 homology domain. The gene family includes proto-oncogenes, thus broadly implicating I-
 kappaB in the control of both normal gene expression and the aberrant gene expression that
 15 makes cells cancerous. (Nolan and Baltimore, *Curr Opin Genet Dev.* (1992) 2(2):211-220).
 In the case of rel/NF-kappaB and pp40/I-kappaB β , both the ankyrin repeats and the carboxy-
 terminal domain are required for inhibiting DNA-binding activity and direct association of
 pp40/I-kappaB β with rel/NF-kappaB protein. The ankyrin repeats and the carboxy-terminal
 of pp40/I-kappaB β form a structure that associates with the rel homology domain to inhibit
 20 DNA binding activity (Inoue *et al.*, *PNAS USA* (1992) 89:4333).

The 4 ankyrin repeats in the amino terminus of the transcription factor subunit
 GABP β are required for its interaction with the GABP α subunit to form a functional high
 affinity DNA-binding protein. These repeats can be crosslinked to DNA when GABP is
 bound to its target sequence. (Thompson *et al.*, *Science* (1991) 253:762; LaMarco *et al.*,
 25 *Science* (1991) 253:789).

Myotrophin, a 12.5 kDa protein having a key role in the initiation of cardiac
 hypertrophy, comprises ankyrin repeats. The ankyrin repeats are characteristic of a hairpin-
 like protruding tip followed by a helix-turn-helix motif. The V-shaped helix-turn-helix of
 the repeats stack sequentially in bundles and are stabilized by compact hydrophobic cores,
 30 whereas the protruding tips are less ordered.

d) ATPases Associated with Various Cellular Activities (AAA). SEQ ID NOS: 63,
 116, 134, 136, 151, 384, and 404 polynucleotides encoding novel members of the "ATPases
 Associated with diverse cellular Activities" (AAA) protein family The AAA protein family

WO 99/33982

PCT/US98/27610

is composed of a large number of ATPases that share a conserved region of about 220 amino acids that contains an ATP-binding site (Froehlich *et al.*, *J. Cell Biol.* (1991) 114:443; Erdmann *et al.* *Cell* (1991) 64:499; Peters *et al.*, *EMBO J.* (1990) 9:1757; Kunau *et al.*, *Biochimie* (1993) 75:209-224; Confalonieri *et al.*, *BioEssays* (1995) 17:639;

- 5 <http://yeamob.pci.chemie.uni-tuebingen.de/AAA/Description.html>). The proteins that belong to this family either contain one or two AAA domains.

Proteins containing two AAA domains include: 1) Mammalian and drosophila NSF (N-ethylmaleimide-sensitive fusion protein) and the fungal homolog, SEC18, which are involved in intracellular transport between the endoplasmic reticulum and Golgi, as well as
10 between different Golgi cisternae; 2) Mammalian transitional endoplasmic reticulum ATPase (previously known as p97 or VCP), which is involved in the transfer of membranes from the endoplasmic reticulum to the golgi apparatus. This ATPase forms a ring-shaped homooligomer composed of six subunits. The yeast homolog, CDC48, plays a role in spindle pole proliferation; 3) Yeast protein PAS1 essential for peroxisome assembly and the
15 related protein PAS1 from *Pichia pastoris*; 4) Yeast protein AFG2; 5) *Sulfolobus acidocaldarius* protein SAV and *Halobacterium salinarium* cdcH, which may be part of a transduction pathway connecting light to cell division.

Proteins containing a single AAA domain include: 1) *Escherichia coli* and other bacteria *ftsH* (or *hflB*) protein. *FtsH* is an ATP-dependent zinc metallopeptidase that
20 degrades the heat-shock sigma-32 factor, and is an integral membrane protein with a large cytoplasmic C-terminal domain that contain both the AAA and the protease domains; 2) Yeast protein YME1, a protein important for maintaining the integrity of the mitochondrial compartment. YME1 is also a zinc-dependent protease; 3) Yeast protein AFG3 (or YTA10). This protein also contains an AAA domain followed by a zinc-dependent protease domain;
25 4) Subunits from regulatory complex of the 26S proteasome (Hilt *et al.*, *Trends Biochem. Sci.* (1996) 21:96), which is involved in the ATP-dependent degradation of ubiquitinated proteins, which subunits include: a) Mammalian 4 and homologs in other higher eukaryotes, in yeast (gene YTA5) and fission yeast (gene *mts2*); b) Mammalian 6 (TBP7) and homologs in other higher eukaryotes and in yeast (gene YTA2); c) Mammalian subunit 7 (MSS1) and
30 homologs in other higher eukaryotes and in yeast (gene CIM5 or YTA3); d) Mammalian subunit 8 (P45) and homologs in other higher eukaryotes and in yeast (SUG1 or CIM3 or TBY1) and fission yeast (gene *let1*); e) Other probable subunits include human TBP1, which influences HIV gene expression by interacting with the virus tat transactivator protein, and yeast YTA1 and YTA6; 5) Yeast protein BCS1, a mitochondrial protein essential for the

WO 99/33982

PCT/US98/27610

expression of the Rieske iron-sulfur protein; 6) Yeast protein MSP1, a protein involved in intramitochondrial sorting of proteins; 7) Yeast protein PAS8, and the corresponding proteins PAS5 from *Pichia pastoris* and PAY4 from *Yarrowia lipolytica*; 8) Mouse protein SKD1 and its fission yeast homolog (SpAC2G11.06); 9) *Caenorhabditis elegans* meiotic spindle formation protein mei-1; 10) Yeast protein SAP1' 11) Yeast protein YTA7; and 12) *Mycobacterium leprae* hypothetical protein A2126A.

In general, the AAA domains in these proteins act as ATP-dependent protein clamps (Confalonieri *et al.* (1995) *BioEssays* 17:639). In addition to the ATP-binding 'A' and 'B' motifs, which are located in the N-terminal half of this domain, there is a highly conserved region located in the central part of the domain which was used in the development of the signature pattern. The consensus pattern is: [LIVMT]-x-[LIVMT]-[LIVMF]-x-[GATMC]-[ST]-[NS]-x(4)-[LIVM]-D-x-A-[LIFA]-x-R.

e) Basic Region Plus Leucine Zipper Transcription Factors. SEQ ID NO:374 correspond to a polynucleotide encoding a novel member of the family of basic region plus leucine zipper transcription factors. The bZIP superfamily (Hurst, *Protein Prof.* (1995) 2:105; and Ellenberger, *Curr. Opin. Struct. Biol.* (1994) 4:12) of eukaryotic DNA-binding transcription factors encompasses proteins that contain a basic region mediating sequence-specific DNA-binding followed by a leucine zipper required for dimerization. Members of the family include transcription factor AP-1, which binds selectively to enhancer elements in the cis control regions of SV40 and metallothionein IIA. AP-1, also known as c-jun, is the cellular homolog of the avian sarcoma virus 17 (ASV17) oncogene v-jun.

Other members of this protein family include jun-B and jun-D, probable transcription factors that are highly similar to jun/AP-1; the fos protein, a proto-oncogene that forms a non-covalent dimer with c-jun; the fos-related proteins fra-1, and fos B; and mammalian cAMP response element (CRE) binding proteins CREB, CREM, ATF-1, ATF-3, ATF-4, ATF-5, ATF-6 and LRF-1. The consensus pattern for this protein family is: [KR]-x(1,3)-[RKSAQ]-N-x(2)-[SAQ](2)-x-[RKTAENQ]-x-R-x-[RK].

f) Bromodomain. SEQ ID NO:97 corresponds to a polynucleotide encoding a polypeptide having a bromodomain region (Haynes *et al.*, 1992, *Nucleic Acids Res.* 20:2693-2603, Tamkun *et al.*, 1992, *Cell* 68:561-572, and Tamkun, 1995, *Curr. Opin. Genet. Dev.* 5:473-477), which is a conserved region of about 70 amino acids found in the following proteins: 1) Higher eukaryotes transcription initiation factor TFIID 250 Kd subunit (TBP-associated factor p250) (gene CCG1); P250 is associated with the TFIID TATA-box binding protein and seems essential for progression of the G1 phase of the cell

WO 99/33982

PCT/US98/27610

cycle. 2) Human RING3, a protein of unknown function encoded in the MHC class II locus;
3) Mammalian CREB-binding protein (CBP), which mediates cAMP-gene regulation by
binding specifically to phosphorylated CREB protein; 4) Mammalian homologs of brahma,
including three brahma-like human: SNF2a(hBRM), SNF2b, and BRG1; 5) Human BS69,
5 a protein that binds to adenovirus E1A and inhibits E1A transactivation; 6) Human peregrin
(or Br140).

The bromodomain is thought to be involved in protein-protein interactions and may
be important for the assembly or activity of multicomponent complexes involved in
transcriptional activation. The consensus pattern, which spans a major part of the
10 bromodomain, is: [STANVF]-x(2)-F-x(4)-[DNS]-x(5,7)-[DENQTF]-Y-[HFY]-x(2)-
[LIVMFY]-x(3)-[LIVM]-x(4)-[LIVM]-x(6,8)-Y-x(12,13)-[LIVM]-x(2)-N-[SACF]-x(2)-
[FY].

g) EF-Hand. SEQ ID NOS:136, 242, and 379 correspond to polynucleotides
encoding a novel protein in the family of EF-hand proteins. Many calcium-binding proteins
15 belong to the same evolutionary family and share a type of calcium-binding domain known
as the EF-hand (Kawasaki *et al.*, *Protein. Prof.* (1995) 2:305-490). This type of domain
consists of a twelve residue loop flanked on both sides by a twelve residue alpha-helical
domain. In an EF-hand loop the calcium ion is coordinated in a pentagonal bipyramidal
configuration. The six residues involved in the binding are in positions 1, 3, 5, 7, 9 and 12;
20 these residues are denoted by X, Y, Z, -Y, -X and -Z. The invariant Glu or Asp at position
12 provides two oxygens for liganding Ca (bidentate ligand).

Proteins known to contain EF-hand regions include: Calmodulin (Ca=4, except in
yeast where Ca=3) ("Ca=" indicates approximate number of EF-hand regions);
diacylglycerol kinase (EC 2.7.1.107) (DGK) (Ca=2); 2) FAD-dependent glycerol-3-
25 phosphate dehydrogenase (EC 1.1.99.5) from mammals (Ca=1); guanylate cyclase activating
protein (GCAP) (Ca=3); MIF related proteins 8 (MRP-8 or CFAG) and 14 (MRP-14)
(Ca=2); myosin regulatory light chains (Ca=1); oncomodulin (Ca=2); osteonectin (basement
membrane protein BM-40) (SPARC); and proteins that contain an "osteonectin" domain
(QR1, matrix glycoprotein SC1).

30 The consensus pattern includes the complete EF-hand loop as well as the first residue
which follows the loop and which seem to always be hydrophobic.

Consensus pattern: D-x-[DNS]-{ILVIFYW}-[DENSTG]-[DNQGHRK]-{GP}-
[LIVMC]-[DENQSTAGC]-x(2)-[DE]-[LIVMFYW]

WO 99/33982

PCT/US98/27610

h) Eukaryotic Aspartyl Proteases. SEQ ID NO:308 corresponds to a gene encoding a novel eukaryotic aspartyl protease. Aspartyl proteases, known as acid proteases, (EC 3.4.23.-) are a widely distributed family of proteolytic enzymes (Foltmann B., *Essays Biochem.* (1981) 17:52; Davies D.R., *Annu. Rev. Biophys. Chem.* (1990) 19:189; Rao J.K.M., *et al.*, *Biochemistry* (1991) 30:4663) known to exist in vertebrates, fungi, plants, retroviruses and some plant viruses. Aspartate proteases of eukaryotes are monomeric enzymes which consist of two domains. Each domain contains an active site centered on a catalytic aspartyl residue. The two domains most probably evolved from the duplication of an ancestral gene encoding a primordial domain. Currently known eukaryotic aspartyl proteases include: 1) Vertebrate gastric pepsins A and C (also known as gastricsin); 2) Vertebrate chymosin (rennin), involved in digestion and used for making cheese; 3) Vertebrate lysosomal cathepsins D (EC 3.4.23.5) and E (EC 3.4.23.34); 4) Mammalian renin (EC 3.4.23.15) whose function is to generate angiotensin I from angiotensinogen in the plasma; 5) Fungal proteases such as aspergillopepsin A (EC 3.4.23.18), candidapepsin (EC 3.4.23.24), mucoropepsin (EC 3.4.23.23) (mucor rennin), endothiapepsin (EC 3.4.23.22), polyporopepsin (EC 3.4.23.29), and rhizopuspepsin (EC 3.4.23.21); and 6) Yeast saccharopepsin (EC 3.4.23.25) (proteinase A) (gene PEP4). PEP4 is implicated in posttranslational regulation of vacuolar hydrolases; 7) Yeast barrierpepsin (EC 3.4.23.35) (gene BAR1); a protease that cleaves alpha-factor and thus acts as an antagonist of the mating pheromone; and 8) Fission yeast *ssa1* which is involved in degrading or processing the mating pheromones.

Most retroviruses and some plant viruses, such as badnaviruses, encode for an aspartyl protease which is an homodimer of a chain of about 95 to 125 amino acids. In most retroviruses, the protease is encoded as a segment of a polyprotein which is cleaved during the maturation process of the virus. It is generally part of the pol polyprotein and, more rarely, of the gag polyprotein. Because the sequence around the two aspartates of eukaryotic aspartyl proteases and around the single active site of the viral proteases is conserved, a single signature pattern can be used to identify members of both groups of proteases. The consensus pattern is: [LIVMFGAC]-[LIVMTADN]-[LIVFSA]-D-[ST]-G-[STAV]-[STAPDENQ]-x-[LIVMFSTNC]-x-[LIVMFGTA], where D is the active site residue.

i) GATA Family of Transcription Factors. SEQ ID NO:213 corresponds to a novel member of the GATA family of transcription factors. The GATA family of transcription factors are proteins that bind to DNA sites with the consensus sequence (A/T)GATA(A/G), found within the regulatory region of a number of genes. Proteins currently known to belong

WO 99/33982

PCT/US98/27610

to this family are: 1) GATA-1 (Trainor, C.D., *et al.*, *Nature* (1990) 343:92) (also known as Eryf1, GF-1 or NF-E1), which binds to the GATA region of globin genes and other genes expressed in erythroid cells. It is a transcriptional activator which probably serves as a general 'switch' factor for erythroid development; 2) GATA-2 (Lee, M.E., *et al.*, *J. Biol. Chem.* (1991) 266:16188), a transcriptional activator which regulates endothelin-1 gene expression in endothelial cells; 3) GATA-3 (Ho, I.-C., *et al.*, *EMBO J.* (1991) 10:1187), a transcriptional activator which binds to the enhancer of the T-cell receptor alpha and delta genes; 4) GATA-4 (Spieth, J., *et al.*, *Mol. Cell. Biol.* (1991) 11:4651), a transcriptional activator expressed in endodermally derived tissues and heart; 5) *Drosophila* protein pannier (or DGATAa) (gene *pnr*) which acts as a repressor of the achaete-scute complex (*as-c*); 6) *Bombyx mori* BCF1 (Drevet, J.R., *et al.*, *J. Biol. Chem.* (1994) 269:10660), which regulates the expression of chorion genes; 7) *Caenorhabditis elegans* elt-1 and elt-2, transcriptional activators of genes containing the GATA region, including vitellogenin genes (Hawkins, M.G., *et al.*, *J. Biol. Chem.* (1995) 270:14666); 8) *Ustilago maydis* urbs1 (Voisard, C.P.O., *et al.*, *Mol. Cell. Biol.* (1993) 13:7091), a protein involved in the repression of the biosynthesis of siderophores; 9) Fission yeast protein GAF2.

All these transcription factors contain a pair of highly similar 'zinc finger' type domains with the consensus sequence C-x2-C-x17-C-x2-C. Some other proteins contain a single zinc finger motif highly related to those of the GATA transcription factors. These proteins are: 1) *Drosophila* box A-binding factor (ABF) (also known as protein serpent (gene *srp*)) which may function as a transcriptional activator protein and may play a key role in the organogenesis of the fat body; 2) *Emericella nidulans* are (Arst, H.N., Jr., *et al.*, *Trends Genet.* (1989) 5:291) a transcriptional activator which mediates nitrogen metabolite repression; 3) *Neurospora crassa* nit-2 (Fu, Y.-H., *et al.*, *Mol. Cell. Biol.* (1990) 10:1056), a transcriptional activator which turns on the expression of genes coding for enzymes required for the use of a variety of secondary nitrogen sources, during conditions of nitrogen limitation; 4) *Neurospora crassa* white collar proteins 1 and 2 (WC-1 and WC-2), which control expression of light-regulated genes; 5) *Saccharomyces cerevisiae* DAL81 (or UGA43), a negative nitrogen regulatory protein; 6) *Saccharomyces cerevisiae* GLN3, a positive nitrogen regulatory protein; 7) *Saccharomyces cerevisiae* GAT1; 8) *Saccharomyces cerevisiae* GZF3.

The consensus pattern for the GATA family is: C-x-[DN]-C-x(4,5)-[ST]-x(2)-W-[HR]-[RK]-x(3)-[GN]-x(3,4)-C-N-[AS]-C, where the four C's are zinc ligands.

WO 99/33982

PCT/US98/27610

j) G-Protein Alpha Subunit. SEQ ID NO:367 corresponds to a gene encoding a novel polypeptide of the G-protein alpha subunit family. Guanine nucleotide binding proteins (G-proteins) are a family of membrane-associated proteins that couple extracellularly-activated integral-membrane receptors to intracellular effectors, such as ion channels and enzymes that vary the concentration of second messenger molecules. G-proteins are composed of 3 subunits (alpha, beta and gamma) which, in the resting state, associate as a trimer at the inner face of the plasma membrane. The alpha subunit has a molecule of guanosine diphosphate (GDP) bound to it. Stimulation of the G-protein by an activated receptor leads to its exchange for GTP (guanosine triphosphate). This results in the separation of the alpha from the beta and gamma subunits, which always remain tightly associated as a dimer. Both the alpha and beta-gamma subunits are then able to interact with effectors, either individually or in a cooperative manner. The intrinsic GTPase activity of the alpha subunit hydrolyses the bound GTP to GDP. This returns the alpha subunit to its inactive conformation and allows it to reassociate with the beta-gamma subunit, thus restoring the system to its resting state.

G-protein alpha subunits are 350-400 amino acids in length and have molecular weights in the range 40-45 kDa. Seventeen distinct types of alpha subunit have been identified in mammals. These fall into 4 main groups on the basis of both sequence similarity and function: alpha-s, alpha-q, alpha-i and alpha-12 (Simon *et al.*, *Science* (1993) 252:802). Many alpha subunits are substrates for ADP-ribosylation by cholera or pertussis toxins. They are often N-terminally acylated, usually with myristate and/or palmitoylate, and these fatty acid modifications are probably important for membrane association and high-affinity interactions with other proteins. The atomic structure of the alpha subunit of the G-protein involved in mammalian vision, transducin, has been elucidated in both GTP- and GDB-bound forms, and shows considerable similarity in both primary and tertiary structure in the nucleotide-binding regions to other guanine nucleotide binding proteins, such as p21-ras and EF-Tu.

k) Phorbol Esters/Diacylglycerol Binding. SEQ ID NO:188 and 251 represent polynucleotides encoding a protein belonging to the family including phorbol esters/diacylglycerol binding proteins. Diacylglycerol (DAG) is an important second messenger. Phorbol esters (PE) are analogues of DAG and potent tumor promoters that cause a variety of physiological changes when administered to both cells and tissues. DAG activates a family of serine/threonine protein kinases, collectively known as protein kinase C (PKC) (Azzi *et al.*, *Eur. J. Biochem.* (1992) 208:547). Phorbol esters can directly stimulate PKC. The N-terminal region of PKC, known as C1, has been shown (Ono *et al.*, *Proc. Natl.*

WO 99/33982

PCT/US98/27610

Acad. Sci. USA (1989) 86:4868) to bind PE and DAG in a phospholipid and zinc-dependent fashion. The C1 region contains one or two copies (depending on the isozyme of PKC) of a cysteine-rich domain about 50 amino-acid residues long and essential for DAG/PE-binding. Such a domain has also been found in, for example, the following proteins.

5 (1) Diacylglycerol kinase (EC 2.7.1.107) (DGK) (Sakane *et al.*, *Nature* (1990) 344:345), the enzyme that converts DAG into phosphatidate. It contains two copies of the DAG/PE-binding domain in its N-terminal section. At least five different forms of DGK are known in mammals; and

(2) N-chimaerin, a brain specific protein which shows sequence similarities with the
10 BCR protein at its C-terminal part and contains a single copy of the DAG/PE-binding domain at its N-terminal part. It has been shown (Ahmed *et al.*, *Biochem. J.* (1990) 272:767, and Ahmed *et al.*, *Biochem. J.* (1991) 280:233) to be able to bind phorbol esters.

The DAG/PE-binding domain binds two zinc ions; the ligands of these metal ions are probably the six cysteines and two histidines that are conserved in this domain. The
15 signature pattern completely spans the DAG/PE domain. The consensus pattern is: H-x-[LIVMFYW]-x(8,11)-C-x(2)-C-x(3)-[LIVMFC]-x(5,10)-C-x(2)-C-x(4)-[HD]-x(2)-C-x(5,9)-C. All the C and H are probably involved in binding zinc.

1) Protein Kinase. SEQ ID NOS:202, 315, 367, and 397 represent polynucleotides encoding protein kinases. Protein kinases catalyze phosphorylation of proteins in a variety of
20 pathways, and are implicated in cancer. Eukaryotic protein kinases (Hanks S.K., *et al.*, *FASEB J.* (1995) 9:576; Hunter T., *Meth. Enzymol.* (1991) 200:3; Hanks S.K., *et al.*, *Meth. Enzymol.* (1991) 200:38; Hanks S.K., *Curr. Opin. Struct. Biol.* (1991) 1:369; Hanks S.K., *et al.*, *Science* (1988) 241:42) are enzymes that belong to a very extensive family of proteins which share a conserved catalytic core common to both serine/threonine and tyrosine protein
25 kinases. There are a number of conserved regions in the catalytic domain of protein kinases. Two of the conserved regions are the basis for the signature pattern in the protein kinase profile. The first region, which is located in the N-terminal extremity of the catalytic domain, is a glycine-rich stretch of residues in the vicinity of a lysine residue, which has been shown to be involved in ATP binding. The second region, which is located in the
30 central part of the catalytic domain, contains a conserved aspartic acid residue which is important for the catalytic activity of the enzyme (Knighton D.R., *et al.*, *Science* (1991) 253:407). The protein kinase profile includes two signature patterns for this second region: one specific for serine/threonine kinases and the other for tyrosine kinases. A third profile is

based on the alignment in (Hanks S.K., *et al.*, *FASEB J.* (1995) 9:576) and covers the entire catalytic domain. The consensus patterns are as follows:

- 1) Consensus pattern: [LIV]-G-{P}-G-{P}-[FYWMGSTNH]-[SGA]-[PW]-[LIVCAT]-[PD]-x-[GSTACLIVMFY]-x(5,18)-[LIVMFYWCSTAR]-[AIVP]-
 5 [LIVMFAGCKR]-K, where K binds ATP. The majority of known protein kinases are detected by this pattern. Proteins kinases that are not detected by this consensus include viral kinases, which are quite divergent in this region and are completely missed by this pattern.
- 2) Consensus pattern: [LIVMFYC]-x-[HY]-x-D-[LIVMFY]-K-x(2)-N-[LIVMFYCT](3), where D is an active site residue. This consensus sequence identifies most
 10 serine/threonine-specific protein kinases with only 10 exceptions. Half of the exceptions are viral kinases, while the other exceptions include Epstein-Barr virus BGLF4 and Drosophila ninaC, which have Ser and Arg, respectively, instead of the conserved Lys. These latter two protein kinases are detected by the tyrosine kinase specific pattern described below.
- 3) Consensus pattern: [LIVMFYC]-x-[HY]-x-D-[LIVMFY]-[RSTAC]-x(2)-N-[LIVMFYC], where D is an active site residue. All tyrosine-specific protein kinases are
 15 detected by this consensus pattern, with the exception of human ERBB3 and mouse blk. This pattern also detects most bacterial aminoglycoside phosphotransferases (Benner S., *Nature* (1987) 329:21; Kirby R., *J. Mol. Evol.* (1992) 30:489) and herpesviruses ganciclovir
 20 kinases (Littler E., *et al.*, *Nature* (1992) 358:160), which are structurally and evolutionary related to protein kinases.

The protein kinase profile also detects receptor guanylate cyclases and 2-5A-dependent ribonucleases. Sequence similarities between these two families and the eukaryotic protein kinase family have been noticed previously. The profile also detects
 25 *Arabidopsis thaliana* kinase-like protein TMKL1 which seems to have lost its catalytic activity.

If a protein analyzed includes the two of the above protein kinase signatures, the probability of it being a protein kinase is close to 100%. Eukaryotic-type protein kinases have also been found in prokaryotes such as *Myxococcus xanthus* (Munoz-Dorado J., *et al.*,
 30 *Cell* (1991) 67:995) and *Yersinia pseudotuberculosis*. The patterns shown above has been updated since their publication in (Bairoch A., *et al.*, *Nature* (1988) 331:22).

m) Protein Phosphatase 2C. SEQ ID NO:256 corresponds to a polynucleotide encoding a novel protein phosphatase 2C (PP2C), which is one of the four major classes of mammalian serine/threonine specific protein phosphatases. PP2C (Wenk *et al.*, *FEBS Lett.*

WO 99/33982

PCT/US98/27610

(1992) 297:135) is a monomeric enzyme of about 42 Kd which shows broad substrate specificity and is dependent on divalent cations (mainly manganese and magnesium) for its activity. Three isozymes are currently known in mammals: PP2C- α , - β and - γ .

- n) Protein Tyrosine Phosphatase. SEQ ID NO:382 represents a polynucleotide
5 encoding a protein tyrosine kinase. Tyrosine specific protein phosphatases (EC 3.1.3.48) (PTPase) (Fischer *et al.*, *Science* (1991) 253:401; Charbonneau *et al.*, *Annu. Rev. Cell Biol.* (1992) 8:463; Trowbridge, *J. Biol. Chem.* (1991) 266:23517; Tonks *et al.*, *Trends Biochem. Sci.* (1989) 14:497; and Hunter, *Cell* (1989) 58:1013) catalyze the removal of a phosphate group attached to a tyrosine residue. These enzymes are very important in the control of cell
10 growth, proliferation, differentiation and transformation. Multiple forms of PTPase have been characterized and can be classified into two categories: soluble PTPases and transmembrane receptor proteins that contain PTPase domain(s).

- Soluble PTPases include PTPN3 (H1) and PTPN4 (MEG), enzymes that contain an N-terminal band 4.1-like domain and could act at junctions between the membrane and
15 cytoskeleton; PTPN6 (PTP-1C; HCP; SHP) and PTPN11 (PTP-2C; SH-PTP3; Syp), enzymes that contain two copies of the SH2 domain at its N-terminal extremity.

- Dual specificity PTPases include DUSP1 (PTPN10; MAP kinase phosphatase-1; MKP-1) which dephosphorylates MAP kinase on both Thr-183 and Tyr-185; and DUSP2 (PAC-1), a nuclear enzyme that dephosphorylates MAP kinases ERK1 and ERK2 on both
20 Thr and Tyr residues.

- Structurally, all known receptor PTPases are made up of a variable length extracellular domain, followed by a transmembrane region and a C-terminal catalytic cytoplasmic domain. Some of the receptor PTPases contain fibronectin type III (FN-III) repeats, immunoglobulin-like domains, MAM domains or carbonic anhydrase-like domains
25 in their extracellular region. The cytoplasmic region generally contains two copies of the PTPase domain. The first seems to have enzymatic activity, while the second is inactive but seems to affect substrate specificity of the first. In these domains, the catalytic cysteine is generally conserved but some other, presumably important, residues are not.

- PTPase domains consist of about 300 amino acids. There are two conserved
30 cysteines and the second one has been shown to be absolutely required for activity. Furthermore, a number of conserved residues in its immediate vicinity have also been shown to be important. The consensus pattern for PTPases is: [LIVMF]-H-C-x(2)-G-x(3)-[STC]-[STAGP]-x-[LIVMFY]; C is the active site residue.

PCT/US98/27610

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WO 99/33982

PCT/US98/27610

factors B, D and I; 6) Complement-activating component of RA-reactive factor; 7) Cytotoxic cell proteases (granzymes A to H); 8) Duodenase I; 9) Elastases 1, 2, 3A, 3B (protease E), leukocyte (medullasin); 10) Enterokinase (EC 3.4.21.9) (enteropeptidase); 11) Hepatocyte growth factor activator; 12) Hepsin; 13) Glandular (tissue) kallikreins (including EGF-binding protein types A, B, and C, NGF-gamma chain, gamma-renin, prostate specific antigen (PSA) and tonin); 14) Plasma kallikrein; 15) Mast cell proteases (MCP) 1 (chymase) to 8; 16) Myeloblastin (proteinase 3) (Wegener's autoantigen); 17) Plasminogen activators (urokinase-type, and tissue-type); 18) Trypsins I, II, III, and IV; 19) Tryptases; 20) Snake venom proteases such as ancrod, batroxobin, cerastobin, flavoxobin, and protein C activator; 21) Collagenase from common cattle grub and collagenolytic protease from Atlantic sand fiddler crab; 22) Apolipoprotein(a); 23) Blood fluke cercarial protease; 24) Drosophila trypsin like proteases: alpha, easter, snake-locus; 25) Drosophila protease stubble (gene sb); and 26) Major mite fecal allergen Der p III. All the above proteins belong to family S1 in the classification of peptidases (Rawlings N.D., *et al.*, *Meth. Enzymol.* (1994) 244:19; <http://www.expasy.ch/cgi-bin/lists?peptidas.txt>) and originate from eukaryotic species. It should be noted that bacterial proteases that belong to family S2A are similar enough in the regions of the active site residues that they can be picked up by the same patterns.

The consensus patterns for this trypsin protein family are: 1) [LIVM]-[ST]-A-[STAG]-H-C, where H is the active site residue. All sequences known to belong to this class detected by the pattern, except for complement components C1r and C1s, pig plasminogen, bovine protein C, rodent urokinase, ancrod, gyroxin and two insect trypsins; 2) [DNSTAGC]-[GSTAPIMVQH]-x(2)-G-[DE]-S-G-[GS]-[SAPHV]-[LIVMFYWH]-[LIVMFYSTANQH], where S is the active site residue. All sequences known to belong to this family are detected by the above consensus sequences, except for 18 different proteases which have lost the first conserved glycine. If a protein includes both the serine and the histidine active site signatures, the probability of it being a trypsin family serine protease is 100%.

q) WD Domain, G-Beta Repeats. SEQ ID NOS:188 and 335 represent novel members of the WD domain/G-beta repeat family. Beta-transducin (G-beta) is one of the three subunits (alpha, beta, and gamma) of the guanine nucleotide-binding proteins (G proteins) which act as intermediaries in the transduction of signals generated by transmembrane receptors (Gilman, *Annu. Rev. Biochem.* (1987) 56:615). The alpha subunit binds to and hydrolyzes GTP; the functions of the beta and gamma subunits are less clear but

WO 99/33982

PCT/US98/27610

they seem to be required for the replacement of GDP by GTP as well as for membrane anchoring and receptor recognition.

In higher eukaryotes, G-beta exists as a small multigene family of highly conserved proteins of about 340 amino acid residues. Structurally, G-beta consists of eight tandem repeats of about 40 residues, each containing a central Trp-Asp motif (this type of repeat is sometimes called a WD-40 repeat). Such a repetitive segment has been shown to exist in a number of other proteins including: human LIS1, a neuronal protein involved in type-1 lissencephaly; and mammalian coatmer beta' subunit (beta'-COP), a component of a cytosolic protein complex that reversibly associates with Golgi membranes to form vesicles that mediate biosynthetic protein transport.

The consensus pattern for the WD domain/G-Beta repeat family is: [LIVMSTAC]-[LIVMFYWSTAGC]-[LIMSTAG]-[LIVMSTAGC]-x(2)-[DN]-x(2)-[LIVMWSTAC]-x-[LIVMFSTAG]-W-[DEN]-[LIVMFSTAGCN].

r) wnt Family of Developmental Signaling Proteins. SEQ ID NO: 23, 291, 324, 330, 341, and 353 correspond to novel members of the wnt family of developmental signaling proteins. Wnt-1 (previously known as int-1), the seminal member of this family, (Nusse R., *Trends Genet.* (1988) 4:291) is a proto-oncogene induced by the integration of the mouse mammary tumor virus. It is thought to play a role in intercellular communication and seems to be a signalling molecule important in the development of the central nervous system (CNS). The sequence of wnt-1 is highly conserved in mammals, fish, and amphibians. Wnt-1 was found to be a member of a large family of related proteins (Nusse R., *et al.*, *Cell* (1992) 69:1073; McMahon A.P., *Trends Genet.* (1992) 8:1; Moon R.T., *BioEssays* (1993) 15:91) that are all thought to be developmental regulators. These proteins are known as wnt-2 (also known as irp), wnt-3, -3A, -4, -5A, -5B, -6, -7A, -7B, -8, -8B, -9 and -10. At least four members of this family are present in *Drosophila*; one of them, wingless (wg), is implicated in segmentation polarity. All these proteins share the following features characteristics of secretory proteins: a signal peptide, several potential N-glycosylation sites and 22 conserved cysteines that are probably involved in disulfide bonds. The Wnt proteins seem to adhere to the plasma membrane of the secreting cells and are therefore likely to signal over only few cell diameters. The consensus pattern, which is based upon a highly conserved region including three cysteines, is as follows: C-K-C-H-G-[LIVMT]-S-G-x-C. All sequences known to belong to this family are detected by the provided consensus pattern.

s) Ww/rsp5/WWP Domain-Containing Proteins. SEQ ID NOS:188, 379, and 395 represent polynucleotides encoding a polypeptide in the family of WW/rsp5/WWP domain-

WO 99/33982

PCT/US98/27610

containing proteins. The WW domain (Bork *et al.*, *Trends Biochem. Sci.* (1994) 19:531; Andre *et al.*, *Biochem. Biophys. Res. Commun.* (1994) 205:1201; Hofmann *et al.*, *FEBS Lett.* (1995) 358:153; and Sudol *et al.*, *FEBS Lett.* (1995) 369:67), also known as rsp5 or WWP), was originally discovered as a short conserved region in a number of unrelated proteins, among them dystrophin, the gene responsible for Duchenne muscular dystrophy. The domain, which spans about 35 residues, is repeated up to 4 times in some proteins. It has been shown (Chen *et al.*, *Proc. Natl. Acad. Sci. USA* (1995) 92:7819) to bind proteins with particular proline-motifs, [AP]-P-P-[AP]-Y, and thus resembles somewhat SH3 domains. It appears to contain beta-strands grouped around four conserved aromatic positions, generally Trp. The name WW or WWP derives from the presence of these Trp as well as that of a conserved Pro. It is frequently associated with other domains typical for proteins in signal transduction processes.

Proteins containing the WW domain include:

1. Dystrophin, a multidomain cytoskeletal protein. Its longest alternatively spliced form consists of an N-terminal actin-binding domain, followed by 24 spectrin-like repeats, a cysteine-rich calcium-binding domain and a C-terminal globular domain. Dystrophins form tetramers and is thought to have multiple functions including involvement in membrane stability, transduction of contractile forces to the extracellular environment and organization of membrane specialization. Mutations in the dystrophin gene lead to muscular dystrophy of Duchenne or Becker type. Dystrophin contains one WW domain C-terminal of the spectrin-repeats.
2. Vertebrate YAP protein, which is a substrate of an unknown serine kinase. It binds to the SH3 domain of the Yes oncoprotein via a proline-rich region. This protein appears in alternatively spliced isoforms, containing either one or two WW domains.
3. IQGAP, which is a human GTPase activating protein acting on ras. It contains an N-terminal domain similar to fly muscle mp20 protein and a C-terminal ras GTPase activator domain.

For the sensitive detection of WW domains, the profile spans the whole homology region as well as a pattern. The consensus for this family is: W-x(9,11)-[VFY]-[FYW]-x(6,7)-[GSTNE]-[GSTQCR]-[FYW]-x(2)-P.

i) Zinc Finger, C2H2 Type. SEQ ID NO:61, 306, and 386 correspond to

polynucleotides encoding novel members of the of the C2H2 type zinc finger protein family. Zinc finger domains (Klug *et al.*, *Trends Biochem. Sci.* (1987) 12:464; Evans *et al.*, *Cell* (1988) 52:1; Payre *et al.*, *FEBS Lett.* (1988) 234:245; Miller *et al.*, *EMBO J.* (1985) 4:1609;

WO 99/33982

PCT/US98/27610

and Berg, *Proc. Natl. Acad. Sci. USA* (1988) 85:99) are nucleic acid-binding protein structures first identified in the *Xenopus* transcription factor TFIIIA. These domains have since been found in numerous nucleic acid-binding proteins. A zinc finger domain is composed of 25 to 30 amino acid residues. Two cysteine or histidine residues are positioned at both extremities of the domain, which are involved in the tetrahedral coordination of a zinc atom. It has been proposed that such a domain interacts with about five nucleotides.

Many classes of zinc fingers are characterized according to the number and positions of the histidine and cysteine residues involved in the zinc atom coordination. In the first class to be characterized, called C2H2, the first pair of zinc coordinating residues are cysteines, while the second pair are histidines. A number of experimental reports have demonstrated the zinc-dependent DNA or RNA binding property of some members of this class.

Mammalian proteins having a C2H2 zipper include (number in parenthesis indicates number of zinc finger regions in the protein): basonuclin (6), BCL-6/LAZ-3 (6), erythroid krueppel-like transcription factor (3), transcription factors Sp1 (3), Sp2 (3), Sp3 (3) and Sp4 (3), transcriptional repressor YY1 (4), Wilms' tumor protein (4), EGR1/Krox24 (3), EGR2/Krox20 (3), EGR3/Pilot (3), EGR4/AT133 (4), Evi-1 (10), GLI1 (5), GLI2 (4+), GLI3 (3+), HIV-EP1/ZNF40 (4), HIV-EP2 (2), KR1 (9+), KR2 (9), KR3 (15+), KR4 (14+), KR5 (11+), HF.12 (6+), REX-1 (4), Zfx (13), Zfy (13), Zfp-35 (18), ZNF7 (15), ZNF8 (7), ZNF35 (10), ZNF42/MZF-1 (13), ZNF43 (22), ZNF46/Kup (2), ZNF76 (7), ZNF91 (36), ZNF133 (3).

In addition to the conserved zinc ligand residues, it has been shown that a number of other positions are also important for the structural integrity of the C2H2 zinc fingers. (Rosenfeld *et al.*, *J. Biomol. Struct. Dyn.* (1993) 11:557) The best conserved position is found four residues after the second cysteine; it is generally an aromatic or aliphatic residue.

The consensus pattern for C2H2 zinc fingers is: C-x(2,4)-C-x(3)-[LIVMFYWC]-x(8)-H-x(3,5)-H. The two C's and two H's are zinc ligands.

u) Zinc Finger, CCHC Class. SEQ ID NO:322 corresponds to a polynucleotide encoding a novel member of the zinc finger CCHC family. The CCHC zinc finger protein family to date has been mostly composed of retroviral gag proteins (nucleocapsid). The prototype structure of this family is from HIV. The family also contains members involved in eukaryotic gene regulation, such as *C. elegans* GLH-1. The consensus sequence of this family is based upon the common structure of an 18-residue zinc finger.

PCT/US98/27610

polynucleotides encoding novel members of the zinc-binding metalloprotease domain protein family. The majority of zinc-dependent metalloproteases (with the notable exception of the carboxypeptidases) share a common pattern of primary structure (Jongeneel *et al.*, *FEBS Lett.* (1989) 242:211; Murphy *et al.*, *FEBS Lett.* (1991) 289:4; and Bodé *et al.*, *Zoology* (1996) 99:237) in the part of their sequence involved in the binding of zinc, and can be grouped together as a superfamily, known as the metzincins, on the basis of this sequence similarity. Examples of these proteins include: 1) Angiotensin-converting enzyme (EC 3.4.15.1) (dipeptidyl carboxypeptidase I) (ACE), the enzyme responsible for hydrolyzing angiotensin I to angiotensin II. 2) Mammalian extracellular matrix metalloproteinases (known as matrixins) (Woessner, *FASEB J.* (1991) 5:2145): MMP-1 (EC 3.4.24.7) (interstitial collagenase), MMP-2 (EC 3.4.24.24) (72 Kd gelatinase), MMP-9 (EC 3.4.24.35) (92 Kd gelatinase), MMP-7 (EC 3.4.24.23) (matrylisin), MMP-8 (EC 3.4.24.34) (neutrophil collagenase), MMP-3 (EC 3.4.24.17) (stromelysin-1), MMP-10 (EC 3.4.24.22) (stromelysin-2), and MMP-11 (stromelysin-3), MMP-12 (EC 3.4.24.65) (macrophage metalloelastase). 3) Endothelin-converting enzyme 1 (EC 3.4.24.71) (ECE-1), which processes the precursor of endothelin to release the active peptide.

A signature pattern which includes the two histidine and the glutamic acid residues is sufficient to detect this superfamily of proteins, having the consensus pattern: [GSTALIVN]-x(2)-H-E-[LIVMFYW]-{DEHRKP}-H-x-[LIVMFYWGSPQ]. The two H's are zinc ligands, and E is the active site residue.

Example 4: Differential Expression of Polynucleotides of the Invention : Description of Libraries and Detection of Differential Expression

The relative expression levels of the polynucleotides of the invention was assessed in several libraries prepared from various sources, including cell lines and patient tissue samples. Table 4 provides a summary of these libraries, including the shortened library name (used hereafter), the mRNA source used to prepared the cDNA library, the "nickname" of the library that is used in the tables below (in quotes), and the approximate number of clones in the library.

Table 4 Description of cDNA Libraries

Library (lib #)	Description	Number of Clones in this Clustering
1	Km12 L4 Human Colon Cell Line, High Metastatic Potential (derived from Km12C) "High Colon"	307133
2	Km12C Human Colon Cell Line, Low Metastatic Potential "Low Colon"	284755
3	MDA-MB-231 Human Breast Cancer Cell Line, High Metastatic Potential; micro-metastases in lung "High Breast"	326937
4	MCF7 Human Breast Cancer Cell, Non Metastatic "Low Breast"	318979
8	MV-522 Human Lung Cancer Cell Line, High Metastatic Potential "High Lung"	223620
9	UCP-3 Human Lung Cancer Cell Line, Low Metastatic Potential "Low Lung"	312503
12	Human microvascular endothelial cells (HMEC) – Untreated PCR (OligodT) cDNA library	41938
13	Human microvascular endothelial cells (HMEC) – bFGF treated PCR (OligodT) cDNA library	42100
14	Human microvascular endothelial cells (HMEC) – VEGF treated PCR (OligodT) cDNA library	42825
15	Normal Colon – UC#2 Patient PCR (OligodT) cDNA library "Normal Colon Tumor Tissue"	34285
16	Colon Tumor – UC#2 Patient PCR (OligodT) cDNA library "Normal Colon Tumor Tissue"	35625
17	Liver Metastasis from Colon Tumor of UC#2 Patient PCR (OligodT) cDNA library "High Colon Metastasis Tissue"	36984
18	Normal Colon – UC#3 Patient PCR (OligodT) cDNA library "Normal Colon Tumor Tissue"	36216
19	Colon Tumor – UC#3 Patient PCR (OligodT) cDNA library "High Colon Tumor Tissue"	41388
20	Liver Metastasis from Colon Tumor of UC#3 Patient PCR (OligodT) cDNA library "High Colon Metastasis Tissue"	30956

WO 99/33982

PCT/US98/27610

The KM12L4 and KM12C cell lines are described in Example 1 above. The MDA-MB-231 cell line was originally isolated from pleural effusions (Cailleau, *J. Natl. Cancer Inst.* (1974) 53:661), is of high metastatic potential, and forms poorly differentiated adenocarcinoma grade II in nude mice consistent with breast carcinoma. The MCF7 cell line was derived from a pleural effusion of a breast adenocarcinoma and is non-metastatic. The MV-522 cell line is derived from a human lung carcinoma and is of high metastatic potential. The UCP-3 cell line is a low metastatic human lung carcinoma cell line; the MV-522 is a high metastatic variant of UCP-3. These cell lines are well-recognized in the art as models for the study of human breast and lung cancer (see, e.g., Chandrasekaran *et al.*, *Cancer Res.* (1979) 39:870 (MDA-MB-231 and MCF-7); Gastpar *et al.*, *J Med Chem* (1998) 41:4965 (MDA-MB-231 and MCF-7); Ranson *et al.*, *Br J Cancer* (1998) 77:1586 (MDA-MB-231 and MCF-7); Kuang *et al.*, *Nucleic Acids Res* (1998) 26:1116 (MDA-MB-231 and MCF-7); Varki *et al.*, *Int J Cancer* (1987) 40:46 (UCP-3); Varki *et al.*, *Tumour Biol.* (1990) 11:327; (MV-522 and UCP-3); Varki *et al.*, *Anticancer Res.* (1990) 10:637; (MV-522); Kelner *et al.*, *Anticancer Res* (1995) 15:867 (MV-522); and Zhang *et al.*, *Anticancer Drugs* (1997) 8:696 (MV522)). The samples of libraries 15-20 are derived from two different patients (UC#2, and UC#3).

Each of the libraries is composed of a collection of cDNA clones that in turn are representative of the mRNAs expressed in the indicated mRNA source. In order to facilitate the analysis of the millions of sequences in each library, the sequences were assigned to clusters. The concept of "cluster of clones" is derived from a sorting/grouping of cDNA clones based on their hybridization pattern to a panel of roughly 300 7bp oligonucleotide probes (see Drmanac *et al.*, *Genomics* (1996) 37(1):29). Random cDNA clones from a tissue library are hybridized at moderate stringency to 300 7bp oligonucleotides. Each oligonucleotide has some measure of specific hybridization to that specific clone. The combination of 300 of these measures of hybridization for 300 probes equals the "hybridization signature" for a specific clone. Clones with similar sequence will have similar hybridization signatures. By developing a sorting/grouping algorithm to analyze these signatures, groups of clones in a library can be identified and brought together computationally. These groups of clones are termed "clusters". Depending on the stringency of the selection in the algorithm (similar to the stringency of hybridization in a classic library cDNA screening protocol), the "purity" of each cluster can be controlled. For example, artifacts of clustering may occur in computational clustering just as artifacts can occur in "wet-lab" screening of a cDNA library with 400 bp cDNA fragments, at even the

WO 99/33982 PCT/US98/27610
highest stringency. The stringency used in the implementation of cluster herein provides groups of clones that are in general from the same cDNA or closely related cDNAs. Closely related clones can be a result of different length clones of the same cDNA, closely related clones from highly related gene families, or splice variants of the same cDNA.

5 Differential expression for a selected cluster was assessed by first determining the number of cDNA clones corresponding to the selected cluster in the first library (Clones in 1st), and the determining the number of cDNA clones corresponding to the selected cluster in the second library (Clones in 2nd). Differential expression of the selected cluster in the first library relative to the second library is expressed as a "ratio" of percent expression between
10 the two libraries. In general, the "ratio" is calculated by: 1) calculating the percent expression of the selected cluster in the first library by dividing the number of clones corresponding to a selected cluster in the first library by the total number of clones analyzed from the first library; 2) calculating the percent expression of the selected cluster in the second library by dividing the number of clones corresponding to a selected cluster in a
15 second library by the total number of clones analyzed from the second library; 3) dividing the calculated percent expression from the first library by the calculated percent expression from the second library. If the "number of clones" corresponding to a selected cluster in a library is zero, the value is set at 1 to aid in calculation. The formula used in calculating the ratio takes into account the "depth" of each of the libraries being compared, i.e., the total
20 number of clones analyzed in each library.

In general, a polynucleotide is said to be significantly differentially expressed between two samples when the ratio value is greater than at least about 2, preferably greater than at least about 3, more preferably greater than at least about 5, where the ratio value is calculated using the method described above. The significance of differential expression is
25 determined using a z score test (Zar, Biostatistical Analysis, Prentice Hall, Inc., USA, "Differences between Proportions," pp 296-298 (1974).

Tables 5 to 7 (inserted before the claims) show the number of clones in each of the above libraries that were analyzed for differential expression. Examples of differentially expressed polynucleotides of particular interest are described in more detail below.

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Example 5: Polynucleotides Differentially Expressed in High Metastatic Potential Breast Cancer Cells Versus Low Metastatic Breast Cancer Cells

A number of polynucleotide sequences have been identified that are differentially expressed between cells derived from high metastatic potential breast cancer tissue and low

WO 99/33982

PCT/US98/27610

metastatic breast cancer cells. Expression of these sequences in breast cancer can be valuable in determining diagnostic, prognostic and/or treatment information. For example, sequences that are highly expressed in the high metastatic potential cells can be indicative of increased expression of genes or regulatory sequences involved in the metastatic process. A patient sample displaying an increased level of one or more of these polynucleotides may thus warrant more aggressive treatment. In another example, sequences that display higher expression in the low metastatic potential cells can be associated with genes or regulatory sequences that inhibit metastasis, and thus the expression of these polynucleotides in a sample may warrant a more positive prognosis than the gross pathology would suggest.

The differential expression of these polynucleotides can be used as a diagnostic marker, a prognostic marker, for risk assessment, patient treatment and the like. These polynucleotide sequences can also be used in combination with other known molecular and/or biochemical markers.

The following table summarizes identified polynucleotides with differential expression between high metastatic potential breast cancer cells and low metastatic potential breast cancer cells.

WO 99/33982

PCT/US98/27610

Table 8. Differentially expressed polynucleotides: High metastatic potential breast cancer vs. low metastatic breast cancer cells

SEQ ID NO.	Differential Expression	Cluster ID	Clones in 1 st Library	Clones in 2 nd Library	Ratio
			Library	Library	
9	High Breast > Low Breast (Lib3 > Lib4)	2623	31	4	7.561356
42	High Breast > Low Breast (Lib3 > Lib4)	307	196	75	2.549721
52	High Breast > Low Breast (Lib3 > Lib4)	19	1364	525	2.534854
62	High Breast > Low Breast (Lib3 > Lib4)	2623	31	4	7.561356
65	High Breast > Low Breast (Lib3 > Lib4)	5749	9	0	8.780930
66	High Breast > Low Breast (Lib3 > Lib4)	6455	6	0	5.853953
68	High Breast > Low Breast (Lib3 > Lib4)	6455	6	0	5.853953
114	High Breast > Low Breast (Lib3 > Lib4)	2030	32	4	7.805271
123	High Breast > Low Breast (Lib3 > Lib4)	3389	13	2	6.341782
144	High Breast > Low Breast (Lib3 > Lib4)	4623	12	2	5.853953
172	High Breast > Low Breast (Lib3 > Lib4)	102	278	116	2.338217
178	High Breast > Low Breast (Lib3 > Lib4)	3681	10	1	9.756589
214	High Breast > Low Breast (Lib3 > Lib4)	3900	8	1	7.805271
219	High Breast > Low Breast (Lib3 > Lib4)	3389	13	2	6.341782
223	High Breast > Low Breast (Lib3 > Lib4)	1399	19	7	2.648217
258	High Breast > Low Breast (Lib3 > Lib4)	4837	10	0	9.756589
317	High Breast > Low Breast (Lib3 > Lib4)	1577	25	3	8.130490
379	High Breast > Low Breast (Lib3 > Lib4)	260	27	2	13.17139
4	Low Breast > High Breast (Lib4 > Lib3)	3706	22	4	5.637215
39	Low Breast > High Breast (Lib4 > Lib3)	4016	6	0	6.149690
74	Low Breast > High Breast (Lib4 > Lib3)	6268	18	3	6.149690
81	Low Breast > High Breast (Lib4 > Lib3)	40392	8	1	8.199586
130	Low Breast > High Breast (Lib4 > Lib3)	13183	7	0	7.174638
157	Low Breast > High Breast (Lib4 > Lib3)	5417	9	0	9.224535
162	Low Breast > High Breast (Lib4 > Lib3)	9685	7	0	7.174638
183	Low Breast > High Breast (Lib4 > Lib3)	7337	16	3	5.466391
202	Low Breast > High Breast (Lib4 > Lib3)	6124	9	1	9.224535
298	Low Breast > High Breast (Lib4 > Lib3)	1037	22	4	5.637215
338	Low Breast > High Breast (Lib4 > Lib3)	689	36	17	2.170478
384	Low Breast > High Breast (Lib4 > Lib3)	697	72	30	2.459876
386	Low Breast > High Breast (Lib4 > Lib3)	4568	9	0	9.224535
388	Low Breast > High Breast (Lib4 > Lib3)	5622	13	2	6.662164

5 Example 6: Polynucleotides Differentially Expressed in High Metastatic Potential Lung Cancer Cells Versus Low Metastatic Lung Cancer Cells

A number of polynucleotide sequences have been identified that are differentially expressed between cells derived from high metastatic potential lung cancer tissue and low metastatic lung cancer cells. Expression of these sequences in lung cancer tissue can be valuable in determining diagnostic, prognostic and/or treatment information. For example, sequences that are highly expressed in the high metastatic potential cells are associated can be indicative of increased expression of genes or regulatory sequences involved in the metastatic process. A patient sample displaying an increased level of one or more of these

WO 99/33982

PCT/US98/27610

polynucleotides may thus warrant more aggressive treatment. In another example, sequences that display higher expression in the low metastatic potential cells can be associated with genes or regulatory sequences that inhibit metastasis, and thus the expression of these polynucleotides in a sample may warrant a more positive prognosis than the gross pathology would suggest.

The differential expression of these polynucleotides can be used as a diagnostic marker, a prognostic marker, for risk assessment, patient treatment and the like. These polynucleotide sequences can also be used in combination with other known molecular and/or biochemical markers.

The following table summarizes identified polynucleotides with differential expression between high metastatic potential lung cancer cells and low metastatic potential lung cancer cells:

Table 9 Differentially expressed polynucleotides: High metastatic potential lung cancer vs. low metastatic lung cancer cells

SEQ ID NO.	Differential Expression	Cluster ID	Clones in 1 st Library	Clones in 2 nd Library	Ratio
400	High Lung > Low Lung (Lib8 > Lib9)	14929	23	16	2.008868
9	High Lung > Low Lung (Lib8 > Lib9)	2623	6	1	8.384840
34	High Lung > Low Lung (Lib8 > Lib9)	5832	5	0	6.987366
42	High Lung > Low Lung (Lib8 > Lib9)	307	79	27	4.088903
62	High Lung > Low Lung (Lib8 > Lib9)	2623	6	1	8.384840
74	High Lung > Low Lung (Lib8 > Lib9)	6268	5	0	6.987366
106	High Lung > Low Lung (Lib8 > Lib9)	10717	8	0	11.17978
119	High Lung > Low Lung (Lib8 > Lib9)	8	1355	122	15.52111
361	High Lung > Low Lung (Lib8 > Lib9)	1120	5	0	6.987366
369	High Lung > Low Lung (Lib8 > Lib9)	2790	6	0	8.384840
371	High Lung > Low Lung (Lib8 > Lib9)	8847	6	1	8.384840
379	High Lung > Low Lung (Lib8 > Lib9)	260	15	0	20.96210
395	High Lung > Low Lung (Lib8 > Lib9)	13538	9	1	12.57726
135	Low Lung > High Lung (Lib9 > Lib8)	36313	30	1	21.46731
154	Low Lung > High Lung (Lib9 > Lib8)	5345	27	6	3.220097
160	Low Lung > High Lung (Lib9 > Lib8)	4386	21	3	5.009039
260	Low Lung > High Lung (Lib9 > Lib8)	4141	27	4	4.830145
308	Low Lung > High Lung (Lib9 > Lib8)	15855	213	12	12.70149
323	Low Lung > High Lung (Lib9 > Lib8)	5257	25	5	3.577885
349	Low Lung > High Lung (Lib9 > Lib8)	2797	14	1	10.01807
381	Low Lung > High Lung (Lib9 > Lib8)	2428	19	2	6.797982

Example 7: Polynucleotides Differentially Expressed in High Metastatic Potential Colon Cancer Cells Versus Low Metastatic Colon Cancer Cells

A number of polynucleotide sequences have been identified that are differentially expressed between cells derived from high metastatic potential colon cancer tissue and low

WO 99/33982

PCT/US98/27610

metastatic colon cancer cells. Expression of these sequences in colon cancer tissue can be valuable in determining diagnostic, prognostic and/or treatment information. For example, sequences that are highly expressed in the high metastatic potential cells can be indicative of increased expression of genes or regulatory sequences involved in the metastatic process. A patient sample displaying an increased level of one or more of these polynucleotides may thus warrant more aggressive treatment. In another example, sequences that display higher expression in the low metastatic potential cells can be associated with genes or regulatory sequences that inhibit metastasis, and thus the expression of these polynucleotides in a sample may warrant a more positive prognosis than the gross pathology would suggest.

The differential expression of these polynucleotides can be used as a diagnostic marker, a prognostic marker, for risk assessment, patient treatment and the like. These polynucleotide sequences can also be used in combination with other known molecular and/or biochemical markers.

The following table summarizes identified polynucleotides with differential expression between high metastatic potential colon cancer cells and low metastatic potential colon cancer cells:

Table 11: Differentially expressed polynucleotides: High metastatic potential colon cancer vs. low metastatic colon cancer cells

SEQ ID NO.	Differential Expression	Cluster ID	Clones in 1 st Library	Clones in 2 nd Library	Ratio
1	High Colon > Low Colon (Lib1 > Lib2)	6660	7	0	6.489973
176	High Colon > Low Colon (Lib1 > Lib2)	3765	19	6	2.935940
241	High Colon > Low Colon (Lib1 > Lib2)	4275	11	2	5.099264
362	High Colon > Low Colon (Lib1 > Lib2)	6420	8	0	7.417112
374	High Colon > Low Colon (Lib1 > Lib2)	6420	8	0	7.417112
39	Low Colon > High Colon (Lib2 > Lib1)	4016	14	5	3.020043
97	Low Colon > High Colon (Lib2 > Lib1)	945	21	9	2.516702
134	Low Colon > High Colon (Lib2 > Lib1)	2464	19	5	4.098630
317	Low Colon > High Colon (Lib2 > Lib1)	1577	40	12	3.595289
357	Low Colon > High Colon (Lib2 > Lib1)	4309	13	4	3.505407

Example 8: Polynucleotides Differentially Expressed at Higher Levels in High Metastatic Potential Colon Cancer Patient Tissue Versus Normal Patient Tissue

A number of polynucleotide sequences have been identified that are differentially expressed between cells derived from high metastatic potential colon cancer tissue and normal tissue. Expression of these sequences in colon cancer tissue can be valuable in determining diagnostic, prognostic and/or treatment information. For example, sequences that are highly expressed in the high metastatic potential cells are associated can be

WO 99/33982

PCT/US98/27610

indicative of increased expression of genes or regulatory sequences involved in the advanced disease state which involves processes such as angiogenesis, dedifferentiation, cell replication, and metastasis. A patient sample displaying an increased level of one or more of these polynucleotides may thus warrant more aggressive treatment.

5 The differential expression of these polynucleotides can be used as a diagnostic marker, a prognostic marker, for risk assessment, patient treatment and the like. These polynucleotide sequences can also be used in combination with other known molecular and/or biochemical markers.

10 The following table summarizes identified polynucleotides with differential expression between high metastatic potential colon cancer cells and normal colon cells:

Table 11: Differentially expressed polynucleotides: High metastatic potential colon tissue vs. normal colon tissue

SEQ ID NO.	Differential Expression	Cluster ID	Clones in 1 st Library	Clones in 2 nd Library	Ratio
52	High Colon Metastasis Tissue > Normal Colon Tissue of UC#3 (Lib20 > Lib18)	19	10	0	11.69918
52	High Colon Metastasis Tissue > Normal Tissue in UC#2 (Lib17 > Lib15)	19	13	2	6.025646
172	High Colon Metastasis Tissue > Normal Tissue in UC#2 (Lib17 > Lib15)	102	65	22	2.738930

15 Example 9: Polynucleotides Differentially Expressed at Higher Levels in High Colon Tumor Potential Patient Tissue Versus Metastasized Colon Cancer Patient Tissue

A number of polynucleotide sequences have been identified that are differentially expressed between cells derived from high tumor potential colon cancer tissue and cells
20 derived from high metastatic potential colon cancer cells. Expression of these sequences in colon cancer tissue can be valuable in determining diagnostic, prognostic and/or treatment information associated with the transformation of precancerous tissue to malignant tissue. This information can be useful in the prevention of achieving the advanced malignant state in these tissues, and can be important in risk assessment for a patient.

25 The following table summarizes identified polynucleotides with differential expression between high tumor potential colon cancer tissue and cells derived from high metastatic potential colon cancer cells:

WO 99/33982

PCT/US98/27610

Table 12: Differentially expressed polynucleotides: High tumor potential colon tissue vs. metastatic colon tissue

SEQ ID NO.	Differential Expression	Cluster ID	Clones in 1 st Library	Clones in 2 nd Library	Ratio
52	High Colon Tumor Tissue > Metastasis Tissue of UC#3 (Lib19 > Lib20)	19	69	10	5.160829
119	High Colon Tumor Tissue > Metastasis Tissue of UC#3 (Lib19 > Lib20)	8	14	1	10.47124
172	High Colon Tumor Tissue > Metastasis Tissue of UC#3 (Lib19 > Lib20)	102	43	10	3.216168

5 Example 10: Polynucleotides Differentially Expressed at Higher Levels in High Tumor Potential Colon Cancer Patient Tissue Versus Normal Patient Tissue

A number of polynucleotide sequences have been identified that are differentially expressed between cells derived from high tumor potential colon cancer tissue and normal tissue. Expression of these sequences in colon cancer tissue can be valuable in determining diagnostic, prognostic and/or treatment information associated with the prevention of achieving the malignant state in these tissues, and can be important in risk assessment for a patient. For example, sequences that are highly expressed in the potential colon cancer cells are associated with or can be indicative of increased expression of genes or regulatory sequences involved in early tumor progression. A patient sample displaying an increased level of one or more of these polynucleotides may thus warrant closer attention or more frequent screening procedures to catch the malignant state as early as possible.

The following table summarizes identified polynucleotides with differential expression between high metastatic potential colon cancer cells and normal colon cells:

20 **Table 13:** Differentially expressed polynucleotides: High tumor potential colon tissue vs. normal colon tissue

SEQ ID NO.	Differential Expression	Cluster ID	Clones in 1 st Library	Clones in 2 nd Library	Ratio
52	High Colon Tumor Tissue > Normal Tissue of UC#2 (Lib16 > Lib15)	19	13	2	6.255508
288	High Colon Tumor Tissue > Normal Tissue of UC#2 (Lib16 > Lib15)	1267	7	0	6.125253
52	High Colon Tumor Tissue > Normal Tissue of UC#3 (Lib19 > Lib18)	19	69	0	60.37750
119	High Colon Tumor Tissue > Normal Tissue of UC#3 (Lib19 > Lib18)	8	14	1	12.25050
172	High Colon Tumor Tissue > Normal Tissue of UC#3 (Lib19 > Lib18)	102	43	7	5.375222

Example 11: Polynucleotides Differentially Expressed Across Multiple Libraries

A number of polynucleotide sequences have been identified that are differentially expressed between cancerous cells and normal cells across all three tissue types tested (*i.e.*, breast, colon, and lung). Expression of these sequences in a tissue or any origin can be valuable in determining diagnostic, prognostic and/or treatment information associated with the prevention of achieving the malignant state in these tissues, and can be important in risk assessment for a patient. These polynucleotides can also serve as non-tissue specific markers of, for example, risk of metastasis of a tumor. The following table summarizes identified polynucleotides that were differentially expressed but without tissue type-specificity in the breast, colon, and lung libraries tested.

Table 14: Polynucleotides Differentially Expressed Across Multiple Library Comparisons

SEQ ID NO.	Differential Expression	Cluster ID	Clones in 1 st Library	Clones in 2 nd Library	Ratio
9	High Breast > Low Breast (Lib3 > Lib4)	2623	31	4	7.561356
	High Lung > Low Lung (Lib8 > Lib9)	2623	6	1	8.384840
39	Low Breast > High Breast (Lib4 > Lib3)	4016	6	0	6.149690
	Low Colon > High Colon (Lib2 > Lib1)	4016	14	5	3.020043
42	High Breast > Low Breast (Lib3 > Lib4)	307	196	75	2.549721
	High Lung > Low Lung (Lib8 > Lib9)	307	79	27	4.088903
52	High Breast > Low Breast (Lib3 > Lib4)	19	1364	525	2.534854
	High Colon Metastasis Tissue > Normal Colon Tissue of UC#3 (Lib20 > Lib18)	19	10	0	11.69918
	High Colon Metastasis Tissue > Normal Tissue in UC#2 (Lib17 > Lib15)	19	13	2	6.025646
	High Colon Tumor Tissue > Metastasis Tissue of UC#3 (Lib19 > Lib20)	19	69	10	5.160829
	High Colon Tumor Tissue > Normal Tissue of UC#2 (Lib16 > Lib15)	19	13	2	6.255508
	High Colon Tumor Tissue > Normal Tissue of UC#3 (Lib19 > Lib18)	19	69	0	60.37750
62	High Breast > Low Breast (Lib3 > Lib4)	2623	31	4	7.561356
	High Lung > Low Lung (Lib8 > Lib9)	2623	6	1	8.384840
74	High Lung > Low Lung (Lib8 > Lib9)	6268	5	0	6.987366
	Low Breast > High Breast (Lib4 > Lib3)	6268	18	3	6.149690
119	High Colon Tumor Tissue > Metastasis Tissue of UC#3 (Lib19 > Lib20)	8	14	1	10.47124
	High Colon Tumor Tissue > Normal Tissue of UC#3 (Lib19 > Lib18)	8	14	1	12.25050
	High Lung > Low Lung (Lib8 > Lib9)	8	1355	122	15.52111
172	High Breast > Low Breast (Lib3 > Lib4)	102	278	116	2.338217
	High Colon Metastasis Tissue > Normal Tissue in UC#2 (Lib17 > Lib15)	102	65	22	2.738930
	High Colon Tumor Tissue > Metastasis	102	43	10	3.216168

WO 99/33982		PCT/US98/27610			
SEQ ID NO.	Differential Expression	Cluster ID	Clones in 1 st Library	Clones in 2 nd Library	Ratio
	Tissue of UC#3 (Lib19 > Lib20)				
	High Colon Tumor Tissue > Normal Tissue of UC#3 (Lib19 > Lib18)	102	43	7	5.375222
317	High Breast > Low Breast (Lib3 > Lib4)	1577	25	3	8.130490
	Low Colon > High Colon (Lib2 > Lib1)	1577	40	12	3.595289
379	High Breast > Low Breast (Lib3 > Lib4)	260	27	2	13.17139
	High Lung > Low Lung (Lib8 > Lib9)	260	15	0	20.96210

Example 12: Polynucleotides Exhibiting Colon-Specific Expression

The cDNA libraries described herein were also analyzed to identify those polynucleotides that were specifically expressed in colon cells or tissue, *i.e.*, the

- 5 polynucleotides were identified in libraries prepared from colon cell lines or tissue, but not in libraries of breast or lung origin. The polynucleotides that were expressed in a colon cell line and/or in colon tissue, but were present in the breast or lung cDNA libraries described herein, are shown in Table 15.

10 **Table 15** Polynucleotides specifically expressed in colon cells.

SEQ ID NO.	Cluster	Clones in 1 st Library	Clones in 2 nd Library	SEQ ID NO.	Cluster	Clones in 1 st Library	Clones in 2 nd Library
5	36535	2	0	229	39648	2	0
13	27250	2	0	231	85064	1	0
19	16283	3	0	234	39391	2	0
24	16918	4	0	236	39498	2	0
26	40108	2	0	242	22113	3	0
32	32663	1	1	247	19255	2	0
43	39833	2	0	252	22814	3	0
47	18957	3	0	253	39563	2	0
48	39508	2	0	254	39420	2	0
56	7005	8	2	257	39412	2	0
58	18957	3	0	261	38085	2	0
59	18957	3	0	265	40054	1	0
60	16283	3	0	266	39423	2	0
64	13238	4	1	267	39453	2	0
70	39442	2	0	270	78091	1	0
71	17036	4	0	276	39168	2	0
73	7005	8	2	277	39458	2	0
83	11476	6	0	278	14391	3	1
86	39425	2	0	279	39195	2	0
94	21847	2	1	282	12977	5	0
100	16731	3	1	284	14391	3	1
101	12439	4	0	290	16347	4	0
113	17055	4	0	293	39478	2	0
120	67907	1	0	294	39392	2	0
121	12081	4	0	297	39180	2	0
124	39174	2	0	299	6867	7	3

WO 99/33982				PCT/US98/27610			
SEQ ID NO.	Cluster	Clones in 1 st Library	Clones in 2 nd Library	SEQ ID NO.	Cluster	Clones in 1 st Library	Clones in 2 nd Library
126	8210	2	6	301	41633	1	1
128	40455	2	0	302	23218	3	0
139	22195	3	0	303	39380	2	0
143	86859	1	0	309	84328	1	0
150	8672	4	4	314	14367	3	0
153	16977	4	0	320	39886	2	0
156	17036	4	0	324	9061	5	2
159	40044	2	0	327	16653	3	1
161	40044	2	0	328	16985	4	0
163	22155	3	0	329	12977	5	0
166	15066	4	0	330	9061	5	2
170	11465	5	0	333	16392	3	0
176	3765	19	6	342	39486	2	0
181	86110	1	0	344	6874	6	3
182	39648	2	0	345	6874	6	3
185	17076	4	0	353	11494	4	0
186	22794	2	0	354	17062	3	0
187	39171	2	0	355	16245	4	0
194	40455	2	0	356	83103	1	0
199	16317	3	0	358	13072	4	1
210	39186	2	0	366	14364	1	0
211	40122	2	0	368	84182	1	0
218	26295	2	0	372	56020	1	0
222	4665	5	9	389	7514	5	3
226	82498	1	0	391	7570	5	3
227	35702	2	0	393	23210	3	0

In addition to the above, SEQ ID NOS:159 and 161 were each present in one clone in each of Lib16 (Normal Colon Tumor Tissue), and SEQ ID NOS:344 and 345 were each present in one clone in Lib17 (High Colon Metastasis Tissue). No clones corresponding to the colon-specific polynucleotides in the table above were present in any of Libraries 3, 4, 8, or 9. The polynucleotide provided above can be used as markers of cells of colon origin, and find particular use in reference arrays, as described above.

Example 13: Identification of Contiguous Sequences Having a Polynucleotide of the Invention

The novel polynucleotides were used to screen publicly available and proprietary databases to determine if any of the polynucleotides of SEQ ID NOS:1-404 would facilitate identification of a contiguous sequence, *e.g.*, the polynucleotides would provide sequence that would result in 5' extension of another DNA sequence, resulting in production of a longer contiguous sequence composed of the provided polynucleotide and the other DNA sequence(s). Contigging was performed using the AssemblyLign program with the following

WO 99/33982

PCT/US98/27610

parameters: 1) Overlap: Minimum Overlap Length: 30; % Stringency: 50; Minimum Repeat Length: 30; Alignment: gap creation penalty: 1.00, gap extension penalty: 1.00; 2) Consensus: % Base designation threshold: 80.

Using these parameters, 44 polynucleotides provided contiged sequences. These
5 contiged sequences are provided as SEQ ID NOS:801-844. The contiged sequences can be correlated with the sequences of SEQ ID NOS:1-404 upon which the contiged sequences are based by identifying those sequences of SEQ ID NOS:1-404 and the contiged sequences of SEQ ID NOS:801-844 that share the same clone name in Table 1. It should be noted that of these 44 sequences that provided a contiged sequence, the following members of that group
10 of 44 did not contig using the overlap settings indicated in parentheses (Stringency/Overlap): SEQ ID NO:804 (30%/10); SEQ ID NO:810 (20%/20); SEQ ID NO:812 (30%/10); SEQ ID NO:814 (40%/20); SEQ ID NO:816 (30%/10); SEQ ID NO:832 (30%/10); SEQ ID NO:840 (20%/20); SEQ ID NO:841 (40%/20). To generalize, the indicated polynucleotides did not contig using a minimum 20% stringency, 10 overlap. There was a corresponding increase in
15 the number of degenerate codons in these sequences.

The contiged sequences (SEQ ID NO:801-844) thus represent longer sequences that encompass a polynucleotide sequence of the invention. The contiged sequences were then translated in all three reading frames to determine the best alignment with individual sequences using the BLAST programs as described above for SEQ ID NOS:1-404 and the
20 validation sequences SEQ ID NOS:405-800. Again the sequences were masked using the XBLAST program for masking low complexity as described above in Example 1 (Table 2). Several of the contiged sequences were found to encode polypeptides having characteristics of a polypeptide belonging to a known protein families (and thus represent new members of these protein families) and/or comprising a known functional domain (Table 16). Thus the
25 invention encompasses fragments, fusions, and variants of such polynucleotides that retain biological activity associated with the protein family and/or functional domain identified herein.

Table 16. Profile hits using contiged sequences

SEQ ID NO.	Sequence Name	Profile	Start (Stop)	Score
809	Contig_RTA00000177AF.n.18.3. Seq_THC123051	ATPases	778 (1612)	6040
824	Contig_RTA00000187AF.g.24.1. Seq_THC168636	homeobox	531 (707)	12080
824	Contig_RTA00000187AF.g.24.1. Seq_THC168636	MAP kinase kinase	769 (1494)	5784
833	Contig_RTA00000190AF.j.4.1. Seq_THC228776	protein kinase	170 (1010)	5027
833	Contig_RTA00000190AF.j.4.1. Seq_THC228776	protein kinase	170 (1010)	5027

All stop/start sequences are provided in the forward direction.

5 The profiles for the ATPases (AAA) and protein kinase families are described above in Example 2. The homeobox and MAP kinase kinase protein families are described further below.

Homeobox domain. The 'homeobox' is a protein domain of 60 amino acids (Gehring In: Guidebook to the Homeobox Genes, Duboule D., Ed., pp1-10, Oxford University Press, Oxford, (1994); Buerklin In: Guidebook to the Homeobox Genes, pp25-72, Oxford University Press, Oxford, (1994); Gehring *Trends Biochem. Sci.* (1992) 17:277-280; Gehring *et al Annu. Rev. Genet.* (1986) 20:147-173; Schofield *Trends Neurosci.* (1987) 10:3-6; <http://copan.bioz.unibas.ch/homeo.html>) first identified in number of *Drosophila* homeotic and segmentation proteins. It is extremely well conserved in many other animals, including vertebrates. This domain binds DNA through a helix-turn-helix type of structure. Several proteins that contain a homeobox domain play an important role in development. Most of these proteins are sequence-specific DNA-binding transcription factors. The homeobox domain is also very similar to a region of the yeast mating type proteins. These are sequence-specific DNA-binding proteins that act as master switches in yeast differentiation by controlling gene expression in a cell type-specific fashion.

A schematic representation of the homeobox domain is shown below. The helix-turn-helix region is shown by the symbols 'H' (for helix), and 't' (for turn).

XXXXXXXXXXXXXXXXXXXXXXXXXXXXHHHHHHHttHHHHHHHHHXXXXXXXXXX
25 1 60

WO 99/33982

PCT/US98/27610

The pattern detects homeobox sequences 24 residues long and spans positions 34 to 57 of the homeobox domain. The consensus pattern is as follows: [LIVMFYVG]-[ASLVR]-x(2)-[LIVMSTACN]-x-[LIVM]-x(4)-[LIV]-[RKNQESTAIV]-[LIVFSTNKH]-W-[FYVC]-x-[NDQTAH]-x(5)-[RKNAIMW].

- 5 MAP kinase kinase (MAPKK). MAP kinases (MAPK) are involved in signal transduction, and are important in cell cycle and cell growth controls. The MAP kinase kinases (MAPKK) are dual-specificity protein kinases which phosphorylate and activate MAP kinases. MAPKK homologues have been found in yeast, invertebrates, amphibians, and mammals. Moreover, the MAPKK/MAPK phosphorylation switch constitutes a basic
- 10 module activated in distinct pathways in yeast and in vertebrates. MAPKK regulation studies have led to the discovery of at least four MAPKK convergent pathways in higher organisms. One of these is similar to the yeast pheromone response pathway which includes the ste11 protein kinase. Two other pathways require the activation of either one or both of the serine/threonine kinase-encoded oncogenes c-Raf-1 and c-Mos. Additionally, several
- 15 studies suggest a possible effect of the cell cycle control regulator cyclin-dependent kinase 1 (cdc2) on MAPKK activity. Finally, MAPKKs are apparently essential transducers through which signals must pass before reaching the nucleus. For review, see, *e.g.*, Biologique *Biol Cell* (1993) 79:193-207; Nishida *et al.*, *Trends Biochem Sci* (1993) 18:128-31; Ruderman *Curr Opin Cell Biol* (1993) 5:207-13; Dhanasekaran *et al.*, *Oncogene* (1998) 17:1447-55;
- 20 Kiefer *et al.*, *Biochem Soc Trans* (1997) 25:491-8; and Hill, *Cell Signal* (1996) 8:533-44.

Those skilled in the art will recognize, or be able to ascertain, using not more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such specific embodiments and equivalents are intended to be encompassed by the following claims.

- 25 All publications and patent applications cited in this specification are herein incorporated by reference as if each individual publication or patent application were specifically and individually indicated to be incorporated by reference. The citation of any publication is for its disclosure prior to the filing date and should not be construed as an admission that the present invention is not entitled to antedate such publication by virtue of
- 30 prior invention.

WO 99/33982

PCT/US98/27610

Although the foregoing invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, it is readily apparent to those of ordinary skill in the art in light of the teachings of this invention that certain changes and modifications may be made thereto without departing from the spirit or scope of the appended claims.

Deposit Information:

The following materials were deposited with the American Type Culture Collection: CMCC = (Chiron Master Culture Collection)

Cell Lines Deposited with ATCC

Cell Line	Deposit Date	ATCC Accession No.	CMCC Accession No.
KM12L4-A	March 19, 1998	CRL-12496	11606
Km12C	May 15, 1998	CRL-12533	11611
MDA-MB-231	May 15, 1998	CRL-12532	10583
MCF-7	October 9, 1998	CRL-12584	10377

WO 99/33982
CDNA Library Deposits

PCT/US98/27610

cDNA Library ES1 - ATCC#
 Deposit Date - December 22, 1998

Clone Name	Cluster ID	Sequence Name
M00001395A:C03	4016	79.A1.sp6:130016.Seq
M00001395A:C03	4016	RTA00000118A.c.4.1
M00001449A:D12	3681	RTA00000131A.g.15.2
M00001449A:D12	3681	79.E1.sp6:130064.Seq
M00001452A:D08	1120	79.C2.sp6:130041.Seq
M00001452A:D08	1120	RTA00000118A.p.15.3
M00001513A:B06	4568	79.D4.sp6:130055.Seq
M00001513A:B06	4568	RTA00000122A.d.15.3
M00001517A:B07	4313	79.F4.sp6:130079.Seq
M00001517A:B07	4313	RTA00000122A.n.3.1
M00001533A:C11	2428	RTA00000123A.l.21.1
M00001533A:C11	2428	79.A5.sp6:130020.Seq
M00001533A:C11	2428	RTA00000123A.l.21.1.Seq_THC205063
M00001542A:A09	22113	79.F5.sp6:130080.Seq
M00001542A:A09	22113	RTA00000125A.c.7.1

cDNA Library ES2 - ATCC#
 Deposit Date - December 22, 1998

Clone Name	Cluster ID	Sequence Name
M00001343C:F10	2790	80.E1.sp6:130256.Seq
M00001343C:F10	2790	RTA00000177AF.e.2.1.Seq_THC229461
M00001343C:F10	2790	RTA00000177AF.e.2.1
M00001343D:H07	23255	100.C1.sp6:131446.Seq
M00001343D:H07	23255	RTA00000177AF.e.14.3.Seq_THC228776
M00001343D:H07	23255	80.F1.sp6:130268.Seq
M00001343D:H07	23255	RTA00000177AF.e.14.3
M00001345A:E01	6420	172.E1.sp6:133925.Seq
M00001345A:E01	6420	RTA00000177AF.f.10.3
M00001345A:E01	6420	RTA00000177AF.f.10.3.Seq_THC226443
M00001345A:E01	6420	80.G1.sp6:130280.Seq
M00001347A:B10	13576	80.D2.sp6:130245.Seq
M00001347A:B10	13576	100.E1.sp6:131470.Seq
M00001347A:B10	13576	RTA00000177AF.g.16.1
M00001353A:G12	8078	80.E3.sp6:130258.Seq
M00001353A:G12	8078	RTA00000177AR.l.13.1
M00001353A:G12	8078	172.C3.sp6:133903.Seq
M00001353D:D10	14929	RTA00000177AF.m.1.2
M00001353D:D10	14929	80.F3.sp6:130270.Seq
M00001353D:D10	14929	172.D3.sp6:133915.Seq
M00001361A:A05	4141	80.B4.sp6:130223.Seq
M00001361A:A05	4141	RTA00000177AF.p.20.3
M00001362B:D10	5622	80.D4.sp6:130247.Seq
M00001362B:D10	5622	RTA00000178AF.a.11.1

WO 99/33982

PCT/US98/27610

cDNA Library ES3 - ATCC#

Deposit Date - December 22, 1998

Clone Name	Cluster ID	Sequence Name
M00001362C:H11	945	RTA00000178AR.a.20.1
M00001362C:H11	945	100.E4.sp6:131473.Seq
M00001362C:H11	945	80.E4.sp6:130259.Seq
M00001362C:H11	945	180.C2.sp6:135940.Seq
M00001376B:G06	17732	RTA00000178AR.i.2.2
M00001376B:G06	17732	80.B5.sp6:130224.Seq
M00001387A:C05	2464	80.D6.sp6:130249.Seq
M00001387A:C05	2464	RTA00000178AF.n.18.1
M00001412B:B10	8551	RTA00000179AF.p.21.1
M00001412B:B10	8551	80.G7.sp6:130286.Seq
M00001415A:H06	13538	80.B8.sp6:130227.Seq
M00001415A:H06	13538	RTA00000180AF.a.24.1
M00001416B:H11	8847	80.C8.sp6:130239.Seq
M00001416B:H11	8847	RTA00000180AF.b.16.1
M00001429D:D07	40392	RTA00000180AF.j.8.1
M00001429D:D07	40392	80.H9.sp6:130300.Seq
M00001448D:H01	36313	80.A11.sp6:130218.Seq
M00001448D:H01	36313	RTA00000181AF.e.23.1

cDNA Library ES4 - ATCC#

Deposit Date - December 22, 1998

Clone Name	Cluster ID	Sequence Name
M00001463C:B11	19	RTA00000182AF.b.7.1
M00001463C:B11	19	89.D1.sp6:130703.Seq
M00001470A:B10	1037	89.F2.sp6:130728.Seq
M00001470A:B10	1037	RTA00000121A.f.8.1
M00001497A:G02	2623	89.F3.sp6:130729.Seq
M00001497A:G02	2623	RTA00000183AF.a.6.1
M00001500A:E11	2623	RTA00000183AF.b.14.1
M00001500A:E11	2623	89.A4.sp6:130670.Seq
M00001501D:C02	9685	RTA00000183AF.c.11.1.Seq_THC109544
M00001501D:C02	9685	RTA00000183AF.c.11.1
M00001501D:C02	9685	89.C4.sp6:130694.Seq
M00001504C:H06	6974	89.F4.sp6:130730.Seq
M00001504C:H06	6974	RTA00000183AF.d.9.1
M00001504C:H06	6974	RTA00000183AF.d.9.1.Seq_THC223129
M00001504D:G06	6420	173.F5.SP6:134133.Seq
M00001504D:G06	6420	89.G4.sp6:130742.Seq
M00001504D:G06	6420	RTA00000183AF.d.11.1.Seq_THC226443
M00001504D:G06	6420	RTA00000183AF.d.11.1
M00001528A:C04	35555	89.B6.sp6:130684.Seq
M00001528A:C04	7337	RTA00000123A.b.17.1
M00001528A:C04	35555	184.A5.sp6:135530.Seq

WO 99/33982

PCT/US98/27610

cDNA Library ES5 - ATCC#

Deposit Date - December 22, 1998

Clone Name	Cluster ID	Sequence Name
M00001537B:G07	3389	RTA00000183AF.m.19.1
M00001537B:G07	3389	89.A8.sp6:130674.Seq
M00001541A:D02	3765	89.C8.sp6:130698.Seq
M00001541A:D02	3765	RTA00000135A.d.1.1
M00001544B:B07	6974	89.A9.sp6:130675.Seq
M00001544B:B07	6974	RTA00000184AF.a.15.1
M00001546A:G11	1267	89.D9.sp6:130711.Seq
M00001546A:G11	1267	RTA00000125A.o.5.1
M00001549B:F06	4193	89.G9.sp6:130747.Seq
M00001549B:F06	4193	RTA00000184AF.e.13.1
M00001556A:F11	1577	173.C9.SP6:134101.Seq
M00001556A:F11	1577	89.F11.sp6:130737.Seq
M00001556A:F11	1577	RTA00000184AF.i.23.1
M00001556B:C08	4386	RTA00000184AF.j.4.1
M00001556B:C08	4386	89.H11.sp6:130761.Seq

cDNA Library ES6 - ATCC#

Deposit Date - December 22, 1998

Clone Name	Cluster ID	Sequence Name
M00001563B:F06	102	RTA00000184AF.o.5.1
M00001563B:F06	102	90.B1.sp6:130871.Seq
M00001571C:H06	5749	90.E1.sp6:130907.Seq
M00001571C:H06	5749	RTA00000185AF.a.19.1
M00001594B:H04	260	90.D2.sp6:130896.Seq
M00001594B:H04	260	RTA00000185AR.i.12.2
M00001597C:H02	4837	90.E2.sp6:130908.Seq
M00001597C:H02	4837	RTA00000185AR.k.3.2
M00001624C:F01	4309	90.C4.sp6:130886.Seq
M00001624C:F01	4309	RTA00000186AF.e.22.1
M00001679A:A06	6660	90.F6.sp6:130924.Seq
M00001679A:A06	6660	122.B5.sp6:132089.Seq
M00001679A:A06	6660	RTA00000187AF.h.15.1
M00003759B:B09	697	90.G8.sp6:130938.Seq
M00003759B:B09	697	RTA00000188AF.d.6.1
M00003759B:B09	697	RTA00000188AF.d.6.1.Seq_THC178884
M00003844C:B11	6539	176.D9.sp6:134556.Seq
M00003844C:B11	6539	RTA00000189AF.d.22.1
M00003844C:B11	6539	90.B10.sp6:130880.Seq
M00003857A:G10	3389	90.A11.sp6:130869.Seq
M00003857A:G10	3389	RTA00000189AF.g.3.1

WO 99/33982

PCT/US98/27610

cDNA Library ES7 - ATCC#

Deposit Date - December 22, 1998

Clone Name	Cluster ID	Sequence Name
M00003914C:F05	3900	99.E1.sp6:131278.Seq
M00003914C:F05	3900	RTA00000190AF.g.13.1
M00003922A:E06	23255	RTA00000190AF.j.4.1
M00003922A:E06	23255	99.F1.sp6:131290.Seq
M00003922A:E06	23255	RTA00000190AF.j.4.1.Seq_THC228776
M00003983A:A05	9105	99.C3.sp6:131256.Seq
M00003983A:A05	9105	RTA00000191AF.a.21.2
M00004028D:A06	6124	RTA00000191AR.e.2.3
M00004028D:A06	6124	99.D3.sp6:131268.Seq
M00004031A:A12	9061	RTA00000191AR.e.11.2
M00004031A:A12	9061	RTA00000191AR.e.11.3
M00004087D:A01	6880	RTA00000191AF.m.20.1
M00004087D:A01	6880	99.A5.sp6:131234.Seq
M00004108A:E06	4937	99.E5.sp6:131282.Seq
M00004108A:E06	4937	RTA00000191AF.p.21.1
M00004114C:F11	13183	123.D5.sp6:132305.Seq
M00004114C:F11	13183	RTA00000192AF.a.24.1
M00004114C:F11	13183	99.G5.sp6:131306.Seq

cDNA Library ES8 - ATCC#

Deposit Date - December 22, 1998

Clone Name	Cluster ID	Sequence Name
M00004146C:C11	5257	99.B6.sp6:131247.Seq
M00004146C:C11	5257	177.F5.sp6:134768.Seq
M00004146C:C11	5257	RTA00000192AF.f.3.1
M00004146C:C11	5257	RTA00000192AF.f.3.1.Seq_THC213833
M00004157C:A09	6455	RTA00000192AF.g.23.1
M00004157C:A09	6455	99.D6.sp6:131271.Seq
M00004157C:A09	6455	123.E7.sp6:132319.Seq
M00004172C:D08	11494	RTA00000192AF.j.6.1
M00004172C:D08	11494	99.G6.sp6:131307.Seq
M00004172C:D08	11494	177.E6.sp6:134757.Seq
M00004229B:F08	6455	RTA00000193AF.b.9.1
M00004229B:F08	6455	99.C8.sp6:131261.Seq

cDNA Library ES9 - ATCC#

Deposit Date - December 22, 1998

Clone Name	Cluster ID	Sequence Name
M00001466A:E07	4275	RTA00000120A.j.14.1
M00001531A:H11		89.F6.sp6:130732.Seq
M00001531A:H11		RTA00000123A.g.19.1
M00001551A:B10	6268	79.G9.sp6:130096.Seq
M00001551A:B10	6268	184.C12.sp6:135561.Seq
M00001551A:B10	6268	RTA00000126A.o.23.1
M00001552A:B12	307	RTA00000136A.o.4.2
M00001552A:B12	307	79.C7.sp6:130046.Seq
M00001556A:H01	15855	RTA00000184AF.j.1.1
M00001586C:C05	4623	RTA00000185AF.f.4.1
M00001604A:B10	1399	79.G8.sp6:130095.Seq
M00001604A:B10	1399	RTA00000129A.o.10.1
M00003879B:C11	5345	RTA00000189AF.1.19.1
M00003879B:C11	5345	90.B12.sp6:130882.Seq

WO 99/33982

PCT/US98/27610

cDNA Library ES10 - ATCC#

Deposit Date - December 22, 1998

Clone Name	Cluster ID	Sequence Name
M00001358C:C06		RTA00000177AF.o.4.3
M00001388D:G05	5832	80.F6.sp6:130273.Seq
M00001388D:G05	5832	RTA00000178AF.o.23.1
M00001394A:F01	6583	RTA00000179AF.d.13.1
M00001394A:F01	6583	172.B8.sp6:133896.Seq
M00001394A:F01	6583	80.H6.sp6:130297.Seq
M00001429A:H04	2797	RTA00000180AF.i.19.1
M00001447A:G03	10717	RTA00000181AF.d.10.1
M00001448D:C09	8	80.H10.sp6:130301.Seq
M00001448D:C09	8	RTA00000181AF.e.17.1
M00001448D:C09	8	100.B11.sp6:131444.Seq
M00001454D:G03	689	RTA00000181AR.I.22.1

cDNA Library ES11 - ATCC#

Deposit Date - December 22, 1998

Clone Name	Cluster ID	Sequence Name
M00003975A:G11	12439	RTA00000190AF.o.24.1
M00003978B:G05	5693	RTA00000190AF.p.17.2.Seq_THC173318
M00003978B:G05	5693	RTA00000190AF.p.17.2
M00004059A:D06	5417	RTA00000191AF.h.19.1
M00004068B:A01	3706	99.C4.sp6:131257.Seq
M00004068B:A01	3706	RTA00000191AF.i.17.2
M00004205D:F06		99.E7.sp6:131284.Seq
M00004205D:F06		177.G7.sp6:134782.Seq
M00004205D:F06		RTA00000192AF.o.11.1
M00004212B:C07	2379	RTA00000192AF.p.8.1
M00004223A:G10	16918	RTA00000193AF.a.16.1

cDNA Library ES12 - ATCC#

Deposit Date - December 22, 1998

Clone Name	Cluster ID	Sequence Name
M00004223B:D09	7899	RTA00000193AF.a.17.1
M00004249D:G12		RTA00000193AF.c.22.1
M00004251C:G07		RTA00000193AF.d.2.1
M00004372A:A03	2030	RTA00000193AF.m.20.1

WO 99/33982
cDNA Library ES13 - ATCC#
Deposit Date - December 22, 1998

PCT/US98/27610

Clone Name	Cluster ID	Sequence Name
M00001340B:A06	17062	80.A1.sp6:130208.Seq
M00001340B:A06	17062	RTA00000177AF.b.8.4
M00001340D:F10	11589	80.B1.sp6:130220.Seq
M00001340D:F10	11589	RTA00000177AF.b.17.4
M00001341A:E12	4443	80.C1.sp6:130232.Seq
M00001341A:E12	4443	RTA00000177AF.b.20.4
M00001342B:E06	39805	80.D1.sp6:130244.Seq
M00001342B:E06	39805	RTA00000177AF.c.21.3
M00001346A:F09	5007	RTA00000177AF.g.2.1
M00001346A:F09	5007	80.H1.sp6:130292.Seq
M00001346D:G06	5779	RTA00000177AF.g.14.3
M00001346D:G06	5779	RTA00000177AF.g.14.1
M00001348B:B04	16927	80.E2.sp6:130257.Seq
M00001348B:B04	16927	RTA00000177AF.h.9.3
M00001348B:B06	16985	RTA00000177AF.h.10.1
M00001348B:G06	16985	80.F2.sp6:130269.Seq
M00001349B:B08	3584	RTA00000177AF.h.20.1
M00001349B:B08	3584	80.G2.sp6:130281.Seq
M00001350A:H01	7187	100.C2.sp6:131447.Seq
M00001350A:H01	7187	80.A3.sp6:130210.Seq
M00001350A:H01	7187	RTA00000177AF.i.8.2
M00001352A:E02	16245	RTA00000177AF.k.9.3
M00001352A:E02	16245	172.D2.sp6:133914.Seq
M00001352A:E02	16245	80.D3.sp6:130246.Seq
M00001355B:G10	14391	RTA00000177AF.m.17.3
M00001355B:G10	14391	80.G3.sp6:130282.Seq
M00001355B:G10	14391	172.H3.sp6:133963.Seq
M00001355B:G10	14391	100.E3.sp6:131472.Seq
M00001361D:F08	2379	80.C4.sp6:130235.Seq
M00001361D:F08	2379	RTA00000178AF.a.6.1
M00001365C:C10	40132	RTA00000178AF.c.7.1
M00001365C:C10	40132	80.F4.sp6:130271.Seq
M00001368D:E03		80.G4.sp6:130283.Seq
M00001368D:E03		RTA00000178AF.d.20.1
M00001370A:C09	6867	80.H4.sp6:130295.Seq
M00001370A:C09	6867	RTA00000178AF.e.12.1
M00001371C:E09	7172	100.A5.sp6:131426.Seq
M00001371C:E09	7172	RTA00000178AF.f.9.1
M00001371C:E09	7172	80.A5.sp6:130212.Seq
M00001378B:B02	39833	80.C5.sp6:130236.Seq
M00001378B:B02	39833	RTA00000178AF.i.23.1
M00001379A:A05	1334	80.D5.sp6:130248.Seq
M00001379A:A05	1334	RTA00000178AF.j.7.1
M00001380D:B09	39886	RTA00000178AF.j.24.1
M00001380D:B09	39886	80.E5.sp6:130260.Seq
M00001381D:E06		80.F5.sp6:130272.Seq
M00001381D:E06		RTA00000178AF.k.16.1
M00001382C:A02	22979	80.G5.sp6:130284.Seq
M00001382C:A02	22979	RTA00000178AF.k.22.1
M00001384B:A11		80.B6.sp6:130225.Seq
M00001384B:A11		RTA00000178AF.m.13.1
M00001386C:B12	5178	80.C6.sp6:130237.Seq

WO 99/33982

PCT/US98/27610

cDNA Library ES13 - ATCC#

Deposit Date - December 22, 1998

Clone Name	Cluster ID	Sequence Name
M00001386C:B12	5178	RTA00000178AF.n.10.1
M00001387B:G03	7587	80.E6.sp6:130261.Seq
M00001387B:G03	7587	RTA00000178AF.n.24.1
M00001389A:C08	16269	RTA00000178AF.p.1.1
M00001389A:C08	16269	80.G6.sp6:130285.Seq
M00001396A:C03	4009	172.D8.sp6:133920.Seq
M00001396A:C03	4009	80.A7.sp6:130214.Seq
M00001396A:C03	4009	RTA00000179AF.e.20.1
M00001400B:H06		172.B9.sp6:133897.Seq
M00001400B:H06		80.B7.sp6:130226.Seq
M00001400B:H06		RTA00000179AF.j.13.1
M00001400B:H06		RTA00000179AF.j.13.1.Seq_THC105720
M00001402A:E08	39563	80.C7.sp6:130238.Seq
M00001402A:E08	39563	RTA00000179AF.k.20.1
M00001407B:D11	5556	RTA00000179AF.n.10.1
M00001407B:D11	5556	80.D7.sp6:130250.Seq
M00001410A:D07	7005	180.H5.sp6:136003.Seq
M00001410A:D07	7005	RTA00000179AF.o.22.1
M00001410A:D07	7005	80.F7.sp6:130274.Seq
M00001414A:B01		RTA00000180AF.a.9.1
M00001414A:B01		80.H7.sp6:130298.Seq
M00001414C:A07		80.A8.sp6:130215.Seq
M00001414C:A07		RTA00000180AF.a.11.1
M00001416A:H01	7674	79.C1.sp6:130040.Seq
M00001416A:H01	7674	RTA00000118A.g.9.1
M00001417A:E02	36393	RTA00000180AF.c.2.1
M00001417A:E02	36393	80.D8.sp6:130251.Seq
M00001423B:E07	15066	RTA00000180AF.e.24.1
M00001423B:E07	15066	80.H8.sp6:130299.Seq
M00001424B:G09	10470	80.A9.sp6:130216.Seq
M00001424B:G09	10470	RTA00000180AF.f.18.1
M00001425B:H08	22195	RTA00000180AF.g.7.1
M00001425B:H08	22195	80.B9.sp6:130228.Seq
M00001426B:D12		RTA00000180AF.g.22.1
M00001426B:D12		80.C9.sp6:130240.Seq
M00001426D:C08	4261	80.D9.sp6:130252.Seq
M00001426D:C08	4261	RTA00000180AF.h.5.1
M00001428A:H10	84182	100.G9.sp6:131502.Seq
M00001428A:H10	84182	RTA00000180AF.h.19.1
M00001428A:H10	84182	80.E9.sp6:130264.Seq
M00001449A:A12	5857	80.B11.sp6:130230.Seq
M00001449A:A12	5857	RTA00000118A.g.14.1
M00001449A:B12	41633	80.C11.sp6:130242.Seq
M00001449A:B12	41633	RTA00000118A.g.16.1
M00001449A:G10	36535	RTA00000181AF.f.5.1
M00001449A:G10	36535	80.D11.sp6:130254.Seq
M00001449A:G10	36535	100.D11.sp6:131468.Seq
M00001449C:D06	86110	RTA00000181AF.f.12.1
M00001449C:D06	86110	80.E11.sp6:130266.Seq
M00001450A:A02	39304	RTA00000118A.j.21.1.Seq_THC151859
M00001450A:A02	39304	RTA00000118A.j.21.1
M00001450A:A02	39304	79.F1.sp6:130076.Seq

WO 99/33982

PCT/US98/27610

cDNA Library ES13 - ATCC#

Deposit Date - December 22, 1998

Clone Name	Cluster ID	Sequence Name
M00001450A:A02	39304	180.G9.sp6:135995.Seq
M00001450A:A11	32663	80.F11.sp6:130278.Seq
M00001450A:A11	32663	RTA00000118A.L.8.1
M00001450A:B12	82498	100.F11.sp6:131492.Seq
M00001450A:B12	82498	RTA00000118A.m.10.1
M00001450A:B12	82498	79.G1.sp6:130088.Seq
M00001450A:D08	27250	80.G11.sp6:130290.Seq
M00001450A:D08	27250	180.B10.sp6:135936.Seq
M00001450A:D08	27250	RTA00000181AF.g.10.1
M00001452A:B04	84328	RTA00000118A.p.10.1
M00001452A:B04	84328	79.A2.sp6:130017.Seq
M00001452A:B12	86859	RTA00000118A.p.8.1
M00001452A:B12	86859	79.B2.sp6:130029.Seq
M00001452A:F05	85064	RTA00000131A.m.23.1
M00001452A:F05	85064	79.D2.sp6:130053.Seq
M00001452C:B06	16970	80.H11.sp6:130302.Seq
M00001452C:B06	16970	100.C12.sp6:131457.Seq
M00001452C:B06	16970	RTA00000181AR.i.18.2
M00001453A:E11	16130	80.A12.sp6:130219.Seq
M00001453A:E11	16130	100.D12.sp6:131469.Seq
M00001453A:E11	16130	RTA00000119A.c.13.1
M00001453C:F06	16653	80.B12.sp6:130231.Seq
M00001453C:F06	16653	RTA00000181AF.k.5.3
M00001454A:A09	83103	RTA00000119A.e.24.2
M00001454A:A09	83103	79.G2.sp6:130089.Seq
M00001454B:C12	7005	121.D1.sp6:131917.Seq
M00001454B:C12	7005	RTA00000181AF.k.24.1
M00001454B:C12	7005	80.C12.sp6:130243.Seq
M00001455B:E12	13072	80.F12.sp6:130279.Seq
M00001455B:E12	13072	RTA00000181AR.m.5.2
M00001460A:F06	2448	89.A1.sp6:130667.Seq
M00001460A:F06	2448	RTA00000119A.j.21.1
M00001461A:D06	1531	89.C1.sp6:130691.Seq
M00001461A:D06	1531	RTA00000119A.o.3.1
M00001465A:B11	10145	79.F3.sp6:130078.Seq
M00001465A:B11	10145	RTA00000120A.g.12.1
M00001467A:B07	38759	89.F1.sp6:130727.Seq
M00001467A:B07	38759	RTA00000120A.m.12.3
M00001467A:D04	39508	RTA00000120A.o.2.1
M00001467A:D04	39508	89.G1.sp6:130739.Seq
M00001467A:E10	39442	89.A2.sp6:130668.Seq
M00001467A:E10	39442	RTA00000120A.o.21.1
M00001468A:F05	7589	RTA00000120A.p.23.1
M00001468A:F05	7589	89.B2.sp6:130680.Seq
M00001469A:A01		RTA00000121A.c.10.1
M00001469A:A01		89.C2.sp6:130692.Seq
M00001469A:C10	12081	89.D2.sp6:130704.Seq
M00001469A:C10	12081	RTA00000133A.d.14.2
M00001469A:H12	19105	89.E2.sp6:130716.Seq
M00001469A:H12	19105	RTA00000133A.e.15.1
M00001470A:C04	39425	89.G2.sp6:130740.Seq
M00001470A:C04	39425	RTA00000133A.f.1.1

WO 99/33982

PCT/US98/27610

cDNA Library ES13 - ATCC#

Deposit Date - December 22, 1998

Clone Name	Cluster ID	Sequence Name
M00001471A:B01	39478	89.H2.sp6:130752.Seq
M00001471A:B01	39478	RTA00000133A.i.5.1
M00001487B:H06		RTA00000182AF.l.15.1
M00001487B:H06		89.B3.sp6:130681.Seq
M00001488B:F12		RTA00000182AF.l.20.1
M00001488B:F12		89.C3.sp6:130693.Seq
M00001494D:F06	7206	RTA00000182AF.o.15.1
M00001494D:F06	7206	89.E3.sp6:130717.Seq
M00001499B:A11	10539	RTA00000183AF.a.24.1
M00001499B:A11	10539	89.G3.sp6:130741.Seq
M00001499B:A11	10539	173.B5.SP6:134085.Seq
M00001500A:C05	5336	RTA00000183AF.b.13.1
M00001500A:C05	5336	89.H3.sp6:130753.Seq
M00001504A:E01		RTA00000183AF.c.24.1
M00001504A:E01		89.D4.sp6:130706.Seq
M00001504A:E01		RTA00000183AF.c.24.1.Seq_THC125912
M00001504C:A07	10185	RTA00000183AF.d.5.1
M00001504C:A07	10185	89.E4.sp6:130718.Seq
M00001505C:C05		89.H4.sp6:130754.Seq
M00001505C:C05		RTA00000183AF.e.1.1
M00001506D:A09		89.A5.sp6:130671.Seq
M00001506D:A09		RTA00000183AF.e.23.1
M00001506D:A09		121.G6.sp6:131958.Seq
M00001507A:H05	39168	RTA00000121A.l.10.1
M00001507A:H05	39168	89.B5.sp6:130683.Seq
M00001535A:F10	39423	79.C5.sp6:130044.Seq
M00001535A:F10	39423	RTA00000134A.k.22.1
M00001541A:H03	39174	79.E5.sp6:130068.Seq
M00001541A:H03	39174	RTA00000124A.n.13.1
M00001544A:G02	19829	79.H5.sp6:130104.Seq
M00001544A:G02	19829	RTA00000125A.h.24.4
M00001545A:D08	13864	RTA00000125A.m.9.1
M00001545A:D08	13864	79.B6.sp6:130033.Seq
M00001551A:F05	39180	RTA00000126A.n.8.2
M00001551A:F05	39180	79.A7.sp6:130022.Seq
M00001552A:D11	39458	RTA00000126A.p.15.2
M00001552A:D11	39458	79.D7.sp6:130058.Seq
M00001557A:F03	39490	RTA00000128A.b.4.1

WO 99/33982

PCT/US98/27610

cDNA Library ES14 - ATCC#

Deposit Date - December 22, 1998

Clone Name	Cluster ID	Sequence Name
M00001511A:H06	39412	RTA00000133A.k.17.1
M00001511A:H06	39412	89.C5.sp6:130695.Seq
M00001512A:A09	39186	89.D5.sp6:130707.Seq
M00001512A:A09	39186	RTA00000121A.p.15.1
M00001512D:G09	3956	89.E5.sp6:130719.Seq
M00001512D:G09	3956	173.H5.SP6:134157.Seq
M00001512D:G09	3956	RTA00000183AF.g.3.1
M00001513B:G03		RTA00000183AF.g.9.1
M00001513B:G03		89.F5.sp6:130731.Seq
M00001513B:G03		RTA00000183AF.g.9.1.Seq_THC198280
M00001513C:E08	14364	RTA00000183AF.g.12.1
M00001513C:E08	14364	89.G5.sp6:130743.Seq
M00001514C:D11	40044	RTA00000183AF.g.22.1
M00001514C:D11	40044	RTA00000183AF.g.22.1.Seq_THC232899
M00001514C:D11	40044	89.H5.sp6:130755.Seq
M00001518C:B11	8952	89.A6.sp6:130672.Seq
M00001518C:B11	8952	RTA00000183AF.h.15.1
M00001528B:H04	8358	89.D6.sp6:130708.Seq
M00001528B:H04	8358	RTA00000183AF.i.5.1
M00001531A:D01	38085	RTA00000123A.e.15.1
M00001531A:D01	38085	89.E6.sp6:130720.Seq
M00001534A:C04	16921	RTA00000183AF.k.6.1
M00001534A:C04	16921	89.H6.sp6:130756.Seq
M00001534A:D09	5097	RTA00000134A.k.1.1
M00001534A:D09	5097	RTA00000134A.k.1.1.Seq_THC215869
M00001534C:A01	4119	RTA00000183AF.k.16.1
M00001534C:A01	4119	89.C7.sp6:130697.Seq
M00001535A:C06	20212	89.E7.sp6:130721.Seq
M00001535A:C06	20212	RTA00000134A.1.22.1.Seq_THC128232
M00001535A:C06	20212	RTA00000134A.1.22.1
M00001536A:B07	2696	RTA00000134A.m.13.1
M00001536A:B07	2696	89.F7.sp6:130733.Seq
M00001537A:F12	39420	89.H7.sp6:130757.Seq
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M00001540A:D06	8286	89.B8.sp6:130686.Seq
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M00001542A:E06	39453	89.E8.sp6:130722.Seq
M00001542A:E06	39453	RTA00000135A.g.11.1
M00001544A:E06		RTA00000184AF.a.8.1
M00001544A:E06		173.G7.SP6:134147.Seq
M00001544A:E06		89.H8.sp6:130758.Seq
M00001545A:B02		89.B9.sp6:130687.Seq
M00001545A:B02		RTA00000135A.1.2.2
M00001548A:E10	5892	89.E9.sp6:130723.Seq
M00001548A:E10	5892	RTA00000184AF.d.11.1
M00001548A:E10	5892	RTA00000184AF.d.11.1.Seq_THC161896
M00001549C:E06	16347	89.H9.sp6:130759.Seq
M00001549C:E06	16347	RTA00000184AF.e.15.1
M00001550A:A03	7239	89.A10.sp6:130676.Seq
M00001550A:A03	7239	RTA00000126A.m.4.2
M00001550A:G01	5175	RTA00000184AF.f.3.1
M00001550A:G01	5175	89.B10.sp6:130688.Seq

WO 99/33982
cDNA Library ES14 - ATCC#
Deposit Date - December 22, 1998

PCT/US98/27610

Clone Name	Cluster ID	Sequence Name
M00001551A:G06	22390	RTA00000136A.j.13.1
M00001551A:G06	22390	89.C10.sp6:130700.Seq
M00001551C:G09	3266	RTA00000184AF.g.1.1
M00001551C:G09	3266	89.D10.sp6:130712.Seq
M00001553A:H06	8298	RTA00000127A.d.19.1
M00001553A:H06	8298	89.G10.sp6:130748.Seq
M00001553B:F12	4573	89.H10.sp6:130760.Seq
M00001553B:F12	4573	RTA00000184AF.h.9.1
M00001555A:B02	39539	RTA00000127A.i.21.1
M00001555A:B02	39539	89.B11.sp6:130689.Seq
M00001555A:C01	39195	89.C11.sp6:130701.Seq
M00001555A:C01	39195	RTA00000137A.c.16.1
M00001555D:G10	4561	RTA00000184AF.i.21.1
M00001555D:G10	4561	89.D11.sp6:130713.Seq
M00001556A:C09	9244	89.E11.sp6:130725.Seq
M00001556A:C09	9244	RTA00000127A.l.3.1
M00001556B:G02	11294	RTA00000184AF.j.6.1
M00001556B:G02	11294	89.A12.sp6:130678.Seq
M00001557B:H10	5192	173.E9.SP6:134125.Seq
M00001557B:H10	5192	RTA00000184AF.k.2.1
M00001557B:H10	5192	89.D12.sp6:130714.Seq
M00001557D:D09	8761	RTA00000184AF.k.12.1
M00001557D:D09	8761	89.E12.sp6:130726.Seq
M00001558B:H11	7514	RTA00000184AF.k.21.1
M00001558B:H11	7514	89.G12.sp6:130750.Seq
M00001559B:F01		89.H12.sp6:130762.Seq
M00001559B:F01		RTA00000184AF.l.11.1
M00001560D:F10	6558	90.A1.sp6:130859.Seq
M00001560D:F10	6558	RTA00000184AF.m.21.1
M00001566B:D11		RTA00000184AF.p.3.1
M00001566B:D11		90.D1.sp6:130895.Seq
M00001583D:A10	6293	RTA00000185AF.e.11.1
M00001583D:A10	6293	90.A2.sp6:130860.Seq
M00001590B:F03		RTA00000185AF.g.11.1
M00001590B:F03		90.C2.sp6:130884.Seq
M00001597D:C05	10470	RTA00000185AF.k.6.1
M00001597D:C05	10470	90.F2.sp6:130920.Seq
M00001598A:G03	16999	90.G2.sp6:130932.Seq
M00001598A:G03	16999	RTA00000185AF.k.9.1
M00001601A:D08	22794	RTA00000138A.b.5.1
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M00001608A:B03	7802	RTA00000185AF.n.5.1
M00001608A:B03	7802	90.B3.sp6:130873.Seq
M00001608B:E03	22155	RTA00000185AF.n.9.1
M00001608B:E03	22155	90.C3.sp6:130885.Seq
M00001608D:A11		RTA00000185AF.n.12.1
M00001608D:A11		90.D3.sp6:130897.Seq
M00001614C:F10	13157	RTA00000186AF.a.6.1
M00001614C:F10	13157	90.E3.sp6:130909.Seq
M00001617C:E02	17004	RTA00000186AF.b.21.1

WO 99/33982

PCT/US98/27610

cDNA Library ES14 - ATCC#

Deposit Date - December 22, 1998

Clone Name	Cluster ID	Sequence Name
M00001617C:E02	17004	90.F3.sp6:130921.Seq
M00001619C:F12	40314	90.G3.sp6:130933.Seq
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M00001621C:C08	40044	RTA00000186AF.d.1.1
M00001621C:C08	40044	RTA00000186AF.d.1.1.Seq_THC232899
M00001621C:C08	40044	90.H3.sp6:130945.Seq
M00001621C:C08	40044	122.E1.sp6:132121.Seq
M00001623D:F10	13913	RTA00000186AF.e.6.1
M00001623D:F10	13913	90.A4.sp6:130862.Seq
M00001632D:H07		RTA00000186AF.h.14.1.Seq_THC112525
M00001632D:H07		RTA00000186AF.h.14.1
M00001632D:H07		90.E4.sp6:130910.Seq
M00001632D:H07		176.A3.sp6:134514.Seq
M00001644C:B07	39171	RTA00000186AF.l.7.1
M00001644C:B07	39171	90.F4.sp6:130922.Seq
M00001644C:B07	39171	217.A12.sp6:139369.Seq
M00001645A:C12	19267	RTA00000186AF.l.12.1.Seq_THC178183
M00001645A:C12	19267	176.G3.sp6:134586.Seq
M00001645A:C12	19267	RTA00000186AF.l.12.1
M00001645A:C12	19267	90.G4.sp6:130934.Seq
M00001648C:A01	4665	90.H4.sp6:130946.Seq
M00001648C:A01	4665	RTA00000186AF.m.3.1
M00001657D:C03	23201	RTA00000187AF.a.14.1
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M00001657D:F08	76760	90.C5.sp6:130887.Seq
M00001657D:F08	76760	RTA00000187AF.a.15.1
M00001662C:A09	23218	RTA00000187AR.c.5.2
M00001662C:A09	23218	90.D5.sp6:130899.Seq
M00001663A:E04	35702	90.E5.sp6:130911.Seq
M00001663A:E04	35702	RTA00000187AR.c.15.2
M00001669B:F02	6468	90.F5.sp6:130923.Seq
M00001669B:F02	6468	RTA00000187AF.d.15.1
M00001670C:H02	14367	90.G5.sp6:130935.Seq
M00001670C:H02	14367	RTA00000187AF.e.8.1
M00001673C:H02	7015	90.H5.sp6:130947.Seq
M00001673C:H02	7015	RTA00000187AF.f.18.1
M00001675A:C09	8773	RTA00000187AF.f.24.1
M00001675A:C09	8773	90.A6.sp6:130864.Seq
M00001675A:C09	8773	RTA00000187AF.f.24.1.Seq_THC220002
M00001676B:F05	11460	RTA00000187AF.g.12.1
M00001676B:F05	11460	90.B6.sp6:130876.Seq
M00001676B:F05	11460	219.F2.sp6:139035.Seq
M00001677D:A07	7570	90.D6.sp6:130900.Seq
M00001677D:A07	7570	RTA00000187AF.g.24.1
M00001677D:A07	7570	RTA00000187AF.g.24.1.Seq_THC168636
M00001678D:F12	4416	90.E6.sp6:130912.Seq
M00001678D:F12	4416	RTA00000187AF.h.13.1
M00001679A:F10	26875	RTA00000187AF.i.1.1
M00001679A:F10	26875	90.A7.sp6:130865.Seq
M00001679B:F01	6298	90.B7.sp6:130877.Seq
M00001679B:F01	6298	RTA00000187AR.i.10.2
M00001680D:F08	10539	90.F7.sp6:130925.Seq

WO 99/33982

PCT/US98/27610

cDNA Library ES14 - ATCC#

Deposit Date - December 22, 1998

Clone Name	Cluster ID	Sequence Name
M00001680D:F08	10539	219.F6.sp6:139039.Seq
M00001680D:F08	10539	RTA00000187AF.l.7.1
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M00001682C:B12	17055	RTA00000187AF.m.3.1
M00001682C:B12	17055	176.D6.sp6:134553.Seq
M00001688C:F09	5382	90.A8.sp6:130866.Seq
M00001688C:F09	5382	RTA00000187AF.m.23.2
M00001693C:G01	4393	RTA00000187AF.n.17.1
M00001693C:G01	4393	90.B8.sp6:130878.Seq
M00001716D:H05	67252	RTA00000187AF.o.6.1
M00001716D:H05	67252	90.C8.sp6:130890.Seq
M00003741D:C09	40108	90.D8.sp6:130902.Seq
M00003741D:C09	40108	RTA00000187AF.o.24.1
M00003747D:C05	11476	RTA00000187AF.p.19.1
M00003747D:C05	11476	90.E8.sp6:130914.Seq
M00003747D:C05	11476	RTA00000187AF.p.19.1.Seq_THC108482
M00003747D:C05	11476	219.H8.sp6:139065.Seq
M00003754C:E09		90.F8.sp6:130926.Seq
M00003754C:E09		RTA00000188AF.b.12.1
M00003761D:A09		RTA00000188AF.d.11.1
M00003761D:A09		90.H8.sp6:130950.Seq
M00003761D:A09		RTA00000188AF.d.11.1.Seq_THC212094
M00003762C:B08	17076	RTA00000188AF.d.21.1.Seq_THC208760
M00003762C:B08	17076	90.A9.sp6:130867.Seq
M00003762C:B08	17076	RTA00000188AF.d.21.1
M00003763A:F06	3108	RTA00000188AF.d.24.1
M00003763A:F06	3108	90.B9.sp6:130879.Seq
M00003774C:A03	67907	RTA00000188AF.g.11.1.Seq_THC123222
M00003774C:A03	67907	RTA00000188AF.g.11.1
M00003774C:A03	67907	90.C9.sp6:130891.Seq
M00003784D:D12		RTA00000188AF.i.8.1
M00003784D:D12		90.D9.sp6:130903.Seq
M00003839A:D08	7798	RTA00000189AF.c.18.1
M00003839A:D08	7798	90.A10.sp6:130868.Seq
M00003851B:D08		90.D10.sp6:130904.Seq
M00003851B:D08		RTA00000189AF.f.7.1
M00003851B:D10	13595	90.E10.sp6:130916.Seq
M00003851B:D10	13595	RTA00000189AF.f.8.1
M00003853A:D04	5619	90.F10.sp6:130928.Seq
M00003853A:D04	5619	RTA00000189AF.f.17.1
M00003853A:F12	10515	90.G10.sp6:130940.Seq
M00003853A:F12	10515	RTA00000189AF.f.18.1
M00003856B:C02	4622	90.H10.sp6:130952.Seq
M00003856B:C02	4622	RTA00000189AF.g.1.1
M00003857A:H03	4718	90.B11.sp6:130881.Seq
M00003857A:H03	4718	RTA00000189AF.g.5.1.Seq_THC196102
M00003857A:H03	4718	RTA00000189AF.g.5.1

WO 99/33982

PCT/US98/27610

cDNA Library ES15 - ATCC#

Deposit Date - December 22, 1998

Clone Name	Cluster ID	Sequence Name
M00003867A:D10		90.C11.sp6:130893.Seq
M00003867A:D10		RTA00000189AF.h.17.1
M00003871C:E02	4573	RTA00000189AF.j.12.1
M00003875C:G07	8479	90.G11.sp6:130941.Seq
M00003875C:G07	8479	RTA00000189AF.j.22.1
M00003875D:D11		90.H11.sp6:130953.Seq
M00003875D:D11		RTA00000189AF.j.23.1
M00003876D:E12	7798	90.A12.sp6:130870.Seq
M00003876D:E12	7798	RTA00000189AF.k.12.1
M00003906C:E10	9285	90.H12.sp6:130954.Seq
M00003906C:E10	9285	RTA00000190AF.d.7.1
M00003907D:A09	39809	99.A1.sp6:131230.Seq
M00003907D:A09	39809	RTA00000190AF.e.3.1.Seq_THC150217
M00003907D:A09	39809	RTA00000190AF.e.3.1
M00003907D:H04	16317	99.B1.sp6:131242.Seq
M00003907D:H04	16317	RTA00000190AF.e.6.1
M00003909D:C03	8672	RTA00000190AF.f.11.1
M00003909D:C03	8672	99.C1.sp6:131254.Seq
M00003968B:F06	24488	RTA00000190AF.n.16.1
M00003968B:F06	24488	99.C2.sp6:131255.Seq
M00003970C:B09	40122	RTA00000190AF.n.23.1
M00003970C:B09	40122	RTA00000190AF.n.23.1.Seq_THC109227
M00003970C:B09	40122	99.D2.sp6:131267.Seq
M00003974D:E07	23210	RTA00000190AF.o.20.1
M00003974D:E07	23210	RTA00000190AF.o.20.1.Seq_THC207240
M00003974D:E07	23210	99.E2.sp6:131279.Seq
M00003974D:H02	23358	RTA00000190AF.o.21.1.Seq_THC207240
M00003974D:H02	23358	RTA00000190AF.o.21.1
M00003974D:H02	23358	99.F2.sp6:131291.Seq
M00003981A:E10	3430	99.A3.sp6:131232.Seq
M00003981A:E10	3430	RTA00000191AF.a.9.1
M00003982C:C02	2433	RTA00000191AF.a.15.2
M00003982C:C02	2433	99.B3.sp6:131244.Seq
M00003982C:C02	2433	RTA00000191AF.a.15.2.Seq_THC79498
M00004028D:C05	40073	RTA00000191AF.e.3.1
M00004028D:C05	40073	99.E3.sp6:131280.Seq
M00004035C:A07	37285	99.H3.sp6:131316.Seq
M00004035C:A07	37285	RTA00000191AF.f.11.1
M00004035D:B06	17036	RTA00000191AF.f.13.1
M00004035D:B06	17036	99.A4.sp6:131233.Seq
M00004072A:C03		RTA00000191AF.j.9.1
M00004072A:C03		99.D4.sp6:131269.Seq
M00004081C:D10	15069	99.F4.sp6:131293.Seq
M00004081C:D10	15069	RTA00000191AF.l.6.1
M00004086D:G06	9285	99.H4.sp6:131317.Seq
M00004086D:G06	9285	RTA00000191AF.m.18.1
M00004105C:A04	7221	99.D5.sp6:131270.Seq
M00004105C:A04	7221	RTA00000191AF.p.9.1
M00004171D:B03	4908	RTA00000192AF.j.2.1
M00004171D:B03	4908	99.F6.sp6:131295.Seq
M00004185C:C03	11443	RTA00000192AF.l.13.2
M00004185C:C03	11443	123.A8.sp6:132272.Seq

WO 99/33982			PCT/US98/27610
cDNA Library ES15 - ATCC#			
Deposit Date - December 22, 1998			
Clone Name	Cluster ID	Sequence Name	
M00004185C:C03	11443	99.A7.sp6:131236.Seq	
M00004191D:B11		RTA00000192AF.m.12.1	
M00004191D:B11		99.B7.sp6:131248.Seq	
M00004191D:B11		123.C8.sp6:132296.Seq	
M00004197D:H01	8210	99.C7.sp6:131260.Seq	
M00004197D:H01	8210	123.E8.sp6:132320.Seq	
M00004197D:H01	8210	RTA00000192AF.n.13.1	
M00004203B:C12	14311	99.D7.sp6:131272.Seq	
M00004203B:C12	14311	RTA00000192AF.o.2.1	
M00004214C:H05	11451	177.D8.sp6:134747.Seq	
M00004214C:H05	11451	RTA00000192AF.p.17.1	
M00004223D:E04	12971	RTA00000193AF.a.20.1	
M00004223D:E04	12971	99.B8.sp6:131249.Seq	
M00004269D:D06	4905	99.H8.sp6:131321.Seq	
M00004269D:D06	4905	RTA00000193AF.e.14.1	
M00004295D:F12	16921	99.D9.sp6:131274.Seq	
M00004295D:F12	16921	RTA00000193AF.h.15.1	
M00004296C:H07	13046	99.E9.sp6:131286.Seq	
M00004296C:H07	13046	RTA00000193AF.h.19.1	
M00004307C:A06	9457	RTA00000193AF.i.14.2	
M00004307C:A06	9457	99.F9.sp6:131298.Seq	
M00004307C:A06	9457	123.D11.sp6:132311.Seq	
M00004312A:G03	26295	RTA00000193AF.i.24.2	
M00004312A:G03	26295	99.G9.sp6:131310.Seq	
M00004312A:G03	26295	RTA00000193AF.i.24.2.Seq_THC197345	
M00004318C:D10	21847	RTA00000193AF.j.9.1	
M00004318C:D10	21847	99.H9.sp6:131322.Seq	
M00004359B:G02		RTA00000193AF.m.5.1.Seq_THC173318	
M00004359B:G02		RTA00000193AF.m.5.1	
M00004505D:F08		RTA00000194AF.b.19.1	
M00004505D:F08		99.H10.sp6:131323.Seq	
M00004692A:H08		99.B11.sp6:131252.Seq	
M00004692A:H08		RTA00000194AF.c.24.1	
M00004692A:H08		377.F4.sp6:141957.Seq	
M00005180C:G03		RTA00000194AF.f.4.1	

WO 99/33982
cDNA Library ES16 - ATCC#
Deposit Date - December 22, 1998

PCT/US98/27610

Clone Name	Cluster ID	Sequence Name
M00001346D:E03	6806	RTA00000177AF.g.13.3
M00001350A:B08		80.H2.sp6:130293.Seq
M00001350A:B08		RTA00000177AF.i.6.2
M00001357D:D11	4059	RTA00000177AF.n.18.3.Seq_THC123051
M00001357D:D11	4059	RTA00000177AF.n.18.3
M00001409C:D12	9577	RTA00000179AF.o.17.1
M00001409C:D12	9577	80.E7.sp6:130262.Seq
M00001418B:F03	9952	RTA00000180AF.c.20.1
M00001418B:F03	9952	RTA00000180AF.c.20.1.Seq_THC162284
M00001418B:F03	9952	80.E8.sp6:130263.Seq
M00001418D:B06	8526	RTA00000180AF.d.1.1
M00001421C:F01	9577	RTA00000180AF.d.23.1
M00001421C:F01	9577	80.G8.sp6:130287.Seq
M00001429B:A11	4635	RTA00000180AF.i.20.1
M00001432C:F06		RTA00000180AF.k.24.1
M00001439C:F08	40054	RTA00000180AF.p.10.1
M00001442C:D07	16731	RTA00000181AF.a.20.1
M00001442C:D07	16731	80.C10.sp6:130241.Seq
M00001443B:F01		80.D10.sp6:130253.Seq
M00001443B:F01		RTA00000181AF.b.7.1
M00001445A:F05	13532	80.E10.sp6:130265.Seq
M00001445A:F05	13532	RTA00000181AF.c.4.1
M00001446A:F05	7801	RTA00000181AF.c.21.1
M00001455A:E09	13238	RTA00000181AF.m.4.1
M00001455A:E09	13238	RTA00000181AF.m.4.1.Seq_THC140691
M00001460A:F12	39498	RTA00000119A.j.20.1
M00001481D:A05	7985	RTA00000182AR.j.2.1
M00001490B:C04	18699	RTA00000182AF.m.16.1
M00001490B:C04	18699	89.D3.sp6:130705.Seq
M00001500C:E04	9443	89.B4.sp6:130682.Seq
M00001500C:E04	9443	RTA00000183AF.c.1.1
M00001532B:A06	3990	89.G6.sp6:130744.Seq
M00001532B:A06	3990	RTA00000183AF.j.11.1
M00001534A:F09	5321	89.B7.sp6:130685.Seq
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M00001535A:B01	7665	RTA00000134A.l.19.1
M00001536A:C08	39392	89.G7.sp6:130745.Seq
M00001536A:C08	39392	RTA00000134A.m.16.1
M00001541A:F07	22085	RTA00000135A.e.5.2
M00001542B:B01		RTA00000183AF.p.4.1
M00001542B:B01		89.F8.sp6:130734.Seq
M00001544A:E03	12170	RTA00000125A.h.18.4
M00001545A:C03	19255	RTA00000135A.m.18.1
M00001545A:C03	19255	184.B10.sp6:135547.Seq
M00001545A:C03	19255	89.C9.sp6:130699.Seq
M00001548A:H09	1058	RTA00000126A.e.20.3.Seq_THC217534
M00001548A:H09	1058	RTA00000126A.e.20.3
M00001548A:H09	1058	79.F6.sp6:130081.Seq
M00001549A:B02	4015	RTA00000136A.e.12.1
M00001549A:B02	4015	79.G6.sp6:130093.Seq
M00001549A:D08	10944	RTA00000126A.h.17.2
M00001552B:D04	5708	RTA00000184AF.g.12.1

WO 99/33982			PCT/US98/27610
cDNA Library ES16 - ATCC#			
Deposit Date - December 22, 1998			
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M00001552D:A01		89.F10.sp6:130736.Seq	
M00001552D:A01		RTA00000184AF.g.22.1	
M00001553D:D10	22814	RTA00000184AF.h.14.1	
M00001553D:D10	22814	89.A11.sp6:130677.Seq	
M00001558A:H05		RTA00000128A.c.20.1	
M00001558A:H05		89.F12.sp6:130738.Seq	
M00001561A:C05	39486	RTA00000128A.m.22.2	
M00001561A:C05	39486	79.B8.sp6:130035.Seq	
M00001564A:B12	5053	RTA00000184AF.o.12.1	
M00001578B:E04	23001	RTA00000185AF.c.24.1	
M00001579D:C03	6539	90.G1.sp6:130931.Seq	
M00001579D:C03	6539	173.A12.SP6:134080.Seq	
M00001579D:C03	6539	RTA00000185AF.d.11.1	
M00001582D:F05		RTA00000185AF.d.24.1	
M00001587A:B11	39380	RTA00000129A.e.24.1	
M00001587A:B11	39380	79.E8.sp6:130071.Seq	
M00001604A:F05	39391	RTA00000138A.c.3.1	
M00001604A:F05	39391	79.A9.sp6:130024.Seq	
M00001624A:B06	3277	RTA00000138A.15.1	
M00001624A:B06	3277	217.E1.sp6:139406.Seq	
M00001624A:B06	3277	90.B4.sp6:130874.Seq	
M00001630B:H09	5214	90.D4.sp6:130898.Seq	
M00001630B:H09	5214	122.C2.sp6:132098.Seq	
M00001630B:H09	5214	RTA00000186AF.g.11.1	
M00001651A:H01		RTA00000186AF.n.7.1	
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M00001677C:E10	14627	RTA00000187AF.g.23.1	
M00001679C:F01	78091	90.C7.sp6:130889.Seq	
M00001679C:F01	78091	RTA00000187AF.j.6.1	
M00001679C:F01	78091	176.G5.sp6:134588.Seq	
M00001686A:E06	4622	RTA00000187AF.m.15.2	
M00003796C:D05	5619	RTA00000188AF.I.9.1.Seq_THC167845	
M00003796C:D05	5619	RTA00000188AF.I.9.1	
M00003826B:A06	11350	RTA00000189AF.a.24.2	
M00003826B:A06	11350	90.F9.sp6:130927.Seq	
M00003833A:E05	21877	RTA00000189AF.b.21.1	
M00003837D:A01	7899	90.H9.sp6:130951.Seq	
M00003837D:A01	7899	RTA00000189AF.c.10.1	
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M00003846B:D06	6874	90.C10.sp6:130892.Seq	
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M00003879D:A02	14507	90.D12.sp6:130906.Seq	
M00003879D:A02	14507	RTA00000189AR.L23.2	
M00003891C:H09		90.G12.sp6:130942.Seq	
M00003891C:H09		RTA00000189AF.p.8.1	
M00003912B:D01	12532	99.D1.sp6:131266.Seq	
M00003912B:D01	12532	RTA00000190AF.g.2.1	
M00004072B:B05	17036	RTA00000191AF.j.10.1	
M00004081C:D12	14391	RTA00000191AF.I.7.1	
M00004111D:A08	6874	RTA00000192AF.a.14.1	

WO 99/33982		PCT/US98/27610
cDNA Library ES16 - ATCC#		
Deposit Date - December 22, 1998		
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M00004111D:A08	6874	99.F5.sp6:131294.Seq
M00004121B:G01		177.H4.sp6:134791.Seq
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M00004121B:G01		RTA00000192AF.c.2.1
M00004138B:H02	13272	99.A6.sp6:131235.Seq
M00004138B:H02	13272	RTA00000192AF.e.3.1
M00004151D:B08	16977	RTA00000192AF.g.3.1
M00004169C:C12	5319	99.E6.sp6:131283.Seq
M00004169C:C12	5319	RTA00000192AF.i.12.1
M00004169C:C12	5319	123.F7.sp6:132331.Seq
M00004183C:D07	16392	RTA00000192AF.l.1.1
M00004183C:D07	16392	RTA00000192AF.l.1.1.Seq_THC202071
M00004230B:C07	7212	RTA00000193AF.b.14.1
M00004230B:C07	7212	99.D8.sp6:131273.Seq
M00004249D:F10		RTA00000193AF.c.21.1.Seq_THC222602
M00004249D:F10		RTA00000193AF.c.21.1
M00004275C:C11	16914	99.A9.sp6:131238.Seq
M00004275C:C11	16914	RTA00000193AF.f.5.1
M00004283B:A04	14286	RTA00000193AF.f.22.1
M00004285B:E08	56020	RTA00000193AF.g.2.1
M00004327B:H04		RTA00000193AF.j.20.1
M00004377C:F05	2102	RTA00000193AF.n.7.1
M00004384C:D02		RTA00000193AF.n.15.1
M00004384C:D02		RTA00000193AF.n.15.1.Seq_THC215687
M00004461A:B08		RTA00000194AF.a.10.2
M00004461A:B09		RTA00000194AF.a.11.1
M00004691D:A05		RTA00000194AF.c.23.1
M00004896A:C07		RTA00000194AF.d.13.1

The above material has been deposited with the American Type Culture Collection, Rockville, Maryland, under the accession number indicated. This deposit will be maintained under the terms of the Budapest Treaty on the International Recognition of the Deposit of Microorganisms for purposes of Patent Procedure. The deposit will be maintained for a period of 30 years following issuance of this patent, or for the enforceable life of the patent, whichever is greater. Upon issuance of the patent, the deposit will be available to the public from the ATCC without restriction.

This deposit is provided merely as convenience to those of skill in the art, and is not an admission that a deposit is required under 35 U.S.C. §112. The sequence of the polynucleotides contained within the deposited material, as well as the amino acid sequence of the polypeptides encoded thereby, are incorporated herein by reference and are controlling in the event of any conflict with the written description of sequences herein. A license may

WO 99/33982

PCT/US98/27610

be required to make, use, or sell the deposited material, and no such license is granted hereby.

Retrieval of Individual Clones from Deposit of Pooled Clones

5 Where the ATCC deposit is composed of a pool of cDNA clones, the deposit was prepared by first transfecting each of the clones into separate bacterial cells. The clones were then deposited as a pool of equal mixtures in the composite deposit. Particular clones can be obtained from the composite deposit using methods well known in the art. For example, a bacterial cell containing a particular clone can be identified by isolating single
10 colonies, and identifying colonies containing the specific clone through standard colony hybridization techniques, using an oligonucleotide probe or probes designed to specifically hybridize to a sequence of the clone insert (*e.g.*, a probe based upon unmasked sequence of the encoded polynucleotide having the indicated SEQ ID NO). The probe should be designed to have a T_m of approximately 80°C (assuming 2°C for each A or T and 4°C for
15 each G or C). Positive colonies can then be picked, grown in culture, and the recombinant clone isolated. Alternatively, probes designed in this manner can be used to PCR to isolate a nucleic acid molecule from the pooled clones according to methods well known in the art, *e.g.*, by purifying the cDNA from the deposited culture pool, and using the probes in PCR reactions to produce an amplified product having the corresponding desired polynucleotide
20 sequence.

WO 99/33982

PCT/US98/27610

Table 1. Sequence identification numbers, cluster ID, sequence name, and clone name

SEQ ID NO:	Cluster ID	Sequence Name	Clone Name
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2		RTA00000185AF.n.12.1	M00001608D:A11
3	4622	RTA00000187AF.m.15.2	M00001686A:E06
4	3706	RTA00000191AF.i.17.2	M00004068B:A01
5	36535	RTA00000181AF.f.5.1	M00001449A:G10
6	3990	RTA00000183AF.j.11.1	M00001532B:A06
7	5319	RTA00000192AF.i.12.1	M00004169C:C12
8	36393	RTA00000180AF.c.2.1	M00001417A:E02
9	2623	RTA00000183AF.a.6.1	M00001497A:G02
10	7587	RTA00000178AF.n.24.1	M00001387B:G03
11	7065	RTA00000137A.g.6.1	M00001557A:D02
12	10539	RTA00000187AF.l.7.1	M00001680D:F08
13	27250	RTA00000181AF.g.10.1	M00001450A:D08
14	5556	RTA00000179AF.n.10.1	M00001407B:D11
15		RTA00000192AF.m.12.1	M00004191D:B11
16	8761	RTA00000184AF.k.12.1	M00001557D:D09
17	4622	RTA00000189AF.g.1.1	M00003856B:C02
18	11460	RTA00000187AF.g.12.1	M00001676B:F05
19	16283	RTA00000120A.o.20.1	M00001467A:D08
20	3430	RTA00000191AF.a.9.1	M00003981A:E10
21	7065	RTA00000184AF.j.21.1	M00001557A:D02
22		RTA00000182AF.l.20.1	M00001488B:F12
23		RTA00000123A.g.19.1	M00001531A:H11
24	16918	RTA00000193AF.a.16.1	M00004223A:G10
25	16914	RTA00000193AF.f.5.1	M00004275C:C11
26	40108	RTA00000187AF.o.24.1	M00003741D:C09
27	14286	RTA00000193AF.f.22.1	M00004283B:A04
28	17004	RTA00000186AF.b.21.1	M00001617C:E02
29		RTA00000180AF.g.22.1	M00001426B:D12
30	13272	RTA00000192AF.e.3.1	M00004138B:H02
31		RTA00000194AF.f.4.1	M00005180C:G03
32	32663	RTA00000118A.l.8.1	M00001450A:A11
33		RTA00000180AF.a.9.1	M00001414A:B01
34	5832	RTA00000178AF.o.23.1	M00001388D:G05
35	7801	RTA00000181AF.c.21.1	M00001446A:F05
36	76760	RTA00000187AF.a.15.1	M00001657D:F08
37	40132	RTA00000178AF.c.7.1	M00001365C:C10
38		RTA00000183AF.e.1.1	M00001505C:C05
39	4016	RTA00000118A.c.4.1	M00001395A:C03
40	5382	RTA00000187AF.m.23.2	M00001688C:F09

WO 99/33982			PCT/US98/27610
SEQ ID NO:	Cluster ID	Sequence Name	Clone Name
41	5693	RTA00000190AF.p.17.2	M00003978B:G05
42	307	RTA00000136A.o.4.2	M00001552A:B12
43	39833	RTA00000178AF.i.23.1	M00001378B:B02
44		RTA00000193AF.m.5.1	M00004359B:G02
45	5325	RTA00000191AF.o.6.1	M00004093D:B12
46	5325	RTA00000191AF.o.6.2	M00004093D:B12
47	18957	RTA00000190AR.m.9.1	M00003958A:H02
48	39508	RTA00000120A.o.2.1	M00001467A:D04
49	22390	RTA00000136A.j.13.1	M00001551A:G06
50	12170	RTA00000125A.h.18.4	M00001544A:E03
51	4393	RTA00000187AF.n.17.1	M00001693C:G01
52	19	RTA00000182AF.b.7.1	M00001463C:B11
53		RTA00000193AF.c.21.1	M00004249D:F10
54	7899	RTA00000189AF.c.10.1	M00003837D:A01
55	40073	RTA00000191AF.e.3.1	M00004028D:C05
56	7005	RTA00000179AF.o.22.1	M00001410A:D07
57		RTA00000187AF.h.22.1	M00001679A:F06
58	18957	RTA00000190AF.m.9.2	M00003958A:H02
59	18957	RTA00000183AF.h.23.1	M00001528A:F09
60	16283	RTA00000182AF.c.22.1	M00001467A:D08
61	6974	RTA00000183AF.d.9.1	M00001504C:H06
62	2623	RTA00000183AF.b.14.1	M00001500A:E11
63	9105	RTA00000191AF.a.21.2	M00003983A:A05
64	13238	RTA00000181AF.m.4.1	M00001455A:E09
65	5749	RTA00000185AF.a.19.1	M00001571C:H06
66	6455	RTA00000193AF.b.9.1	M00004229B:F08
67	23001	RTA00000185AF.c.24.1	M00001578B:E04
68	6455	RTA00000192AF.g.23.1	M00004157C:A09
69	13595	RTA00000189AF.f.8.1	M00003851B:D10
70	39442	RTA00000120A.o.21.1	M00001467A:E10
71	17036	RTA00000191AF.f.13.1	M00004035D:B06
72		RTA00000183AF.g.9.1	M00001513B:G03
73	7005	RTA00000181AF.k.24.1	M00001454B:C12
74	6268	RTA00000126A.o.23.1	M00001551A:B10
75	16130	RTA00000119A.c.13.1	M00001453A:E11
76	23201	RTA00000187AF.a.14.1	M00001657D:C03
77	5321	RTA00000183AF.k.8.1	M00001534A:F09
78	13157	RTA00000186AF.a.6.1	M00001614C:F10
79	2102	RTA00000193AF.n.7.1	M00004377C:F05
80	1058	RTA00000126A.e.20.3	M00001548A:H09
81	40392	RTA00000180AF.j.8.1	M00001429D:D07
82		RTA00000183AF.e.23.1	M00001506D:A09
83	11476	RTA00000187AF.p.19.1	M00003747D:C05

WO 99/33982			PCT/US98/27610
SEQ ID NO:	Cluster ID	Sequence Name	Clone Name
84	3584	RTA00000177AF.h.20.1	M00001349B:B08
85	10470	RTA00000180AF.f.18.1	M00001424B:G09
86	39425	RTA00000133A.f.1.1	M00001470A:C04
87	5175	RTA00000184AF.f.3.1	M00001550A:G01
88	13576	RTA00000189AF.o.13.1	M00003885C:A02
89	7665	RTA00000134A.l.19.1	M00001535A:B01
90	16927	RTA00000177AF.h.9.3	M00001348B:B04
91	6660	RTA00000187AF.h.15.1	M00001679A:A06
92	2433	RTA00000191AF.a.15.2	M00003982C:C02
93	5097	RTA00000134A.k.1.1	M00001534A:D09
94	21847	RTA00000193AF.j.9.1	M00004318C:D10
95	3277	RTA00000138A.l.5.1	M00001624A:B06
96	5708	RTA00000184AF.g.12.1	M00001552B:D04
97	945	RTA00000178A.a.20.1	M00001362C:H11
98	16269	RTA00000178AF.p.1.1	M00001389A:C08
99		RTA00000183AF.c.24.1	M00001504A:E01
100	16731	RTA00000181AF.a.20.1	M00001442C:D07
101	12439	RTA00000190AF.o.24.1	M00003975A:G11
102	3162	RTA00000177AF.j.12.3	M00001351B:A08
103		RTA00000194AF.b.19.1	M00004505D:F08
104		RTA00000193AF.n.15.1	M00004384C:D02
105		RTA00000186AF.n.7.1	M00001651A:H01
106	10717	RTA00000181AF.d.10.1	M00001447A:G03
107	4573	RTA00000189AF.j.12.1	M00003871C:E02
108		RTA00000186AF.h.14.1	M00001632D:H07
109	11443	RTA00000192AF.l.13.2	M00004185C:C03
110	5892	RTA00000184AF.d.11.1	M00001548A:E10
111	3162	RTA00000177AF.j.12.1	M00001351B:A08
112	10470	RTA00000185AF.k.6.1	M00001597D:C05
113	17055	RTA00000187AF.m.3.1	M00001682C:B12
114	2030	RTA00000193AF.m.20.1	M00004372A:A03
115	6558	RTA00000184AF.m.21.1	M00001560D:F10
116	23255	RTA00000190AF.j.4.1	M00003922A:E06
117	9577	RTA00000179AF.o.17.1	M00001409C:D12
118		RTA00000180AF.a.11.1	M00001414C:A07
119	8	RTA00000181AF.e.17.1	M00001448D:C09
120	67907	RTA00000188AF.g.11.1	M00003774C:A03
121	12081	RTA00000133A.d.14.2	M00001469A:C10
122	2448	RTA00000119A.j.21.1	M00001460A:F06
123	3389	RTA00000189AF.g.3.1	M00003857A:G10
124	39174	RTA00000124A.n.13.1	M00001541A:H03
125	24488	RTA00000190AF.n.16.1	M00003968B:F06
126	8210	RTA00000192AF.n.13.1	M00004197D:H01

WO 99/33982		PCT/US98/27610	
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128	40455	RTA00000190AF.m.10.2	M00003958C:G10
129	9577	RTA00000180AF.d.23.1	M00001421C:F01
130	13183	RTA00000192AF.a.24.1	M00004114C:F11
131	5214	RTA00000186AF.g.11.1	M00001630B:H09
132	67252	RTA00000187AF.o.6.1	M00001716D:H05
133	3108	RTA00000188AF.d.24.1	M00003763A:F06
134	2464	RTA00000178AF.n.18.1	M00001387A:C05
135	36313	RTA00000181AF.e.23.1	M00001448D:H01
136	23255	RTA00000177AF.e.14.3	M00001343D:H07
137	7985	RTA00000182AR.j.2.1	M00001481D:A05
138	8286	RTA00000183AF.o.1.1	M00001540A:D06
139	22195	RTA00000180AF.g.7.1	M00001425B:H08
140	4573	RTA00000184AF.h.9.1	M00001553B:F12
141	26875	RTA00000187AF.i.1.1	M00001679A:F10
142	7187	RTA00000177AF.i.8.2	M00001350A:H01
143	86859	RTA00000118A.p.8.1	M00001452A:B12
144	4623	RTA00000185AF.f.4.1	M00001586C:C05
145		RTA00000121A.c.10.1	M00001469A:A01
146	10185	RTA00000183AF.d.5.1	M00001504C:A07
147		RTA00000183AF.p.4.1	M00001542B:B01
148	15069	RTA00000191AF.l.6.1	M00004081C:D10
149	39304	RTA00000118A.j.21.1	M00001450A:A02
150	8672	RTA00000190AF.f.11.1	M00003909D:C03
151	13576	RTA00000177AF.g.16.1	M00001347A:B10
152	6293	RTA00000185AF.e.11.1	M00001583D:A10
153	16977	RTA00000192AF.g.3.1	M00004151D:B08
154	5345	RTA00000189AF.l.19.1	M00003879B:C11
155	4905	RTA00000193AF.e.14.1	M00004269D:D06
156	17036	RTA00000191AF.j.10.1	M00004072B:B05
157	5417	RTA00000191AF.h.19.1	M00004059A:D06
158	7172	RTA00000178AF.f.9.1	M00001371C:E09
159	40044	RTA00000186AF.d.1.1	M00001621C:C08
160	4386	RTA00000184AF.j.4.1	M00001556B:C08
161	40044	RTA00000183AF.g.22.1	M00001514C:D11
162	9685	RTA00000183AF.c.11.1	M00001501D:C02
163	22155	RTA00000185AF.n.9.1	M00001608B:E03
164	10515	RTA00000189AF.f.18.1	M00003853A:F12
165	6539	RTA00000185AF.d.11.1	M00001579D:C03
166	15066	RTA00000180AF.e.24.1	M00001423B:E07
167	4261	RTA00000180AF.h.5.1	M00001426D:C08
168	13864	RTA00000125A.m.9.1	M00001545A:D08
169	6539	RTA00000189AF.d.22.1	M00003844C:B11

WO 99/33982			PCT/US98/27610
SEQ ID NO:	Cluster ID	Sequence Name	Clone Name
170	11465	RTA00000185AF.m.19.1	M00001607A:E11
171	3266	RTA00000184AR.g.1.1	M00001551C:G09
172	102	RTA00000184AF.o.5.1	M00001563B:F06
173	16970	RTA00000181AR.i.18.2	M00001452C:B06
174	12971	RTA00000193AF.a.20.1	M00004223D:E04
175	5007	RTA00000177AF.g.2.1	M00001346A:F09
176	3765	RTA00000135A.d.1.1	M00001541A:D02
177	11294	RTA00000184AF.j.6.1	M00001556B:G02
178	3681	RTA00000131A.g.15.2	M00001449A:D12
179	9283	RTA00000181AR.m.21.2	M00001455D:F09
180	18699	RTA00000182AF.m.16.1	M00001490B:C04
181	86110	RTA00000181AF.f.12.1	M00001449C:D06
182	39648	RTA00000178AR.l.8.2	M00001383A:C03
183	7337	RTA00000123A.b.17.1	M00001528A:C04
184	1334	RTA00000178AF.j.7.1	M00001379A:A05
185	17076	RTA00000188AF.d.21.1	M00003762C:B08
186	22794	RTA00000138A.b.5.1	M00001601A:D08
187	39171	RTA00000186AF.l.7.1	M00001644C:B07
188	8551	RTA00000179AF.p.21.1	M00001412B:B10
189	5857	RTA00000118A.g.14.1	M00001449A:A12
190	9443	RTA00000183AF.c.1.1	M00001500C:E04
191	9457	RTA00000193AF.i.14.2	M00004307C:A06
192	7206	RTA00000182AF.o.15.1	M00001494D:F06
193	22979	RTA00000178AF.k.22.1	M00001382C:A02
194	40455	RTA00000190AR.m.10.1	M00003958C:G10
195	7221	RTA00000191AF.p.9.1	M00004105C:A04
196		RTA00000191AF.j.9.1	M00004072A:C03
197	7239	RTA00000126A.m.4.2	M00001550A:A03
198	31587	RTA00000189AF.l.20.1	M00003879B:D10
199	16317	RTA00000190AF.e.6.1	M00003907D:H04
200	13576	RTA00000189AR.o.13.1	M00003885C:A02
201	5779	RTA00000177AF.g.14.3	M00001346D:G06
202	6124	RTA00000191AR.e.2.3	M00004028D:A06
203	9952	RTA00000180AF.c.20.1	M00001418B:F03
204		RTA00000188AF.i.8.1	M00003784D:D12
205	5779	RTA00000177AF.g.14.1	M00001346D:G06
206	39490	RTA00000128A.b.4.1	M00001557A:F03
207	4416	RTA00000187AF.h.13.1	M00001678D:F12
208	4009	RTA00000179AF.e.20.1	M00001396A:C03
209	5336	RTA00000183AF.b.13.1	M00001500A:C05
210	39186	RTA00000121A.p.15.1	M00001512A:A09
211	40122	RTA00000190AF.n.23.1	M00003970C:B09
212	12532	RTA00000190AF.g.2.1	M00003912B:D01

WO 99/33982			PCT/US98/27610
SEQ ID NO:	Cluster ID	Sequence Name	Clone Name
213	8078	RTA00000177AR.l.13.1	M00001353A:G12
214	3900	RTA00000190AF.g.13.1	M00003914C:F05
215	7589	RTA00000120A.p.23.1	M00001468A:F05
216	8298	RTA00000127A.d.19.1	M00001553A:H06
217	4443	RTA00000177AF.b.20.4	M00001341A:E12
218	26295	RTA00000193AF.i.24.2	M00004312A:G03
219	3389	RTA00000183AF.m.19.1	M00001537B:G07
220	7015	RTA00000187AF.f.18.1	M00001673C:H02
221	8526	RTA00000180AF.d.1.1	M00001418D:B06
222	4665	RTA00000186AF.m.3.1	M00001648C:A01
223	1399	RTA00000129A.o.10.1	M00001604A:B10
224	9244	RTA00000127A.l.3.1	M00001556A:C09
225		RTA00000179AF.j.13.1	M00001400B:H06
226	82498	RTA00000118A.m.10.1	M00001450A:B12
227	35702	RTA00000187AR.c.15.2	M00001663A:E04
228	38759	RTA00000120A.m.12.3	M00001467A:B07
229	39648	RTA00000178AF.l.8.1	M00001383A:C03
230	19105	RTA00000133A.e.15.1	M00001469A:H12
231	85064	RTA00000191A.m.23.1	M00001452A:F05
232	9285	RTA00000191AF.m.18.1	M00004086D:G06
233	9285	RTA00000190AF.d.7.1	M00003906C:E10
234	39391	RTA00000138A.c.3.1	M00001604A:F05
235		RTA00000178AF.d.20.1	M00001368D:E03
236	39498	RTA00000119A.j.20.1	M00001460A:F12
237	7798	RTA00000189AF.k.12.1	M00003876D:E12
238	7798	RTA00000189AF.c.18.1	M00003839A:D08
239	19829	RTA00000125A.h.24.4	M00001544A:G02
240		RTA00000188AF.d.11.1	M00003761D:A09
241	4275	RTA00000120A.j.14.1	M00001466A:E07
242	22113	RTA00000125A.c.7.1	M00001542A:A09
243	40314	RTA00000186AF.c.15.1	M00001619C:F12
244	10944	RTA00000126A.h.17.2	M00001549A:D08
245	39809	RTA00000190AF.e.3.1	M00003907D:A09
246	22085	RTA00000135A.e.5.2	M00001541A:F07
247	19255	RTA00000135A.m.18.1	M00001545A:C03
248	14311	RTA00000192AF.o.2.1	M00004203B:C12
249	8479	RTA00000189AF.j.22.1	M00003875C:G07
250		RTA00000189AF.j.23.1	M00003875D:D11
251	4193	RTA00000184AF.e.13.1	M00001549B:F06
252	22814	RTA00000184AF.h.14.1	M00001553D:D10
253	39563	RTA00000179AF.k.20.1	M00001402A:E08
254	39420	RTA00000134A.o.23.1	M00001537A:F12
255	11589	RTA00000177AF.b.17.4	M00001340D:F10

WO 99/33982		PCT/US98/27610	
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256	4937	RTA00000191AF.p.21.1	M00004108A:E06
257	39412	RTA00000133A.k.17.1	M00001511A:H06
258	4837	RTA00000185AR.k.3.2	M00001597C:H02
259	13046	RTA00000193AF.b.19.1	M00004296C:H07
260	4141	RTA00000177AF.p.20.3	M00001361A:A05
261	38085	RTA00000123A.e.15.1	M00001531A:D01
262		RTA00000189AF.p.8.1	M00003891C:H09
263	11451	RTA00000192AF.p.17.1	M00004214C:H05
264	14507	RTA00000189AR.1.23.2	M00003879D:A02
265	40054	RTA00000180AF.p.10.1	M00001439C:F08
266	39423	RTA00000134A.k.22.1	M00001535A:F10
267	39453	RTA00000135A.g.11.1	M00001542A:E06
268	10751	RTA00000187AF.k.7.1	M00001679D:D03
269	10751	RTA00000187AF.k.6.1	M00001679D:D03
270	78091	RTA00000187AF.j.6.1	M00001679C:F01
271	39539	RTA00000127A.i.21.1	M00001555A:B02
272		RTA00000182AF.l.15.1	M00001487B:H06
273		RTA00000194AF.d.13.1	M00004896A:C07
274		RTA00000128A.c.20.1	M00001558A:H05
275	9283	RTA00000181AR.m.22.2	M00001455D:F09
276	39168	RTA00000121A.l.10.1	M00001507A:H05
277	39458	RTA00000126A.p.15.2	M00001552A:D11
278	14391	RTA00000177AF.m.17.3	M00001355B:G10
279	39195	RTA00000137A.c.16.1	M00001555A:C01
280	7212	RTA00000193AF.b.14.1	M00004230B:C07
281	4015	RTA00000136A.e.12.1	M00001549A:B02
282	12977	RTA00000189AF.j.19.1	M00003875B:F04
283		RTA00000178AF.m.13.1	M00001384B:A11
284	14391	RTA00000191AF.l.7.1	M00004081C:D12
285		RTA00000194AF.c.23.1	M00004691D:A05
286		RTA00000181AF.b.7.1	M00001443B:F01
287	8358	RTA00000183AF.i.5.1	M00001528B:H04
288	1267	RTA00000125A.o.5.1	M00001546A:G11
289		RTA00000189AF.f.7.1	M00003851B:D08
290	16347	RTA00000184AF.e.15.1	M00001549C:E06
291	7899	RTA00000193AF.a.17.1	M00004223B:D09
292	2379	RTA00000178AF.a.6.1	M00001361D:F08
293	39478	RTA00000133A.i.5.1	M00001471A:B01
294	39392	RTA00000134A.m.16.1	M00001536A:C08
295	5053	RTA00000184AF.o.12.1	M00001564A:B12
296	16999	RTA00000185AF.k.9.1	M00001598A:G03
297	39180	RTA00000126A.n.8.2	M00001551A:F05
298	1037	RTA00000121A.f.8.1	M00001470A:B10

WO 99/33982			PCT/US98/27610
SEQ ID NO:	Cluster ID	Sequence Name	Clone Name
299	6867	RTA00000178AF.e.12.1	M00001370A:C09
300	10539	RTA00000183AF.a.24.1	M00001499B:A11
301	41633	RTA00000118A.g.16.1	M00001449A:B12
302	23218	RTA00000187AR.c.5.2	M00001662C:A09
303	39380	RTA00000129A.c.24.1	M00001587A:B11
304		RTA00000185AF.d.24.1	M00001582D:F05
305		RTA00000177AF.o.4.3	M00001358C:C06
306	6974	RTA00000184AF.a.15.1	M00001544B:B07
307		RTA00000185AF.g.11.1	M00001590B:F03
308	15855	RTA00000184AF.j.1.1	M00001556A:H01
309	84328	RTA00000118A.p.10.1	M00001452A:B04
310	10145	RTA00000120A.g.12.1	M00001465A:B11
311	39805	RTA00000177AF.c.21.3	M00001342B:E06
312		RTA00000187AF.h.23.1	M00001679A:F06
313	6298	RTA00000187AR.i.10.2	M00001679B:F01
314	14367	RTA00000187AF.e.8.1	M00001670C:H02
315		RTA00000193AF.c.22.1	M00004249D:G12
316	16921	RTA00000183AF.k.6.1	M00001534A:C04
317	1577	RTA00000184AF.i.23.1	M00001556A:F11
318	8773	RTA00000187AF.f.24.1	M00001675A:C09
319		RTA00000194AF.a.11.1	M00004461A:B09
320	39886	RTA00000178AF.j.24.1	M00001380D:B09
321	13532	RTA00000181AF.c.4.1	M00001445A:F05
322		RTA00000193AF.d.2.1	M00004251C:G07
323	5257	RTA00000192AF.f.3.1	M00004146C:C11
324	9061	RTA00000191AR.e.11.2	M00004031A:A12
325	19267	RTA00000186AF.l.12.1	M00001645A:C12
326	20212	RTA00000134A.L22.1	M00001535A:C06
327	16653	RTA00000181AF.k.5.3	M00001453C:F06
328	16985	RTA00000177AF.h.10.1	M00001348B:G06
329	12977	RTA00000189AR.j.19.1	M00003875B:F04
330	9061	RTA00000191AR.e.11.3	M00004031A:A12
331		RTA00000194AR.a.10.2	M00004461A:B08
332	6468	RTA00000187AF.d.15.1	M00001669B:F02
333	16392	RTA00000192AF.l.1.1	M00004183C:D07
334	14627	RTA00000187AF.g.23.1	M00001677C:E10
335	6583	RTA00000179AF.d.13.1	M00001394A:F01
336	6806	RTA00000177AF.g.13.3	M00001346D:E03
337	9635	RTA00000137A.c.23.4	M00001557A:F01
338	689	RTA00000181AR.L22.1	M00001454D:G03
339	4119	RTA00000183AF.k.16.1	M00001534C:A01
340	8952	RTA00000183AF.h.15.1	M00001518C:B11
341	2379	RTA00000192AF.p.8.1	M00004212B:C07

WO 99/33982			PCT/US98/27610
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342	39486	RTA00000128A.m.22.2	M00001561A:C05
343	21877	RTA00000189AF.b.21.1	M00003833A:E05
344	6874	RTA00000192AF.a.14.1	M00004111D:A08
345	6874	RTA00000189AF.e.9.1	M00003846B:D06
346	37285	RTA00000191AF.f.11.1	M00004035C:A07
347		RTA00000193AF.j.20.1	M00004327B:H04
348	7674	RTA00000118A.g.9.1	M00001416A:H01
349	2797	RTA00000180AF.i.19.1	M00001429A:H04
350		RTA00000184AF.g.22.1	M00001552D:A01
351	7802	RTA00000185AF.n.5.1	M00001608A:B03
352	16921	RTA00000193AF.h.15.1	M00004295D:F12
353	11494	RTA00000192AF.j.6.1	M00004172C:D08
354	17062	RTA00000177AF.b.8.4	M00001340B:A06
355	16245	RTA00000177AF.k.9.3	M00001352A:E02
356	83103	RTA00000119A.e.24.2	M00001454A:A09
357	4309	RTA00000186AF.e.22.1	M00001624C:F01
358	13072	RTA00000181AR.m.5.2	M00001455B:E12
359	4059	RTA00000177AF.n.18.3	M00001357D:D11
360	5178	RTA00000178AF.n.10.1	M00001386C:B12
361	1120	RTA00000118A.p.15.3	M00001452A:D08
362	6420	RTA00000183AF.d.11.1	M00001504D:G06
363	13913	RTA00000186AF.e.6.1	M00001623D:F10
364		RTA00000192AF.c.2.1	M00004121B:G01
365	3956	RTA00000183AF.g.3.1	M00001512D:G09
366	14364	RTA00000183AF.g.12.1	M00001513C:E08
367	6880	RTA00000191AF.m.20.1	M00004087D:A01
368	84182	RTA00000180AF.h.19.1	M00001428A:H10
369	2790	RTA00000177AF.e.2.1	M00001343C:F10
370	4561	RTA00000184AF.i.21.1	M00001555D:G10
371	8847	RTA00000180AF.b.16.1	M00001416B:H11
372	56020	RTA00000193AF.g.2.1	M00004285B:E08
373	1531	RTA00000119A.o.3.1	M00001461A:D06
374	6420	RTA00000177AF.f.10.3	M00001345A:E01
375		RTA00000188AF.b.12.1	M00003754C:E09
376		RTA00000180AF.k.24.1	M00001432C:F06
377		RTA00000184AF.a.8.1	M00001544A:E06
378	2696	RTA00000134A.m.13.1	M00001536A:B07
379	260	RTA00000185AR.i.12.2	M00001594B:H04
380	11350	RTA00000189AF.a.24.2	M00003826B:A06
381	2428	RTA00000123A.l.21.1	M00001533A:C11
382	4313	RTA00000122A.n.3.1	M00001517A:B07
383		RTA00000184AF.p.3.1	M00001566B:D11
384	697	RTA00000188AF.d.6.1	M00003759B:B09

WO 99/33982			PCT/US98/27610
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385	5619	RTA00000188AF.I.9.1	M00003796C:D05
386	4568	RTA00000122A.d.15.3	M00001513A:B06
387		RTA00000177AF.i.6.2	M00001350A:B08
388	5622	RTA00000178AF.a.11.1	M00001362B:D10
389	7514	RTA00000184AF.k.21.1	M00001558B:H11
390	5619	RTA00000189AF.f.17.1	M00003853A:D04
391	7570	RTA00000187AF.g.24.1	M00001677D:A07
392	23358	RTA00000190AF.o.21.1	M00003974D:H02
393	23210	RTA00000190AF.o.20.1	M00003974D:E07
394	5192	RTA00000184AF.k.2.1	M00001557B:H10
395	13538	RTA00000180AF.a.24.1	M00001415A:H06
396		RTA00000189AF.h.17.1	M00003867A:D10
397		RTA00000192AF.o.11.1	M00004205D:F06
398		RTA00000184AF.l.11.1	M00001559B:F01
399	4718	RTA00000189AF.g.5.1	M00003857A:H03
400	14929	RTA00000177AF.m.1.2	M00001353D:D10
401	4908	RTA00000192AF.j.2.1	M00004171D:B03
402		RTA00000178AF.k.16.1	M00001381D:E06
403		RTA00000194AF.c.24.1	M00004692A:H08
404	17732	RTA00000178AR.i.2.2	M00001376B:G06
405	17062	80.A1.sp6:130208.Seq	M00001340B:A06
406	11589	80.B1.sp6:130220.Seq	M00001340D:F10
407	4443	80.C1.sp6:130232.Seq	M00001341A:E12
408	39805	80.D1.sp6:130244.Seq	M00001342B:E06
409	2790	80.E1.sp6:130256.Seq	M00001343C:F10
410	23255	80.F1.sp6:130268.Seq	M00001343D:H07
411	6420	80.G1.sp6:130280.Seq	M00001345A:E01
412	5007	80.H1.sp6:130292.Seq	M00001346A:F09
413	13576	80.D2.sp6:130245.Seq	M00001347A:B10
414	16927	80.E2.sp6:130257.Seq	M00001348B:B04
415	16985	80.F2.sp6:130269.Seq	M00001348B:G06
416	3584	80.G2.sp6:130281.Seq	M00001349B:B08
417		80.H2.sp6:130293.Seq	M00001350A:B08
418	7187	80.A3.sp6:130210.Seq	M00001350A:H01
419	16245	80.D3.sp6:130246.Seq	M00001352A:E02
420	8078	80.E3.sp6:130258.Seq	M00001353A:G12
421	14929	80.F3.sp6:130270.Seq	M00001353D:D10
422	14391	80.G3.sp6:130282.Seq	M00001355B:G10
423	4141	80.B4.sp6:130223.Seq	M00001361A:A05
424	2379	80.C4.sp6:130235.Seq	M00001361D:F08
425	5622	80.D4.sp6:130247.Seq	M00001362B:D10
426	945	80.E4.sp6:130259.Seq	M00001362C:H11
427	40132	80.F4.sp6:130271.Seq	M00001365C:C10

WO 99/33982		PCT/US98/27610	
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428		80.G4.sp6:130283.Seq	M00001368D:E03
429	6867	80.H4.sp6:130295.Seq	M00001370A:C09
430	7172	80.A5.sp6:130212.Seq	M00001371C:E09
431	17732	80.B5.sp6:130224.Seq	M00001376B:G06
432	39833	80.C5.sp6:130236.Seq	M00001378B:B02
433	1334	80.D5.sp6:130248.Seq	M00001379A:A05
434	39886	80.E5.sp6:130260.Seq	M00001380D:B09
435		80.F5.sp6:130272.Seq	M00001381D:E06
436	22979	80.G5.sp6:130284.Seq	M00001382C:A02
437	39648	80.H5.sp6:130296.Seq	M00001383A:C03
438		80.B6.sp6:130225.Seq	M00001384B:A11
439	5178	80.C6.sp6:130237.Seq	M00001386C:B12
440	2464	80.D6.sp6:130249.Seq	M00001387A:C05
441	7587	80.E6.sp6:130261.Seq	M00001387B:G03
442	5832	80.F6.sp6:130273.Seq	M00001388D:G05
443	16269	80.G6.sp6:130285.Seq	M00001389A:C08
444	6583	80.H6.sp6:130297.Seq	M00001394A:F01
445	4009	80.A7.sp6:130214.Seq	M00001396A:C03
446		80.B7.sp6:130226.Seq	M00001400B:H06
447	39563	80.C7.sp6:130238.Seq	M00001402A:E08
448	5556	80.D7.sp6:130250.Seq	M00001407B:D11
449	9577	80.E7.sp6:130262.Seq	M00001409C:D12
450	7005	80.F7.sp6:130274.Seq	M00001410A:D07
451	8551	80.G7.sp6:130286.Seq	M00001412B:B10
452		80.H7.sp6:130298.Seq	M00001414A:B01
453		80.A8.sp6:130215.Seq	M00001414C:A07
454	13538	80.B8.sp6:130227.Seq	M00001415A:H06
455	8847	80.C8.sp6:130239.Seq	M00001416B:H11
456	36393	80.D8.sp6:130251.Seq	M00001417A:E02
457	9952	80.E8.sp6:130263.Seq	M00001418B:F03
458	9577	80.G8.sp6:130287.Seq	M00001421C:F01
459	15066	80.H8.sp6:130299.Seq	M00001423B:E07
460	10470	80.A9.sp6:130216.Seq	M00001424B:G09
461	22195	80.B9.sp6:130228.Seq	M00001425B:H08
462		80.C9.sp6:130240.Seq	M00001426B:D12
463	4261	80.D9.sp6:130252.Seq	M00001426D:C08
464	84182	80.E9.sp6:130264.Seq	M00001428A:H10
465	40392	80.H9.sp6:130300.Seq	M00001429D:D07
466	16731	80.C10.sp6:130241.Seq	M00001442C:D07
467		80.D10.sp6:130253.Seq	M00001443B:F01
468	13532	80.E10.sp6:130265.Seq	M00001445A:F05
469	8	80.H10.sp6:130301.Seq	M00001448D:C09
470	36313	80.A11.sp6:130218.Seq	M00001448D:H01

WO 99/33982			PCT/US98/27610
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473	36535	80.D11.sp6:130254.Seq	M00001449A:G10
474	86110	80.E11.sp6:130266.Seq	M00001449C:D06
475	32663	80.F11.sp6:130278.Seq	M00001450A:A11
476	27250	80.G11.sp6:130290.Seq	M00001450A:D08
477	16970	80.H11.sp6:130302.Seq	M00001452C:B06
478	16130	80.A12.sp6:130219.Seq	M00001453A:E11
479	16653	80.B12.sp6:130231.Seq	M00001453C:F06
480	7005	80.C12.sp6:130243.Seq	M00001454B:C12
481	13072	80.F12.sp6:130279.Seq	M00001455B:E12
482	9283	80.G12.sp6:130291.Seq	M00001455D:F09
483	23255	100.C1.sp6:131446.Seq	M00001343D:H07
484	13576	100.E1.sp6:131470.Seq	M00001347A:B10
485	7187	100.C2.sp6:131447.Seq	M00001350A:H01
486	14391	100.E3.sp6:131472.Seq	M00001355B:G10
487	945	100.E4.sp6:131473.Seq	M00001362C:H11
488	7172	100.A5.sp6:131426.Seq	M00001371C:E09
489	39648	100.A6.sp6:131427.Seq	M00001383A:C03
490	84182	100.G9.sp6:131502.Seq	M00001428A:H10
491	8	100.B11.sp6:131444.Seq	M00001448D:C09
492	36535	100.D11.sp6:131468.Seq	M00001449A:G10
493	82498	100.F11.sp6:131492.Seq	M00001450A:B12
494	16970	100.C12.sp6:131457.Seq	M00001452C:B06
495	16130	100.D12.sp6:131469.Seq	M00001453A:E11
496	7005	121.D1.sp6:131917.Seq	M00001454B:C12
497		121.G6.sp6:131958.Seq	M00001506D:A09
498	18957	121.F7.sp6:131947.Seq	M00001528A:F09
499	40044	122.E1.sp6:132121.Seq	M00001621C:C08
500	5214	122.C2.sp6:132098.Seq	M00001630B:H09
501	6660	122.B5.sp6:132089.Seq	M00001679A:A06
502	13183	123.D5.sp6:132305.Seq	M00004114C:F11
503	6455	123.E7.sp6:132319.Seq	M00004157C:A09
504	5319	123.F7.sp6:132331.Seq	M00004169C:C12
505	11443	123.A8.sp6:132272.Seq	M00004185C:C03
506		123.C8.sp6:132296.Seq	M00004191D:B11
507	8210	123.E8.sp6:132320.Seq	M00004197D:H01
508	9457	123.D11.sp6:132311.Seq	M00004307C:A06
509	6420	172.E1.sp6:133925.Seq	M00001345A:E01
510	16245	172.D2.sp6:133914.Seq	M00001352A:E02
511	8078	172.C3.sp6:133903.Seq	M00001353A:G12
512	14929	172.D3.sp6:133915.Seq	M00001353D:D10
513	14391	172.H3.sp6:133963.Seq	M00001355B:G10

WO 99/33982			PCT/US98/27610
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517		176.A3.sp6:134514.Seq	M00001632D:H07
518	19267	176.G3.sp6:134586.Seq	M00001645A:C12
519	78091	176.G5.sp6:134588.Seq	M00001679C:F01
520	17055	176.D6.sp6:134553.Seq	M00001682C:B12
521	6539	176.D9.sp6:134556.Seq	M00003844C:B11
522		177.H4.sp6:134791.Seq	M00004121B:G01
523	5257	177.F5.sp6:134768.Seq	M00004146C:C11
524	11494	177.E6.sp6:134757.Seq	M00004172C:D08
525		177.G7.sp6:134782.Seq	M00004205D:F06
526	11451	177.D8.sp6:134747.Seq	M00004214C:H05
527	9283	173.D2.SP6:134106.Seq	M00001455D:F09
528	16283	173.F3.SP6:134131.Seq	M00001467A:D08
529	10539	173.B5.SP6:134085.Seq	M00001499B:A11
530	6420	173.F5.SP6:134133.Seq	M00001504D:G06
531	3956	173.H5.SP6:134157.Seq	M00001512D:G09
532		173.G7.SP6:134147.Seq	M00001544A:E06
533	1577	173.C9.SP6:134101.Seq	M00001556A:F11
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535	5192	173.E9.SP6:134125.Seq	M00001557B:H10
536	6539	173.A12.SP6:134080.Seq	M00001579D:C03
537	945	180.C2.sp6:135940.Seq	M00001362C:H11
538	7005	180.H5.sp6:136003.Seq	M00001410A:D07
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542	19255	184.B10.sp6:135547.Seq	M00001545A:C03
543	6268	184.C12.sp6:135561.Seq	M00001551A:B10
544	3277	217.E1.sp6:139406.Seq	M00001624A:B06
545	39171	217.A12.sp6:139369.Seq	M00001644C:B07
546	11460	219.F2.sp6:139035.Seq	M00001676B:F05
547	10539	219.F6.sp6:139039.Seq	M00001680D:F08
548	11476	219.H8.sp6:139065.Seq	M00003747D:C05
549	4016	79.A1.sp6:130016.Seq	M00001395A:C03
550	7674	79.C1.sp6:130040.Seq	M00001416A:H01
551	3681	79.E1.sp6:130064.Seq	M00001449A:D12
552	39304	79.F1.sp6:130076.Seq	M00001450A:A02
553	82498	79.G1.sp6:130088.Seq	M00001450A:B12
554	84328	79.A2.sp6:130017.Seq	M00001452A:B04
555	86859	79.B2.sp6:130029.Seq	M00001452A:B12
556	1120	79.C2.sp6:130041.Seq	M00001452A:D08

WO 99/33982			PCT/US98/27610
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559	10145	79.F3.sp6:130078.Seq	M00001465A:B11
560	16283	79.H3.sp6:130102.Seq	M00001467A:D08
561	4568	79.D4.sp6:130055.Seq	M00001513A:B06
562	4313	79.F4.sp6:130079.Seq	M00001517A:B07
563	2428	79.A5.sp6:130020.Seq	M00001533A:C11
564	39423	79.C5.sp6:130044.Seq	M00001535A:F10
565	39174	79.E5.sp6:130068.Seq	M00001541A:H03
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568	13864	79.B6.sp6:130033.Seq	M00001545A:D08
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571	39180	79.A7.sp6:130022.Seq	M00001551A:F05
572	307	79.C7.sp6:130046.Seq	M00001552A:B12
573	39458	79.D7.sp6:130058.Seq	M00001552A:D11
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575	39486	79.B8.sp6:130035.Seq	M00001561A:C05
576	39380	79.E8.sp6:130071.Seq	M00001587A:B11
577	1399	79.G8.sp6:130095.Seq	M00001604A:B10
578	39391	79.A9.sp6:130024.Seq	M00001604A:F05
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586	16283	89.H1.sp6:130751.Seq	M00001467A:D08
587	39442	89.A2.sp6:130668.Seq	M00001467A:E10
588	7589	89.B2.sp6:130680.Seq	M00001468A:F05
589		89.C2.sp6:130692.Seq	M00001469A:A01
590	12081	89.D2.sp6:130704.Seq	M00001469A:C10
591	19105	89.E2.sp6:130716.Seq	M00001469A:H12
592	1037	89.F2.sp6:130728.Seq	M00001470A:B10
593	39425	89.G2.sp6:130740.Seq	M00001470A:C04
594	39478	89.H2.sp6:130752.Seq	M00001471A:B01
595		89.B3.sp6:130681.Seq	M00001487B:H06
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597	18699	89.D3.sp6:130705.Seq	M00001490B:C04
598	7206	89.E3.sp6:130717.Seq	M00001494D:F06
599	2623	89.F3.sp6:130729.Seq	M00001497A:G02

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604	9685	89.C4.sp6:130694.Seq	M00001501D:C02
605		89.D4.sp6:130706.Seq	M00001504A:E01
606	10185	89.E4.sp6:130718.Seq	M00001504C:A07
607	6974	89.F4.sp6:130730.Seq	M00001504C:H06
608	6420	89.G4.sp6:130742.Seq	M00001504D:G06
609		89.H4.sp6:130754.Seq	M00001505C:C05
610		89.A5.sp6:130671.Seq	M00001506D:A09
611	39168	89.B5.sp6:130683.Seq	M00001507A:H05
612	39412	89.C5.sp6:130695.Seq	M00001511A:H06
613	39186	89.D5.sp6:130707.Seq	M00001512A:A09
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616	14364	89.G5.sp6:130743.Seq	M00001513C:E08
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619	35555	89.B6.sp6:130684.Seq	M00001528A:C04
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624	3990	89.G6.sp6:130744.Seq	M00001532B:A06
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627	4119	89.C7.sp6:130697.Seq	M00001534C:A01
628	20212	89.E7.sp6:130721.Seq	M00001535A:C06
629	2696	89.F7.sp6:130733.Seq	M00001536A:B07
630	39392	89.G7.sp6:130745.Seq	M00001536A:C08
631	39420	89.H7.sp6:130757.Seq	M00001537A:F12
632	3389	89.A8.sp6:130674.Seq	M00001537B:G07
633	8286	89.B8.sp6:130686.Seq	M00001540A:D06
634	3765	89.C8.sp6:130698.Seq	M00001541A:D02
635	39453	89.E8.sp6:130722.Seq	M00001542A:E06
636		89.F8.sp6:130734.Seq	M00001542B:B01
637		89.H8.sp6:130758.Seq	M00001544A:E06
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639		89.B9.sp6:130687.Seq	M00001545A:B02
640	19255	89.C9.sp6:130699.Seq	M00001545A:C03
641	1267	89.D9.sp6:130711.Seq	M00001546A:G11
642	5892	89.E9.sp6:130723.Seq	M00001548A:E10

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645	7239	89.A10.sp6:130676.Seq	M00001550A:A03	
646	5175	89.B10.sp6:130688.Seq	M00001550A:G01	
647	22390	89.C10.sp6:130700.Seq	M00001551A:G06	
648	3266	89.D10.sp6:130712.Seq	M00001551C:G09	
649	5708	89.E10.sp6:130724.Seq	M00001552B:D04	
650		89.F10.sp6:130736.Seq	M00001552D:A01	
651	8298	89.G10.sp6:130748.Seq	M00001553A:H06	
652	4573	89.H10.sp6:130760.Seq	M00001553B:F12	
653	22814	89.A11.sp6:130677.Seq	M00001553D:D10	
654	39539	89.B11.sp6:130689.Seq	M00001555A:B02	
655	39195	89.C11.sp6:130701.Seq	M00001555A:C01	
656	4561	89.D11.sp6:130713.Seq	M00001555D:G10	
657	9244	89.E11.sp6:130725.Seq	M00001556A:C09	
658	1577	89.F11.sp6:130737.Seq	M00001556A:F11	
659	4386	89.H11.sp6:130761.Seq	M00001556B:C08	
660	11294	89.A12.sp6:130678.Seq	M00001556B:G02	
661	5192	89.D12.sp6:130714.Seq	M00001557B:H10	
662	8761	89.E12.sp6:130726.Seq	M00001557D:D09	
663		89.F12.sp6:130738.Seq	M00001558A:H05	
664	7514	89.G12.sp6:130750.Seq	M00001558B:H11	
665		89.H12.sp6:130762.Seq	M00001559B:F01	
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667	102	90.B1.sp6:130871.Seq	M00001563B:F06	
668		90.D1.sp6:130895.Seq	M00001566B:D11	
669	5749	90.E1.sp6:130907.Seq	M00001571C:H06	
670	6539	90.G1.sp6:130931.Seq	M00001579D:C03	
671	6293	90.A2.sp6:130860.Seq	M00001583D:A10	
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673	260	90.D2.sp6:130896.Seq	M00001594B:H04	
674	4837	90.E2.sp6:130908.Seq	M00001597C:H02	
675	10470	90.F2.sp6:130920.Seq	M00001597D:C05	
676	16999	90.G2.sp6:130932.Seq	M00001598A:G03	
677	22794	90.H2.sp6:130944.Seq	M00001601A:D08	
678	11465	90.A3.sp6:130861.Seq	M00001607A:E11	
679	7802	90.B3.sp6:130873.Seq	M00001608A:B03	
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684	40314	90.G3.sp6:130933.Seq	M00001619C:F12	
685	40044	90.H3.sp6:130945.Seq	M00001621C:C08	

WO 99/33982			PCT/US98/27610
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689	5214	90.D4.sp6:130898.Seq	M00001630B:H09
690		90.E4.sp6:130910.Seq	M00001632D:H07
691	39171	90.F4.sp6:130922.Seq	M00001644C:B07
692	19267	90.G4.sp6:130934.Seq	M00001645A:C12
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697	23218	90.D5.sp6:130899.Seq	M00001662C:A09
698	35702	90.E5.sp6:130911.Seq	M00001663A:E04
699	6468	90.F5.sp6:130923.Seq	M00001669B:F02
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703	11460	90.B6.sp6:130876.Seq	M00001676B:F05
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705	4416	90.E6.sp6:130912.Seq	M00001678D:F12
706	6660	90.F6.sp6:130924.Seq	M00001679A:A06
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727	7899	90.H9.sp6:130951.Seq	M00003837D:A01
728	7798	90.A10.sp6:130868.Seq	M00003839A:D08

WO 99/33982			PCT/US98/27610
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733	5619	90.F10.sp6:130928.Seq	M00003853A:D04
734	10515	90.G10.sp6:130940.Seq	M00003853A:F12
735	4622	90.H10.sp6:130952.Seq	M00003856B:C02
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741		90.H11.sp6:130953.Seq	M00003875D:D11
742	7798	90.A12.sp6:130870.Seq	M00003876D:E12
743	5345	90.B12.sp6:130882.Seq	M00003879B:C11
744	31587	90.C12.sp6:130894.Seq	M00003879B:D10
745	14507	90.D12.sp6:130906.Seq	M00003879D:A02
746	13576	90.F12.sp6:130930.Seq	M00003885C:A02
747		90.G12.sp6:130942.Seq	M00003891C:H09
748	9285	90.H12.sp6:130954.Seq	M00003906C:E10
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751	8672	99.C1.sp6:131254.Seq	M00003909D:C03
752	12532	99.D1.sp6:131266.Seq	M00003912B:D01
753	3900	99.E1.sp6:131278.Seq	M00003914C:F05
754	23255	99.F1.sp6:131290.Seq	M00003922A:E06
755	24488	99.C2.sp6:131255.Seq	M00003968B:F06
756	40122	99.D2.sp6:131267.Seq	M00003970C:B09
757	23210	99.E2.sp6:131279.Seq	M00003974D:E07
758	23358	99.F2.sp6:131291.Seq	M00003974D:H02
759	3430	99.A3.sp6:131232.Seq	M00003981A:E10
760	2433	99.B3.sp6:131244.Seq	M00003982C:C02
761	9105	99.C3.sp6:131256.Seq	M00003983A:A05
762	6124	99.D3.sp6:131268.Seq	M00004028D:A06
763	40073	99.E3.sp6:131280.Seq	M00004028D:C05
764	37285	99.H3.sp6:131316.Seq	M00004035C:A07
765	17036	99.A4.sp6:131233.Seq	M00004035D:B06
766	3706	99.C4.sp6:131257.Seq	M00004068B:A01
767		99.D4.sp6:131269.Seq	M00004072A:C03
768	15069	99.F4.sp6:131293.Seq	M00004081C:D10
769	9285	99.H4.sp6:131317.Seq	M00004086D:G06
770	6880	99.A5.sp6:131234.Seq	M00004087D:A01
771	5325	99.C5.sp6:131258.Seq	M00004093D:B12

WO 99/33982			PCT/US98/27610
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774	6874	99.F5.sp6:131294.Seq	M00004111D:A08
775	13183	99.G5.sp6:131306.Seq	M00004114C:F11
776		99.H5.sp6:131318.Seq	M00004121B:G01
777	13272	99.A6.sp6:131235.Seq	M00004138B:H02
778	5257	99.B6.sp6:131247.Seq	M00004146C:C11
779	6455	99.D6.sp6:131271.Seq	M00004157C:A09
780	5319	99.E6.sp6:131283.Seq	M00004169C:C12
781	4908	99.F6.sp6:131295.Seq	M00004171D:B03
782	11494	99.G6.sp6:131307.Seq	M00004172C:D08
783	11443	99.A7.sp6:131236.Seq	M00004185C:C03
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791	4905	99.H8.sp6:131321.Seq	M00004269D:D06
792	16914	99.A9.sp6:131238.Seq	M00004275C:C11
793	16921	99.D9.sp6:131274.Seq	M00004295D:F12
794	13046	99.E9.sp6:131286.Seq	M00004296C:H07
795	9457	99.F9.sp6:131298.Seq	M00004307C:A06
796	26295	99.G9.sp6:131310.Seq	M00004312A:G03
797	21847	99.H9.sp6:131322.Seq	M00004318C:D10
798		99.H10.sp6:131323.Seq	M00004505D:F08
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803	1058	RTA00000126A.e.20.3.Seq_THC217534	
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805	20212	RTA00000134A.l.22.1.Seq_THC128232	
806	23255	RTA00000177AF.e.14.3.Seq_THC228776	
807	2790	RTA00000177AF.e.2.1.Seq_THC229461	
808	6420	RTA00000177AF.f.10.3.Seq_THC226443	
809	4059	RTA00000177AF.n.18.3.Seq_THC123051	
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811	9952	RTA00000180AF.c.20.1.Seq_THC162284	
812	13238	RTA00000181AF.m.4.1.Seq_THC140691	
813	9685	RTA00000183AF.c.11.1.Seq_THC109544	
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WO 99/33982		PCT/US98/27610	
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818		RTA00000183AF.g.9.1.Seq_THC198280	
819	5892	RTA00000184AF.d.11.1.Seq_THC161896	
820	40044	RTA00000186AF.d.1.1.Seq_THC232899	
821		RTA00000186AF.h.14.1.Seq_THC112525	
822	19267	RTA00000186AF.l.12.1.Seq_THC178183	
823	8773	RTA00000187AF.f.24.1.Seq_THC220002	
824	7570	RTA00000187AF.g.24.1.Seq_THC168636	
825	11476	RTA00000187AF.p.19.1.Seq_THC108482	
826		RTA00000188AF.d.11.1.Seq_THC212094	
827	17076	RTA00000188AF.d.21.1.Seq_THC208760	
828	697	RTA00000188AF.d.6.1.Seq_THC178884	
829	67907	RTA00000188AF.g.11.1.Seq_THC123222	
830	5619	RTA00000188AF.l.9.1.Seq_THC167845	
831	4718	RTA00000189AF.g.5.1.Seq_THC196102	
832	39809	RTA00000190AF.e.3.1.Seq_THC150217	
833	23255	RTA00000190AF.j.4.1.Seq_THC228776	
834	40122	RTA00000190AF.n.23.1.Seq_THC109227	
835	23210	RTA00000190AF.o.20.1.Seq_THC207240	
836	23358	RTA00000190AF.o.21.1.Seq_THC207240	
837	5693	RTA00000190AF.p.17.2.Seq_THC173318	
838	2433	RTA00000191AF.a.15.2.Seq_THC79498	
839	5257	RTA00000192AF.f.3.1.Seq_THC213833	
840	16392	RTA00000192AF.l.1.1.Seq_THC202071	
841		RTA00000193AF.c.21.1.Seq_THC222602	
842	26295	RTA00000193AF.i.24.2.Seq_THC197345	
843		RTA00000193AF.m.5.1.Seq_THC173318	
844		RTA00000193AF.n.15.1.Seq_THC215687	

WO 99/33982

PCT/US98/27610

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
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4	<NONE>	<NONE>	<NONE>	BAR3_CHITE	BALBIANI RING PROTEIN 3 PRECURSOR>PIR2:S08167 Balbiani ring 3 protein - midge (Chironomus tentans)>GP:CTBR3_1 C.tentans balbiani ring 3 (BR3) gene	1
5	<NONE>	<NONE>	<NONE>	CYAA_PODAN	ADENYLATE CYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATYLASE) (ADENYL CYCLASE)>PIR2:JC4747 adenylate cyclase (EC 4.6.1.1) - Podospora anserina>GP:PANADCY_1 Podospora anserina adenyl cyclase gene, exons 1-4	1
6	<NONE>	<NONE>	<NONE>	VP03_HSVSA	PROBABLE MEMBRANE ANTIGEN 3 (TEGUMENT PROTEIN)>PIR2:C36806 hypothetical protein ORF3 - saimiriine herpesvirus 1 (strain 11)>GP:HSGEND_3 Herpesvirus saimiri complete genome DNA; ORF 03; similarity to ORF 75 and EBV BNRF1	0.97

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
7	<NONE>	<NONE>	<NONE>	ATFCA2_18	Arabidopsis thaliana DNA chromosome 4, ESSA 1 contig fragment No; 2; Hydroxyproline-rich glycoprotein homolog; Similarity to hydroxyproline-rich glycoprotein precursor-common tobacco	0.93
8	<NONE>	<NONE>	<NONE>	DHAL_ASPN G	ALDEHYDE DEHYDROGENASE (EC 1.2.1.3) (ALDDH)>GP:ASNA LDAA_1 Aspergillus niger aldehyde dehydrogenase (aldA) gene, complete cds	0.9
9	<NONE>	<NONE>	<NONE>	NCU50264_1	Neurospora crassa two-component histidine kinase (nik-1) gene, 5' region and partial cds	0.86
10	<NONE>	<NONE>	<NONE>	NEUG_BOVIN	NEUROGRANIN (P17) (B-50 IMMUNOREACTIVE C-KINASE SUBSTRATE) (BICKS) (FRAGMENT)>PIR2: A39034 neurogranin - bovine (fragment)	0.82
11	<NONE>	<NONE>	<NONE>	HUMBYSTIN_1	Homo sapiens bystin mRNA, complete cds	0.81
12	<NONE>	<NONE>	<NONE>	BTBMP1_1	Bos taurus BMP1 gene, partial sequence; Bone morphogenetic protein 1	0.69
13	<NONE>	<NONE>	<NONE>	TCCYSPROT_1	T;congolense mRNA for (prepro) cysteine proteinase	0.56
14	<NONE>	<NONE>	<NONE>	P60_LISIV	PROTEIN P60 PRECURSOR (INVASION-ASSOCIATED PROTEIN)>GP:LISIA PRELB_1 Listeria	0.15

WO 99/33982

PCT/US98/27610

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					ivanovii extracellular protein homologue (iap) gene, complete cds	
15	<NONE>	<NONE>	<NONE>	HEX_ADE31	HEXON PROTEIN (LATE PROTEIN 2) (FRAGMENT)>PIR2: S37217 hexon protein - human adenovirus 31 (fragment)>GP:HSAT3 1H_1 H;sapiens adenovirus type 31 hexon gene; Hexon protein; Internal fragment containing hypervariable regions	0.15
16	<NONE>	<NONE>	<NONE>	HSU77493_1	Human Notch2 mRNA, partial cds; Transmembrane protein; hN	0.13
17	<NONE>	<NONE>	<NONE>	CYB_PARTE	CYTOCHROME B (EC 1.10.2.2)>PIR2:S07743 cytochrome b - Paramecium tetraurelia mitochondrion (SGC6)>GP:MIPAGE N_19 Paramecium aurelia mitochondrial complete genome; Apocytochrome b (AA 1-391)	0.078
18	<NONE>	<NONE>	<NONE>	HUMERB27_1	Human c-erbB-2 gene, exon 7; C-erb-2 protein	0.054
19	<NONE>	<NONE>	<NONE>	DMTRXIII_2	D;melanogaster DNA for trxl and trxl genes; Trithorax protein trxl; Trithorax; putative>GP:DMTTHO RAX_2 D;melanogaster DNA for (putative) trithorax protein; Predicted trithorax protein	0.047

WO 99/33982

PCT/US98/27610

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
20	<NONE>	<NONE>	<NONE>	CEL.B0281_5	Caenorhabditis elegans cosmid B0281; Similar to reverse transcriptases	0.043
21	<NONE>	<NONE>	<NONE>	MOTY_VIBP A	SODIUM-TYPE FLAGELLAR PROTEIN MOTY PRECURSOR>GP:VP U06949_4 Vibrio parahaemolyticus BB22 RNase T (rnt) gene and flagellar motor component (motY) gene, complete cds	0.041
22	<NONE>	<NONE>	<NONE>	A56263	beta-galactosidase (EC 3.2.1.23) isozyme 12 - Arthrobacter sp. (strain B7)>GP:ASU17417_1 Arthrobacter sp; beta-galactosidase gene, complete cds	0.04
23	<NONE>	<NONE>	<NONE>	GSA_PSEAE	GLUTAMATE-1-SEMIALDEHYDE 2,1-AMINOMUTASE (EC 5.4.3.8) (GSA) (GLUTAMATE-1-SEMIALDEHYDE AMINOTRANSFERASE) (GSA-AT)>PIR2.S57898 glutamate 1-semialdehyde 2,1-aminomutase - Pseudomonas aeruginosa>GP:PAHE ML_1 P:aeruginosa hemL gene; Glutamate 1-sem	0.038
24	<NONE>	<NONE>	<NONE>	S16323	hypothetical protein - Arabidopsis thaliana>GP:ATHB1_1 A;thaliana homeobox gene Athb-1 mRNA; Open reading frame	0.035

WO 99/33982

PCT/US98/27610

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
25	<NONE>	<NONE>	<NONE>	IRS1_RAT	INSULIN RECEPTOR SUBSTRATE-1>PIR2:S16948 hypothetical protein IRS-1 - rat>GP:RNIRS1IRM_1 R;Norvegicus IRS-1 mRNA for insulin-receptor; During insulin stimulation, undergoes tyrosine phosphorylation and binds phosphatidylinositol 3-kinase	0.027
26	<NONE>	<NONE>	<NONE>	CEM02G9_2	Caenorhabditis elegans cosmid M02G9; M02G9;1; Similar to keratin like protein; . cDNA EST yk308g11;5 comes from this gene; cDNA EST yk208e11;5 comes from this gene; cDNA EST yk208e11;3 comes	0.0088
27	<NONE>	<NONE>	<NONE>	S75490_3	competence region: iga=IgA protease, comA=transformation competence [Neisseria gonorrhoeae, MS11, Genomic, 3 genes, 2664 nt]	0.0041
28	<NONE>	<NONE>	<NONE>	EXTN_TOBAC	EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)>PIR2:S06733 hydroxyproline-rich glycoprotein precursor - common tobacco>GP:NTEXT_1 Tobacco HRGPnt3 gene for extensin; Extensin (AA 1-620)	0.0025

WO 99/33982

PCT/US98/27610

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
29	<NONE>	<NONE>	<NONE>	HPCEGS_1	Hepatitis C virus complete genome sequence; Polyprotein	0.0014
30	<NONE>	<NONE>	<NONE>	HHVBC_4	Human hepatitis virus (genotype C, HMA) preS1, preS2, S, C, X, antigens, core antigen, X protein and polymerase	0.00093
31	<NONE>	<NONE>	<NONE>	HSLTGFBP4_1	Homo sapiens mRNA for latent transforming growth factor-beta binding protein-4; Latent TGF-beta binding protein-4	0.00061
32	<NONE>	<NONE>	<NONE>	S74909	transposase - Synechocystis sp. (PCC 6803)>GP:D90909_10 8 Synechocystis sp; PCC6803 complete genome, 11/27, 1311235- 1430418; Transposase; ORF_ID:slr2062	0.00051
33	<NONE>	<NONE>	<NONE>	GRN_MOUSE	GRANULINS PRECURSOR (ACROGRANIN)>GP: MUSAP_1 Mouse gene for acrogranin precursor, complete cds	0.00022
34	<NONE>	<NONE>	<NONE>	CA21_MOUSE	PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR>PIR2:A 43291 collagen alpha 2(I) chain precursor - mouse>GP:MMCOL1 A2_1 Mouse COL1A2 mRNA for pro-alpha-2(I) collagen	0.00016
35	<NONE>	<NONE>	<NONE>	MMMHC29N 7_2	Mus musculus major histocompatibility locus class III region; butyrophilin-like protein gene, partial cds; Notch4, PBX2, RAGE, lysophatidic acid acyl transferase-	8.00E-05

WO 99/33982

PCT/US98/27610

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					alpha, palmitoyl-	
36	<NONE>	<NONE>	<NONE>	NFH_RAT	NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H) (FRAGMENT)	2.40E-05
37	<NONE>	<NONE>	<NONE>	HUMVWFM_1	Human von Willebrand factor mRNA, 3' end; Von Willebrand factor prepropeptide	1.70E-05
38	<NONE>	<NONE>	<NONE>	CGHU2E	collagen alpha 2(XI) chain - human (fragment)	2.00E-06
39	<NONE>	<NONE>	<NONE>	A61183	hypothetical protein (sdsB region) - Pseudomonas sp.	4.90E-08
40	<NONE>	<NONE>	<NONE>	YM8L_YEAS_T	HYPOTHETICAL 71.1 KD PROTEIN IN DSK2-CAT8 INTERGENIC REGION>PIR2:S5458 5 hypothetical protein YMR278w - yeast (Saccharomyces cerevisiae)>GP:SC802 1X_4 S;cerevisiae chromosome XIII cosmid 8021; Unknown; YM8021;04, unknown, len: 622, CAL: 0;16,	1.50E-09
41	<NONE>	<NONE>	<NONE>	MTCY210_31	Mycobacterium tuberculosis cosmid Y210; Unknown; MTCY210;31, unknown, len: 299 aa, slight similarity to carboxykinases	3.10E-10

WO 99/33982

PCT/US98/27610

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
42	<NONE>	<NONE>	<NONE>	CEC01G10_5	Caenorhabditis elegans cosmid C01G10, complete sequence; C01G10:8; CDNA EST CEMSC45R comes from this gene>GP:CEC01G10_5 Caenorhabditis elegans cosmid C01G10; C01G10:8; CDNA EST CEMSC45R comes from this gene	2.30E-12
43	<NONE>	<NONE>	<NONE>	HSU15779_1	Human p70 (ST5) mRNA, alternatively spliced, complete cds; Differentially expressed; alternatively spliced	9.50E-14
44	<NONE>	<NONE>	<NONE>	MTCY210_31	Mycobacterium tuberculosis cosmid Y210; Unknown; MTCY210:31, unknown, len: 299 aa, slight similarity to carboxykinases	1.70E-17
45	U61403	Dietystelium discoideum PrlA (prlA) mRNA, partial cds.	1	U93472_1	Danio rerio PPARB gene, partial cds; Nuclear receptor C domain	0.95
46	Z92832	Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone F31D4; HTGS phase 1.	1	U93472_1	Danio rerio PPARB gene, partial cds; Nuclear receptor C domain	0.94
47	L36557	Oryza sativa (clone pRG3) repetitive element.	1	HSU61262_1	Human neogenin mRNA, complete cds	0.89

WO 99/33982

PCT/US98/27610

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
48	AF005898	Homo sapiens Na,K-ATPase beta-3 subunit pseudogene, complete sequence.	1	LRP1_CHICK	LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 1 PRECURSOR (LRP) (ALPHA-2-MACROGLOBULIN RECEPTOR) (A2MR)>PIR2:A53102 LDL receptor-related protein / alpha-2-macroglobulin receptor precursor - chicken>GP:GGLRPA 2MR_1 G;gallus mRNA for LRP/alp	0.85
49	U18795	Saccharomyces cerevisiae chromosome V cosmids 9669, 8334, 8199, and lambda clone 1160.	1	NKCI_SQUA C	BUMETANIDE-SENSITIVE SODIUM-(POTASSIUM)-CHLORIDE COTRANSPORTER 2 (NA-K-CL SYMPORTER)>PIR2: A53491 bumetanide-sensitive Na-K-Cl cotransporter - spiny dogfish>GP:SANKCC 1_1 Squalus acanthias bumetanide-sensitive Na-K-Cl cotransport protein (NKCC	0.73
50	AC002523	Homo sapiens; HTGS phase 1, 54 unordered pieces.	1	BXEN_CLOB O	BOTULINUM NEUROTOXIN TYPE E, NONTOXIC COMPONENT>GP:C LOENT120_1 C;botulinum gene for nontoxic component of progenitor toxin, complete cds	0.71

WO 99/33982

PCT/US98/27610

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
51	AC002345	*** SEQUENCING IN PROGRESS *** Genomic sequence from Human 17; HTGS phase 1, 10 unordered pieces.	1	P3K2_DICDI	PHOSPHATIDYLINOSITOL 3-KINASE 2 (EC 2.7.1.137) (PI3-KINASE) (PTDINS-3-KINASE) (PI3K)>GP:DDU23477_1 Dictyostelium discoideum phosphatidylinositol-4,5-diphosphate 3-kinase (PIK2) mRNA, complete cds	0.58
52	X14253	Human mRNA for crypto protein.	1	I55651	noradrenaline transporter - bovine>GP:BTU09198_1 Bos taurus noradrenaline transporter mRNA, complete cds	0.55
53	U23516	Caenorhabditis elegans cosmid B0416.	1	I69024	MHC sex-limited protein - mouse (fragment)>GP:MUSM HC4AD_1 Mouse class III H2-Slp sex-limited protein gene, exons 1, 2 and 3; MHC sex-limited protein	0.47
54	AB006698	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCL19.	1	S81293_1	L1 [insertion sequence, provirus] [human papillomavirus type 6b HPV6b, KP4, Genomic Mutant, 121 nt]; Authors note this reading frame results from a 454 bp deletion and resulting	0.25
55	K03458	Human immunodeficiency virus type 1, isolate Zaire 6, vif, tat, rev, env, nef genes and 3' LTR.	1	S13383	hydroxyproline-rich glycoprotein - sorghum	0.24

WO 99/33982

PCT/US98/27610

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
56	B26794	T1016TR TAMU Arabidopsis thaliana genomic clone T1016.	1	RK34_PORP U	CHLOROPLAST 50S RIBOSOMAL PROTEIN L34>PIR2:S73111 ribosomal protein L34 - red alga (Porphyra purpurea) chloroplast>GP:PPU38 804_4 Porphyra purpurea chloroplast genome, complete sequence; 50S ribosomal protein L34	0.021
57	Z98950	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 507115; HTGS phase 1.	1	D41132	collagen-related protein 4 - Hydra magnipapillata (fragment)>PIR2:S219 32 mini-collagen - Hydra sp.>GP:HSNCOL4_1 Hydra N-COL 4 mRNA for mini-collagen; No start codon	0.02
58	U57057	Human WD protein IR10 mRNA, complete cds.	1	DMU15602_1	Drosophila melanogaster (zeste-white 4) mRNA, complete cds; Similar to C. elegans B0464;4 gene product, Swiss-Prot Accession Number Q03562	0.019
59	U57057	Human WD protein IR10 mRNA, complete cds.	1	CR2_MOUSE	COMPLEMENT RECEPTOR TYPE 2 PRECURSOR (CR2) (COMPLEMENT C3D RECEPTOR)>PIR2:A43526 complement C3d/Epstein-Barr virus receptor 2 precursor - mouse>GP:MUSCR2A A_1 Murine complement receptor type 2 (CR2) mRNA, complete cds; Complement receptor type	0.0074

WO 99/33982

PCT/US98/27610

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
60	B65337	CIT-HSP-2021H21.TF CIT-HSP Homo sapiens genomic clone 2021H21.	1	A38096	perlecan precursor - human>GP:HUMHSP G2B_1 Human heparan sulfate proteoglycan (HSPG2) mRNA, complete cds	0.0051
61	U84722	Human vascular endothelial cadherin mRNA, complete cds.	1	HSTAFIII3_1	H;sapiens mRNA for TAFIII35; Subunit of RNA polymerase II transcription factor TFIID	0.0012
62	L41493	Avian rotavirus (strain turkey 1) genomic segment 4 outer capsid protein (VP8*) gene.	1	Y328_MYCP N	HYPOTHETICAL PROTEIN MG328 HOMOLOG>PIR2:S73 693 MG328 homolog P01_orf1033 - Mycoplasma pneumoniae (ATCC 29342) (SGC3)>GP:MPAE000 035_2 Mycoplasma pneumoniae from bases 442306 to 452472 (section 35 of 63) of the complete genome; MG328 homolog.	0.00015
63	D63139	Aeromonas sp. gene for chitinase, complete and partial cds.	1	MTCY16B7_3	Mycobacterium tuberculosis cosmid SCY16B7; Unknown; MTCY16B7;03, initiation factor, len: 900, similar at C-terminal half to eg IF2_BACSU P17889 initiation factor if-2 (716 aa), fasta	6.30E-05

WO 99/33982

PCT/US98/27610

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
64	J04974	Human alpha-2 type XI collagen mRNA (COL11A2).	1	GDF6_BOVIN	GROWTH/DIFFERENTIATION FACTOR GDF-6 PRECURSOR (CARTILAGE-DERIVED MORPHOGENETIC PROTEIN 2) (CDMP-2) (FRAGMENT)>PIR2: B55452 cartilage-derived morphogenetic protein 2 precursor - bovine (fragment)>GP:BTU13661_1 Bos taurus cartilage-derived morp	1.00E-05
65	AC002394	Homo sapiens Chromosome 16 BAC clone CIT987-SKA-211C6 ~complete genomic sequence, complete sequence.	1	CELC14F11_6	Caenorhabditis elegans cosmid C14F11; Similar to aspartate aminotransferase; coded for by C; elegans cDNA CEMS95FB; coded for by C; elegans cDNA yk41e4.3; coded for by C; elegans	4.60E-06
66	AB002312	Human mRNA for KIAA0314 gene, partial cds.	1	NAT1_YEAST	N-TERMINAL ACETYLTRANSFERASE 1 (EC 2.3.1.88) (AMINO-TERMINAL, ALPHA- AMINO, ACETYLTRANSFERASE 1)	1.00E-09
67	AC003085	Human BAC clone RG094H21 from 7q21-q22, complete sequence.	1	DP19_CAEEL	DPY-19 PROTEIN>PIR2:S44629 F22b7.10 protein - Caenorhabditis elegans>GP:CELF22B7_9 C;aenorhabditis elegans (Bristol N2) cosmid F22B7; Putative	4.20E-11
68	X55026	P.anserina complete mitochondrial genome.	1	NAT1_YEAST	N-TERMINAL ACETYLTRANSFERASE 1 (EC 2.3.1.88) (AMINO-TERMINAL, ALPHA- AMINO, ACETYLTRANSFERASE 1)	8.40E-12

WO 99/33982

PCT/US98/27610

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					ASE 1)	
69	Z95399	Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y39B6; HTGS phase 1.	1	CER06B9_5	Caenorhabditis elegans cosmid R06B9, complete sequence; R06B9;b; Protein predicted using Genefinder; preliminary prediction	1.50E-24
70	AC002339	Arabidopsis thaliana chromosome II BAC T11A07 genomic sequence, complete sequence.	0.99	POLG_BVDVS	GENOME POLYPROTEIN>PIR1:A44217 genome polyprotein - bovine viral diarrhea virus (strain SD-1)>GP:BVDPOLYPR O_1 Bovine viral diarrhea virus polyprotein RNA, complete cds; Putative	1
71	Y08559	B.subtilis urease operon and downstream DNA.	0.99	LRP_CAEEL	LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN PRECURSOR (LRP)>PIR2:A47437 LDL-receptor-related protein - Caenorhabditis elegans>GP:CEF29D11_2 Caenorhabditis elegans cosmid F29D11, complete sequence; F29D11;1; Protein predicted using Genefi	1

WO 99/33982

PCT/US98/27610

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
72	U67548	Methanococcus jannaschii from bases 986219 to 996377 (section 90 of 150) of the complete genome.	0.99	YB60_YEAS T	HYPOTHETICAL 16.3 KD PROTEIN IN DUR1.2-NGR1 INTERGENIC REGION>PIR2:S4608 4 probable membrane protein YBR210w - yeast (Saccharomyces cerevisiae)>GP:SCYB R210W_1 S;cerevisiae chromosome II reading frame ORF YBR210w	1
73	U51645	Plasmodium falciparum cytidine triphosphate synthetase gene, complete cds.	0.99	HPSVRPL_1	Sin Nombre virus (NM H10) RNA L segment encoding RNA polymerase (L protein), complete cds; Viral RNA polymerase (L protein); Putative>GP:HPSVRP LA_1 Sin Nombre virus (NM R11) RNA L segment encoding RNA polymerase (L protein), complete cds; Vir	0.99
74	Z49889	Caenorhabditis elegans cosmid T06H11, complete sequence.	0.99	MUSHDPRO B_1	Mouse alternatively spliced HD protein mRNA, complete cds	0.021
75	Z69374	Human DNA sequence from cosmid L174G8, Huntington's Disease Region, chromosome 4p16.3 contains a pair of ESTs.	0.99	NCPR_YEAS T	NADPH-CYTOCHROME P450 REDUCTASE (EC 1.6.2.4) (CPR)	0.017

WO 99/33982

PCT/US98/27610

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
76	Z35847	S.cerevisiae chromosome II reading frame ORF YBL086c.	0.99	CYPA_CAEE L	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE 10 (EC 5.2.1.8) (PPIASE) (ROTAMASE) (CYCLOPHILIN-10)>GP:CELB0252_4 Caenorhabditis elegans cosmid B0252; Similar to peptidyl-prolyl cis-trans isomerase (PPIASE) (CYCLOPHILIN)>GP:CEU34954_1 Caenorhabditis el	0.0044
77	L35330	Rattus norvegicus glutathione S-transferase Yb3 subunit gene, complete cds.	0.99	CELRL148_1	Caenorhabditis elegans cosmid R148; Contains similarity to drosophila DNA-binding protein K10 (NID:g8148); coded for by C; elegans cDNA yk118e11.5; coded for by C; elegans cDNA	0.0032
78	Y00324	Chicken vitellogenin gene 3' flanking region.	0.99	A56922	transcription factor shn - fruit fly (Drosophila melanogaster)	0.0023
79	M32659	D.melanogaster Shab11 protein mRNA, complete cds.	0.99	OMU25146_1	Oncorhynchus mykiss recombination activating protein 2 gene, partial cds	0.0017
80	Z69880	H.sapiens SERCA3 gene (partial).	0.99	M84D_DRO ME	MALE SPECIFIC SPERM PROTEIN MST84DD>PIR2:S25775 testis-specific protein Mst84Dd - fruit fly (Drosophila melanogaster)>GP:DM MST84D_4 D;melanogaster Mst84Da, Mst84Db, Mst84Dc and Mst84Dd genes for put; sperm protein	0.0011

WO 99/33982

PCT/US98/27610

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
81	M99166	Escherichia coli Trp repressor binding protein (wrbA) gene, complete cds.	0.99	MTU88962_1	Mycobacterium tuberculosis unknown protein gene, partial cds	6.50E-07
82	X99257	R.norvegicus mRNA for lamin C2.	0.99	MIU68729_1	Meloidogyne incognita cuticle preprocollagen (col-2) mRNA, complete cds; Putative	1.60E-09
83	AC002432	Human BAC clone RG317G18 from 7q31, complete sequence.	0.98	1FMDC	Foot and mouth disease virus type c-s8c1, chain C - foot and mouth disease virus type c-s8c1 expressed in hamster kidney cells	0.14
84	Z34799	Caenorhabditis elegans cosmid F34D10, complete sequence.	0.98	MMU57368_1	Mus musculus EGF repeat transmembrane protein mRNA, complete cds; Notch like repeats; notch 2	0.0028
85	B15207	344E15.TV CIT978SKA1 Homo sapiens genomic clone A-344E15.	0.98	POLG_HCVJ 6	GENOME POLYPROTEIN (CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE PROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (EC 2.7.7.48) (NS5))>PI	0.00083

WO 99/33982

PCT/US98/27610

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
86	AC002412	*** SEQUENCING IN PROGRESS *** Human Chromosome X; HTGS phase 1, 2 unordered pieces.	0.98	KDG1_ARATH	DIACYLGLYCEROL KINASE 1 (EC 2.7.1.107) (DIGLYCERIDE KINASE) (DGK 1) (DAG KINASE 1)>PIR2:S71467 diacylglycerol kinase (EC 2.7.1.107) ATDGK1 - Arabidopsis thaliana>GP:ATHATDGK1_1 Arabidopsis thaliana mRNA for diacylglycerol kinase, complete c	0.00024
87	X57010	Human COL2A1 gene for collagen II alpha 1 chain, exons E2-E15.	0.98	D80005_1	Human mRNA for KIAA0183 gene, partial cds	5.90E-10
88	M83093	Neurospora crassa cAMP-dependent protein kinase (cot-1) gene, complete cds.	0.98	YA53_SCHPO	HYPOTHETICAL 24.2 KD PROTEIN C13A11.03 IN CHROMOSOME I>GP:SPAC13A11_3 S;pombe chromosome I cosmid c13A11; Unknown; SPAC13A11;03, unknown, len: 210	3.00E-22
89	U96271	Helicobacter pylori heat shock protein 70 (hsp70) gene, complete cds.	0.97	SLMEN6_1	S;latifolia mRNA for Men-6 protein>GP:SLMEN6_1 S;latifolia mRNA for Men-6 protein	0.43
90	U49944	Caenorhabditis elegans cosmid C39E6.	0.97	RON_HUMAN	MACROPHAGE STIMULATING PROTEIN RECEPTOR PRECURSOR (EC 2.7.1.112)>PIR2:I38185 protein-tyrosine kinase (EC 2.7.1.112), receptor type ron - human>GP:HSRON_1 H;sapiens RON mRNA for tyrosine kinase; Putative	0.034

WO 99/33982

PCT/US98/27610

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
91	Y09255	B.cereus dnaI gene, partial.	0.97	CEL T05C1_5	Caenorhabditis elegans cosmid T05C1; Coded for by C; elegans cDNA yk30f6;3; coded for by C; elegans cDNA yk34f10;3	0.00043
92	AC002413	*** SEQUENCING IN PROGRESS *** Human Chromosome X; HTGS phase 1, 2 unordered pieces.	0.96	CEL C44E4_5	Caenorhabditis elegans cosmid C44E4; Weak similarity to the drosophila hyperplastic disc protein (GB:L14644); coded for by C; elegans cDNA yk49h6;5; coded for by C; elegans cDNA	1
93	U41625	Caenorhabditis elegans cosmid K03A1.	0.96	HMGC_HUMAN	HIGH MOBILITY GROUP PROTEIN HMGI-C>PIR2:JC2232 high mobility group I-C phosphoprotein - human>GP:HS_HMGIC G5_1 Human high-mobility group phosphoprotein isoform I-C (HMGIC) gene, exon 5>GP:HS_HMGICP_1 H;sapiens mRNA for HMGI-C protein>GP:HS_HMGIC	1
94	Z82202	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 34P24; HTGS phase 1.	0.96	YTH3_CAEL	HYPOTHETICAL 75.5 KD PROTEIN C14A4.3 IN CHROMOSOME II>GP:CEC14A4_3 Caenorhabditis elegans cosmid C14A4, complete sequence; C14A4;3; Weak similarity with a B; Flavum translocation protein (Swiss Prot accession number P38376)	0.73

WO 99/33982

PCT/US98/27610

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
95	AL008734	Human DNA SEQUENCE *** SEQUENCING IN PROGRESS *** from clone 324M8; HTGS phase 1.	0.96	S25299	extensin precursor (clone Tom L-4) - tomato>GP:TOMEXT ENB_1 L;esculentum extensin (class II) gene, complete cds	0.0004
96	L15388	Human G protein-coupled receptor kinase (GRK5) mRNA, complete cds.	0.96	HUMCOL7A1 X_1	Homo sapiens (clones: CW52-2, CW27-6, CW15-2, CW26-5, 11-67) collagen type VII intergenic region and (COL7A1) gene, complete cds	4.60E-06
97	X97384	A.thaliana atran3 gene.	0.95	<NONE>	<NONE>	<NONE>
98	M62505	Human C5a anaphylatoxin receptor mRNA, complete cds.	0.95	RIPB_BRYDI	RIBOSOME-INACTIVATING PROTEIN BRYODIN (RRNA N-GLYCOSIDASE) (EC 3.2.2.22) (FRAGMENT)>PIR2: S16491 rRNA N-glycosidase (EC 3.2.2.22) bryodin - red bryony (fragment)	0.83
99	D28778	Cucumber mosaic virus RNA 1 for 1a, complete sequence.	0.95	POLS_RUBV M	STRUCTURAL POLYPROTEIN (CONTAINS: NUCLEOCAPSID PROTEIN C; MEMBRANE GLYCOPROTEINS E1 AND E2)>PIR1:GNWVR3 structural polyprotein - rubella virus (strain M33)>GP:TORUB24S_1 Rubella virus 24S subgenomic mRNA for structural proteins E1, E2 and C;	0.00037
100	AF016202	Homo sapiens immunoglobulin heavy chain CDR3 gene,	0.93	HSU79716_1	Human reelin (RELN) mRNA, complete cds	1

WO 99/33982

PCT/US98/27610

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		partial cds.				
101	Z68303	Caenorhabditis elegans cosmid ZK809, complete sequence.	0.93	HS5HT4SAR_1	H;sapiens mRNA for serotonin 4SA receptor (5-HT4SA-R)	0.87
102	X03049	E. coli DNA sequene 5' to origin of replication oriC.	0.93	S37594	mucin - human (fragment)	0.0019
103	M32659	D.melanogaster Shab11 protein mRNA, complete cds.	0.93	S38480	nonstructural protein - rubella virus>GP:RVM33NP_1 Rubella virus M33 RNA for a nonstructural protein; Nonstructural protein genes	2.30E-06
104	D88687	Human mRNA for KM-102-derived reductase-like factor, complete cds.	0.93	BAT3_HUMAN	LARGE PROLINE-RICH PROTEIN BAT3 (HLA-B-ASSOCIATED TRANSCRIPT 3)>PIR2:A35098 MHC class III histocompatibility antigen HLA-B-associated transcript 3 - human>GP:HUMBAT3A_1 Human HLA-B-associated transcript 3 (BAT3) mRNA, complete cds>GP:HUMBAT3	8.70E-07
105	D16847	Mouse mRNA for stromal cell derived protein-1, complete cds.	0.93	S52796	prpL2 protein - human (fragment)>GP:HSPRP L2_1 H;sapiens mRNA for PRPL-2 protein	3.20E-08

WU 99/33982

PCT/US98/27610

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
106	D90915	Synechocystis sp. PCC6803 complete genome, 17/27, 2137259-2267259.	0.92	YEK9_YEAS T	HYPOTHETICAL 53.9 KD PROTEIN IN AFG3-SEB2 INTERGENIC REGION>PIR2:S5047 7 hypothetical protein YER019w - yeast (Saccharomyces cerevisiae)>GP:SCE95 37_20 Saccharomyces cerevisiae chromosome V cosmid 9537, 9581, 9495, 9867, and lambda clone 5898	5.90E-05
107	AJ001101	Mus musculus mRNA for gC1qBP gene.	0.92	DMU58282_1	Drosophila melanogaster Bowl (bowl) mRNA, complete cds; Transcription factor; C2H2 zinc finger protein; zinc fingers have extensive sequence similarity to Drosophila odd-skipped	3.50E-05
108	X57108	Human gene for cerebroside sulfate activator protein, exons 10-14.	0.92	S69032	hypothetical protein YPR144c - yeast (Saccharomyces cerevisiae)>GP:YSCP9 659_17 Saccharomyces cerevisiae chromosome XVI cosmid 9659; Ypr144cp; Weak similarity near C-terminus to RNA Polymerase beta subunit (Swiss Prot; accession number P11213)	4.30E-21

WO 99/33982

PCT/US98/27610

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
109	D14635	Caenorhabditis elegans DNA for EMB-5.	0.91	YM13_YEAS T	PUTATIVE ATP-DEPENDENT RNA HELICASE YMR128W>PIR2:S53 058 probable membrane protein YMR128w - yeast (Saccharomyces cerevisiae)>GP:SC955 3_4 S;cerevisiae chromosome XIII cosmid 9553; Unknown; YMR9553;04, probable ATP-dependent RNA helicase, len:	0.69
110	B55500	CIT-HSP-387J2.TFB CIT-HSP Homo sapiens genomic clone 387J2.	0.91	U97553_79	Murine herpesvirus 68 strain WUMS, complete genome; Unknown	0.00016
111	X03049	E. coli DNA sequene 5' to origin of replication oriC.	0.9	POL_MLVAV	POL POLYPROTEIN (PROTEASE (EC 3.4.23.-); REVERSE TRANSCRIPTASE (EC 2.7.7.49); RIBONUCLEASE H (EC 3.1.26.4))>PIR1:GNM VGV pol polyprotein - AKV murine leukemia virus	0.0019
112	U91327	Human chromosome 12p15 BAC clone CIT987SK-99D8 complete sequence.	0.89	JC5568	serine protease (EC 3.4.-.-) h1 - Serratia marcescens	1
113	X13295	Rat mRNA for alpha-2u globulin-related protein.	0.89	MNGPOLY_1	Mengo virus polyprotein genome, complete cds with repeats	1
114	Z78415	Caenorhabditis elegans cosmid C17G1, complete sequence.	0.89	AB000121_1	Mouse mRNA for TBP1P, complete cds; TBP1 interacting protein	0.39

WO 99/33982

PCT/US98/27610

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
115	AC002308	*** SEQUENCING IN PROGRESS *** Human Chromosome 22q11 BAC Clone 1000e4; HTGS phase 1, 26 unordered pieces.	0.88	YLK2_CAEE L	HYPOTHETICAL 122.7 KD PROTEIN D1044.2 IN CHROMOSOME III>GP:CELD1044_4 Caenorhabditis elegans cosmid D1044	0.0037
116	AC002073	Human PAC clone DJ515N1 from 22q11.2-q22, complete sequence.	0.88	S28499	probable finger protein - rat>GP:RNZFP_1 R;norvegicus mRNA for putative zinc finger protein	1.10E-31
117	Z83848	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 57A13; HTGS phase 1.	0.87	NDL_DROM E	SERINE PROTEASE NUDEL PRECURSOR (EC 3.4.21.-)>PIR2:A57096 nudel protein precursor - fruit fly (Drosophila melanogaster)>GP:DM U29153_1 Drosophila melanogaster nudel (ndl) mRNA, complete cds; Serine protease; Soma dependent gene required matern	1
118	U23449	Caenorhabditis elegans cosmid K06A1.	0.87	AF023268_3	Homo sapiens clk2 kinase (CLK2), propin1, cotel, glucocerebrosidase (GBA), and metaxin genes, complete cds; metaxin pseudogene and glucocerebrosidase pseudogene; and thrombospondin3 (THBS3)	0.21
119	Z68181	H.vulgaris mRNA for elongation factor EF1-alpha.	0.87	RABCY450C_1	Rabbit cytochrome P-450 gene, clone pP-450PBc3, 3' end	0.14

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
120	AC000033	Homo sapiens chromosome 9, complete sequence.	0.87	VWF_CANF_A	VON WILLEBRAND FACTOR PRECURSOR>GP:DO GVWG_1 Canis familiaris von Willebrand factor mRNA, complete cds	0.036
121	U23449	Caenorhabditis elegans cosmid K06A1.	0.86	S48988_1	CRP-1=cystatin-related protein [rats, Wistar albino, mRNA Partial, 213 nt]; Cystatin-related protein; Method: conceptual translation supplied by author; This sequence comes from Fig;	0.64
122	Z89651	F.rubripes GSS sequence, clone 090124cD5.	0.86	CPU65981_1	Cryptosporidium parvum P-ATPase gene (CpPA-E1) gene, complete cds; Putative calcium-ATPase	0.6
123	Z94055	Human DNA sequence from PAC 24M15 on chromosome 1. Contains tenascin-R (restrictin), EST.	0.86	GLTB_SYNY_3	FERREDOXIN-DEPENDENT GLUTAMATE SYNTHASE 1 (EC 1.4.7.1) (FD-GOGAT)>PIR2:S6022 8 glutamate synthase (ferredoxin) (EC 1.4.7.1) gltB - Synechocystis sp. (PCC 6803)>GP:D90902_66 Synechocystis sp; PCC6803 complete genome, 4/27, 402290-524345; Gluta	0.03
124	Z49250	Human DNA sequence from cosmid HW2, Huntington's Disease Region, chromosome 4p16.3.	0.86	TRSCAPSID_1	Tobacco ringspot virus capsid protein gene, complete cds	3.00E-06

WO 99/33982

PCT/US98/27610

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
125	Z92855	Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y48C3; HTGS phase 1.	0.84	AE000809_8	Methanobacterium thermoautotrophicum from bases 161632 to 172569 (section 15 of 148) of the complete genome; Aspartyl-tRNA synthetase; Function Code:10;07 - Metabolism of	1
126	AC002340	*** SEQUENCING IN PROGRESS *** Arabidopsis thaliana 'TAMU' BAC 'T11J7' genomic sequence near marker 'm283'; HTGS phase 1, 2 unordered pieces.	0.83	CET01E8_3	Caenorhabditis elegans cosmid T01E8, complete sequence; T01E8;3; Similar to 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase; cDNA EST CEESG02F comes from this gene;	0.86
127	AL008716	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 206C7; HTGS phase 1.	0.83	HIVU51189_5	HIV-1 clone 93th253 from Thailand, complete genome; Tat protein	0.86
128	AC002340	*** SEQUENCING IN PROGRESS *** Arabidopsis thaliana 'TAMU' BAC 'T11J7' genomic sequence near marker 'm283'; HTGS phase 1, 2 unordered pieces.	0.83	S60257	meltrin alpha - mouse>GP:MUSMAB_1 Mouse mRNA for meltrin alpha, complete cds	0.0013

WO 99/33982

PCT/US98/27610

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			P VALUE	Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			P VALUE
	ACCESSION	DESCRIPTION			ACCESSION	DESCRIPTION		
129	Z83848	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 57A13; HTGS phase 1.		0.82	ARO1_PNEC_A	PENTAFUNCTIONAL AROM POLYPEPTIDE (CONTAINS: 3- DEHYDROQUINATE SYNTHASE (EC 4.6.1.3), 3- DEHYDROQUINATE DEHYDRATASE (EC 4.2.1.10) (3- DEHYDROQUINASE), SHIKIMATE 5- DEHYDROGENASE (EC 1.1.1.25), SHIKIMATE KINASE (EC 2.7.1.71), AND EPSP SYNTHASE (E		0.0098
130	AF029308	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families.		0.8	CELZK84_5	Caenorhabditis elegans cosmid ZK 84; Final exon in repeat region; similar to long tandem repeat region of sialidase (SP:TCNA_TRYCR, P23253) and neurofilament H protein; coded for by C; elegans		2.00E-08
131	AC002458	Human BAC clone RG098M04 from 7q21-q22, complete sequence.		0.78	IGF2_PIG	INSULIN-LIKE GROWTH FACTOR II PRECURSOR (IGF-II)-GP:SSIGF2_1 S;scrofa mRNA IGF2 for insulin-like-growth factor 2; Insulin-like-growth factor 2 preproprotein		0.44
132	Z83843	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 368A4; HTGS phase 1.		0.78	PAR51A_1	P;tetraurelia 51A surface protein gene, complete cds		0.0014

WO 99/33982

PCT/US98/27610

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			P VALUE	Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			P VALUE
	ACCESSION	DESCRIPTION			ACCESSION	DESCRIPTION		
133	X03021	Human gene for granulocyte-macrophage colony stimulating factor (GM-CSF).		0.78	CEF57B1_3	Caenorhabditis elegans cosmid F57B1, complete sequence; F57B1.3; Protein predicted using Genefinder; similar to collagen		2.20E-05
134	Z74825	S.cerevisiae chromosome XV reading frame ORF YOL083w.		0.77	SYLM_SCHPO	PUTATIVE LEUCYL-TRNA SYNTHETASE, MITOCHONDRIAL PRECURSOR (EC 6.1.1.4) (LEUCINE--TRNA LIGASE)>PIR2:S6248 6 hypothetical protein SPAC4G8.09 - fission yeast (Schizosaccharomyces pombe)>GP:SPAC4G8_9 S:pombe chromosome I cosmid c4G8; Unknown; SPAC		0.96
135	Z74825	S.cerevisiae chromosome XV reading frame ORF YOL083w.		0.77	RNU59809_1	Rattus norvegicus mannose 6-phosphate/insulin-like growth factor II receptor (M6P/IGF2r) mRNA, complete cds; Also termed IGF-II/Man 6-P receptor, MPR, CI-MPR		0.01
136	U80445	Caenorhabditis elegans cosmid C50F2.		0.76	S28499	probable finger protein - rat>GP:RNZFP_1 R:norvegicus mRNA for putative zinc finger protein		1.10E-31
137	Z78545	Caenorhabditis elegans cosmid M03B6, complete sequence.		0.75	RRU73586_1	Rattus norvegicus Fanconi anemia group C mRNA, complete cds; Fanconi anemia group C protein; Similar to human FAC protein, GenBank Accession Numbers X66893 and X66894		0.023

WO 99/33982

PCT/US98/27610

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			P VALUE	Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			P VALUE
	ACCESSION	DESCRIPTION			ACCESSION	DESCRIPTION		
138	Z97630	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 466N1; HTGS phase 1.		0.74	HSMHRECA_1	H;sapiens mRNA for MSH receptor; Author-given protein sequence is in conflict with the conceptual translation		0.036
139	AF007269	Arabidopsis thaliana BAC IG002N01.		0.71	HSU95090_1	Homo sapiens chromosome 19 cosmid F19541, complete sequence; F19541_1; Hypothetical (partial) protein similar to proline oxidase		0.16
140	AC002393	Mouse BAC284H12 Chromosome 6, complete sequence.		0.7	RNLTP2_1	Rattus norvegicus mRNA for LTBP-2 like protein; Latent TGF-beta binding protein-2 like protein		4.40E-05
141	B15232	344G8.TV CIT978SKA1 Homo sapiens genomic clone A-344G08.		0.67	DMSEVL2_2	Drosophila melanogaster sevenless mRNA; Put; sevenless protein (AA 1 - 2510)		0.41
142	D13748	Human mRNA for eukaryotic initiation factor 4A1.		0.66	MMU53563_1	Mus musculus Brg1 mRNA, partial cds; N-terminal region of the protein		0.00016
143	S45791	band 3-related protein=renal anion exchanger AE2 homolog [rabbits, New Zealand White, ileal epithelial cells, mRNA, 3964 nt].		0.66	POLSRUBVR	STRUCTURAL POLYPROTEIN (CONTAINS: NUCLEOCAPSID PROTEIN C; MEMBRANE GLYCOPROTEINSE1 AND E2)>PIR1:GNWVRA structural polyprotein - rubella virus (strain RA27/3 vaccine)>GP:RUBCE2 1 1 Rubella virus RA27/3 RNA for capsid, E2 and E1 proteins; Poly		5.60E-05
144	M22462	Chicken protein p54 (ets-1)		0.66	HSH8PROT_1	H;sapiens mRNA for HP8 protein; HP8		2.00E-06

WO 99/33982

PCT/US98/27610

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		mRNA, complete cds.			peptide	
145	U27999	Human clone pDEL52A11 HLA-C region cosmid 52 genomic survey sequence.	0.65	CA18_HUMAN	COLLAGEN ALPHA 1(VIII) CHAIN PRECURSOR (ENDOTHELIAL COLLAGEN)>PIR2:S15435 collagen alpha 1(VIII) chain precursor - human>GP:HSCOL8A1_1 Human COL8A1 mRNA for alpha 1(VIII) collagen	5.70E-06
146	M54787	N.crassa mating type a-1 protein (mt a-1) gene, exons 1-3.	0.64	I50717	vacuolar H+-ATPase A subunit - chicken (fragment)>GP:GGU22078_1 Gallus gallus vacuolar H+-ATPase A subunit gene, partial cds	0.0046
147	AC002094	Genomic sequence from Human 17, complete sequence.	0.63	PVPVA1_1	P;vivax pva1 gene	0.1
148	U32701	Haemophilus influenzae from bases 165345 to 176101 (section 16 of 163) of the complete genome.	0.63	FABG_HAEI	3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE (EC 1.1.1.100) (3-KETOACYL-ACYL CARRIER PROTEIN REDUCTASE)>PIR2:D64051 3-oxoacyl-[acyl-carrier-protein] reductase (EC 1.1.1.100) - Haemophilus influenzae (strain Rd KW20)>GP:HIU32701_7 Haemophilus	2.00E-12
149	Z37159	T.brucei serum resistance associated (SRA) mRNA for VSG-like protein.	0.61	<NONE>	<NONE>	<NONE>

WO 99/33982

PCT/US98/27610

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
150	AF027865	Mus musculus Major Histocompatibility Locus class II region.	0.61	A56514	chromokinesin - chicken>GP:GGU18309_1 Gallus gallus chromokinesin mRNA, complete cds	0.045
151	U40938	Caenorhabditis elegans cosmid D1009.	0.61	YA53_SCHPO	HYPOTHETICAL 24.2 KD PROTEIN C13A11.03 IN CHROMOSOME I>GP:SPAC13A11_3 S.pombe chromosome I cosmid c13A11; Unknown; SPAC13A11.03, unknown, len: 210	1.90E-24
152	116670	Sequence 1 from patent US 5476781.	0.59	CELF21F8_7	Caenorhabditis elegans cosmid F21F8; Similar to eukaryotic aspartyl proteases	0.39
153	Z84468	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 299D3; HTGS phase 1.	0.59	CLG1_YEAST	CYCLIN-LIKE PROTEIN CLG1>PIR2:S37607 cyclin-like protein YGL215w - yeast (Saccharomyces cerevisiae)>GP:SCYG L215W_1 S;cerevisiae chromosome VII reading frame ORF YGL215w>GP:YSCCLG1CPR_1 Saccharomyces cerevisiae cyclin-like protein (CLG1) gene	0.0015
154	U00054	Caenorhabditis elegans cosmid K07E12.	0.57	<NONE>	<NONE>	<NONE>
155	M21207	Synthetic SV40 T antigen mutant pseudogene, 3' end.	0.57	1CJL2	cathepsin L (EC 3.4.22.15) mutant (F(78P)L, C25S, T110A, E176G, D178G), fragment 2 - human	0.43

WO 99/33982

PCT/US98/27610

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
156	AF020282	Dictyostelium discoideum DG2033 gene, partial cds.	0.56	AC002125_4	Homo sapiens DNA from chromosome 19-cosmid F25965, genomic sequence, complete sequence; F25965_5; Hypothetical 35;3 kDa protein similar to GTPase-activating proteins and orf3 from	0.6
157	M86352	Stigmatella aurantiaca reverse transcriptase (163 RT) gene, complete cds.	0.56	AC002398_4	Human DNA from chromosome 19-specific cosmid F25965, genomic sequence, complete sequence; F25965_3; Hypothetical 96 kDa human protein similar to alpha chimaerin; Hypothetical protein>GP:AC002398_4 Human DNA from chromosome 19-specific cosmi	4.50E-06
158	AC003101	*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 17, clone HRPC41C23; HTGS phase 1, 33 unordered pieces.	0.54	<NONE>	<NONE>	<NONE>
159	B12117	F5L15-T7 IGF Arabidopsis thaliana genomic clone F5L15.	0.54	CEF32H2_5	Caenorhabditis elegans cosmid F32H2, complete sequence; F32H2;5; Similarity to Chicken fatty acid synthase (SW:P12276); cDNA EST yk16c2;5 comes from this gene; cDNA EST yk113h6;5 comes	1

WO 99/33982

PCT/US98/27610

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
160	AE000664	Mus musculus TCR beta locus from bases 250554 to 501917 (section 2 of 3) of the complete sequence.	0.54	CET01G9_6	Caenorhabditis elegans cosmid T01G9, complete sequence; T01G9;4; CDNA EST yk29b7;5 comes from this gene	0.84
161	B12117	F5L15-T7 IGF Arabidopsis thaliana genomic clone F5L15.	0.54	A39718	nicotinic acetylcholine receptor alpha chain - marbled electric ray (fragments)	0.27
162	Z71261	Caenorhabditis elegans cosmid F21C3, complete sequence.	0.5	KDGE_DROME	EYE-SPECIFIC DIACYLGLYCEROL KINASE (EC 2.7.1.107) (RETINAL DEGENERATION A PROTEIN) (DIGLYCERIDE KINASE) (DGK)>GP:DRODAG K_1 Fruit fly mRNA for diacylglycerol kinase, complete cds	4.60E-05
163	M61831	Human S-adenosylhomocysteine hydrolase (AHCY) mRNA, complete cds.	0.49	P2C2_ARATH	PROTEIN PHOSPHATASE 2C (EC 3.1.3.16) (PP2C)>PIR2:S55457 phosphoprotein phosphatase (EC 3.1.3.16) 2C - Arabidopsis thaliana>GP:ATHPP2 CA_1 Arabidopsis thaliana mRNA for protein phosphatase 2C	5.60E-08
164	U42608	Glycine max clathrin heavy chain mRNA, complete cds.	0.48	<NONE>	<NONE>	<NONE>

WO 99/33982

PCT/US98/27610

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
165	Z93042	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 6B17; HTGS phase 1.	0.47	PYRD_BACS U	DIHYDROOROTATE DEHYDROGENASE (EC 1.3.3.1) (DIHYDROOROTATE OXIDASE) (DHODEHASE)>PIR1:H39845 dihydroorotate oxidase (EC 1.3.3.1) - Bacillus subtilis>GPN:BSUB0009_25 Bacillus subtilis complete genome (section 9 of 21): from 1598421 to 1807200;	0.002
166	AC000044	Human Chromosome 22q13 Cosmid Clone p76e10, complete sequence.	0.47	MATK_MAR PO	PROBABLE INTRON MATURASE>PIR2:A05034 hypothetical protein 370i - liverwort (Marchantia polymorpha) chloroplast>GP:CHMP XX_21 Liverwort Marchantia polymorpha chloroplast genome DNA; ORF370i	0.0011
167	X51508	Rabbit mRNA for aminopeptidase N (partial).	0.47	S45361	LRR47 protein - fruit fly (Drosophila melanogaster)>GP:DM LRR47_1 D:melanogaster mRNA for LRR47	5.30E-07
168	Z67035	H.sapiens DNA segment containing (CA) repeat; clone AFM323yf1; single read.	0.45	JQ2246	22.5K cathepsin D inhibitor protein precursor - potato>GP:POTCATH D_1 Potato cathepsin D inhibitor protein mRNA, complete cds	0.79
169	Z93042	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 6B17; HTGS phase 1.	0.44	SMU31768_1	Schistosoma mansoni elastase gene, 3045 bp clone, complete cds	0.0022

WO 99/33982

PCT/US98/27610

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
170	L11172	Plasmodium falciparum RNA polymerase I gene, complete cds.	0.43	HUMPKD1G08_1	Homo sapiens polycystic kidney disease (PKD1) gene, exons 43-46; Polycystic kidney disease 1 protein	1
171	Z95889	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 211A9; HTGS phase 1.	0.43	A09811_1	R;norvegicus mRNA for BRL-3A binding protein; Author-given protein sequence is in conflict with the conceptual translation	0.00083
172	U32772	Haemophilus influenzae from bases 954819 to 966363 (section 87 of 163) of the complete genome.	0.43	YPT2_CAEEL	HYPOTHETICAL 21.6 KD PROTEIN F37A4.2 IN CHROMOSOME III>PIR2:S44639 F37A4.2 protein - Caenorhabditis elegans>GP:CEL37A4_8 Caenorhabditis elegans cosmid F37A4	2.50E-28
173	Z99281	Caenorhabditis elegans cosmid Y57G11C, complete sequence.	0.42	PTU19464_1	Paramecium tetraurelia outer arm dynein beta heavy chain gene, complete cds	1
174	X04571	Human mRNA for kidney epidermal growth factor (EGF) precursor.	0.42	YEK9_YEAST	HYPOTHETICAL 53.9 KD PROTEIN IN AFG3-SEB2 INTERGENIC REGION>PIR2:S50477 hypothetical protein YER019w - yeast (Saccharomyces cerevisiae)>GP:SCE9537_20 Saccharomyces cerevisiae chromosome V cosmids 9537, 9581, 9495, 9867, and lambda clone 5898	0.99

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
175	U32772	Haemophilus influenzae from bases 954819 to 966363 (section 87 of 163) of the complete genome.	0.41	YPT2_CAEE L	HYPOTHETICAL 21.6 KD PROTEIN F37A4.2 IN CHROMOSOME III>PIR2:S44639 F37A4.2 protein - Caenorhabditis elegans>GP:CELF37A 4_8 Caenorhabditis elegans cosmid F37A4	7.80E-21
176	AC002053	Human Chromosome 9p22 Cosmid Clone 92f5, complete sequence.	0.4	HSU33837_1	Human glycoprotein receptor gp330 precursor, mRNA, complete cds	1
177	U88309	Caenorhabditis elegans cosmid T23B3.	0.4	DROMTTGN C_1	Drosophila melanogaster mitochondrial cytochrome c oxidase subunit I (COI) gene, 5' end, Trp-, Cys-, and Tyr-tRNA genes, NADH dehydrogenase subunit 2 (ND2) gene, 3' end	0.99
178	M34025	Human fetal Ig heavy chain variable region (clone M44) mRNA, partial cds.	0.39	DNA2_YEAS T	DNA REPLICATION HELICASE DNA2>PIR2:S48904 probable purine nucleotide-binding protein YHR164c - yeast (Saccharomyces cerevisiae)>GPN:YSC H9986_3 Saccharomyces cerevisiae chromosome VIII cosmid 9986; Dna2p: DNA replication helicase; YHR164C>GP:	1
179	AC002395	Homo sapiens; HTGS phase 1, 127 unordered pieces.	0.39	VV_MUMPE	NONSTRUCTURAL PROTEIN V (NONSTRUCTURAL PROTEIN NS1)	0.11

WO 99/33982

PCT/US98/27610

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
180	AC003101	*** . SEQUENCING IN PROGRESS *** Homo sapiens chromosome 17, clone HRPC41C23; HTGS phase 1, 33 unordered pieces.	0.39	YLK2_CAEE L	HYPOTHETICAL 122.7 KD PROTEIN D1044.2 IN CHROMOSOME III>GP:CELD1044_4 Caenorhabditis elegans cosmid D1044	0.0001
181	Z54335	Human DNA sequence from cosmid L17A9, Huntington's Disease Region, chromosome 4p16.3. Contains VNTR and a CpG island.	0.39	HUMNFAT3 A_1	Homo sapiens NF-AT3 mRNA, complete cds	1.60E-06
182	U95743	Homo sapiens chromosome 16 BAC clone CIT987-SK65D3, complete sequence.	0.38	CEZC434_6	Caenorhabditis elegans cosmid ZC434, complete sequence; ZC434;6; CDNA EST CEESO02F comes from this gene; cDNA EST CEES60F comes from this gene	0.18
183	AC001229	Sequence of BAC F5I14 from Arabidopsis thaliana chromosome 1, complete sequence.	0.34	HSOCAM_1	H;sapiens mRNA for immunoglobulin-like domain-containing 1 protein	0.051
184	X01703	Human gene for alpha-tubulin (b alpha 1).	0.33	NTC3_MOUSE E	NEUROGENIC LOCUS NOTCH 3 PROTEIN>PIR2:S453 06 notch 3 protein - mouse>GP:MMNOTC_1 M;musculus mRNA for Notch 3	0.012

WO 99/33982

PCT/US98/27610

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
185	Z82189	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 170A21; HTGS phase 1.	0.31	LG106_3	Lemna gibba negatively light-regulated mRNA (LG106); Second longest ORF (2)	0.27
186	Z98051	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 501A4; HTGS phase 1.	0.3	S34960	NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Crithidia oncopelti mitochondrion (SGC6)>GP:MICO CN NR_3 Crithidia oncopelti mitochondrial ND4, ND5, COI, 12S ribosomal RNA genes for NADH dehydrogenase subunit 4/5, cytochrome oxidase subun	0.25
187	Z98749	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 449O17; HTGS phase 1.	0.3	SCKC_LEIQ H	CHARYBDOTOXIN (CHTX) (CHTX-LQ1)>PIR2:A60963 charybdotoxin 1 - scorpion (Leiurus quinquestriatus)>3D:2 CRD Charybdotoxin (nmr, 12 structures) - scorpion (Leiurus quinquestriatus)	0.12
188	X96763	C.albicans CDC4 gene.	0.29	CECC4_1	Caenorhabditis elegans cosmid CC4, complete sequence; CC4;a; Protein predicted using Genefinder; preliminary prediction	1.30E-17

WO 99/33982

PCT/US98/27610

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
189	U38804	Porphyra purpurea chloroplast genome, complete sequence.	0.28	HIVHCDR3C_1	Human immunodeficiency virus type 1 heavy-chain complementarity-determining region 3 mRNA (clone 11), partial cds; Heavy-chain complementarity-determining region 3 (CDR3) from HIV gp120->GP:HIVHCDR3_1 Human immunodeficiency virus type 1 he	1
190	U20657	Human ubiquitin protease (Unph) proto-oncogene mRNA, complete cds.	0.28	HSU20657_1	Human ubiquitin protease (Unph) proto-oncogene mRNA, complete cds	5.60E-12
191	AC002037	Human Chromosome 11 Overlapping Cosmids cSRL72g7 and cSRL140b8, complete sequence.	0.27	VRP1_YEAST	VERPROLIN>GP:SC VERPRL_1 S;cerevisiae (A364) gene for verprolin	2.00E-11
192	U58748	Caenorhabditis elegans cosmid ZK180.	0.27	EXLP_TOBAC	PISTIL-SECIFIC EXTENSIN-LIKE PROTEIN PRECURSOR (PELP)>PIR2:JQ1696 pistil extensin-like protein precursor (clone pMG15) - common tobacco>GP:NTPMG15_1 N;tabacum mRNA for pistil extensin like protein	4.10E-12
193	Z68013	Caenorhabditis elegans cosmid W02H3, complete sequence.	0.26	<NONE>	<NONE>	<NONE>

WO 99/33982

PCT/US98/27610

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			P VALUE	Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			P VALUE
	ACCESSION	DESCRIPTION			ACCESSION	DESCRIPTION		
194	AF017042	Dictyostelium discoideum LTR-retrotransposon Skipper, partial genomic sequence, 5' end.		0.26	SPBC31F10_14	S.pombe chromosome II cosmid c31F10; Hypothetical protein; SPBC31F10;14c, unknown, len:1586aa, some similarity eg; to YJR140C, YJ9H_YEAST, P47171, involved in cell cycle regulation		1
195	B03174	cSRL-16e2-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-16e2.		0.26	CELC30E1_7	Caenorhabditis elegans cosmid C30E1		0.38
196	X70810	E.gracilis chloroplast complete genome.		0.25	CEK10H10_8	Caenorhabditis elegans cosmid K10H10, complete sequence; K10H10;k; Protein predicted using Genefinder; preliminary prediction		0.98
197	U80024	Caenorhabditis elegans cosmid C18B10.		0.25	MMAF001794_1	Mus musculus Treacher Collins Syndrome protein (Tcof1) mRNA, complete cds; Putative nucleolar phosphoprotein; similar to Homo sapiens Treacher Collins syndrome TCOF1 protein encoded>GP:MMAF001794_1 Mus musculus Treacher Collins Syndrome p		0.017

WO 99/33982

PCT/US98/27610

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			P VALUE	Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			P VALUE
	ACCESSION	DESCRIPTION			ACCESSION	DESCRIPTION		
198	AC000591	Drosophila melanogaster (subclone 9_g3 from P1 DS01486 (D32)) DNA sequence, complete sequence.	0.25	YHGE_ECOL I	HYPOTHETICAL 64.6 KD PROTEIN IN MRCA-PCKA INTERGENIC REGION (F574)>PIR2:E65135 hypothetical 64.6 kD protein in mrcA-pckA intergenic region - Escherichia coli (strain K-12)>GP:ECAE000415_7 Escherichia coli , mrcA, yrfE, yrfF, yrfG, yrfH, yrfI	0.00068		
199	AC000591	Drosophila melanogaster (subclone 9_g3 from P1 DS01486 (D32)) DNA sequence, complete sequence.	0.25	YHGE_ECOL I	HYPOTHETICAL 64.6 KD PROTEIN IN MRCA-PCKA INTERGENIC REGION (F574)>PIR2:E65135 hypothetical 64.6 kD protein in mrcA-pckA intergenic region - Escherichia coli (strain K-12)>GP:ECAE000415_7 Escherichia coli , mrcA, yrfE, yrfF, yrfG, yrfH, yrfI	0.00068		
200	Z99571	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 388N15; HTGS phase 1.	0.24	YA53_SCHP O	HYPOTHETICAL 24.2 KD PROTEIN C13A11.03 IN CHROMOSOME 1>GP:SPAC13A11_3 S.pombe chromosome I cosmid c13A11; Unknown; SPAC13A11:03, unknown, len: 210	0.017		
201	U00672	Human interleukin-10 receptor mRNA, complete cds.	0.24	TFDP00900	- Polypeptides entry for factor Oct-2.5	1.00E-05		

WO 99/33982

PCT/US98/27610

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
202	AC003061	*** SEQUENCING IN PROGRESS *** Mouse Chromosome 6 BAC clone b245c12; HTGS phase 2, 8 ordered pieces.	0.23	CG1_HUMAN	CG1 PROTEIN>GP:HSU46 023_1 Human Xq28 mRNA, complete cds; Orf	0.00078
203	AF009420	Homo sapiens microsatellite sequence in the HNF3a gene.	0.22	PN0675	collagen alpha 1(XVIII) chain - mouse (fragment)>GP:MUSC OLLAG_1 Mouse mRNA for collagen, partial cds	0.00072
204	B18861	F20C18-Sp6 IGF Arabidopsis thaliana genomic clone F20C18.	0.22	TFDP00659	- Polypeptides entry for factor PR	0.0003
205	U00672	Human interleukin-10 receptor mRNA, complete cds.	0.22	TFDP00900	- Polypeptides entry for factor Oct-2.5	1.00E-05
206	X52105	Dictyostelium discoideum SP60 gene for spore coat protein.	0.18	<NONE>	<NONE>	<NONE>
207	L07628	Saccharopolyspora erythraea insertion sequence IS1136, copy B, 3' end.	0.17	D88764_1	Rana catesbeiana mRNA for alpha 2 type I collagen, complete cds	0.00021
208	Z49631	S.cerevisiae chromosome X reading frame ORF YJR131w.	0.16	YSCDAL1A_1	Saccharomyces cerevisiae alantoinase (DAL1) gene, complete cds	1
209	Z87893	F.rubripes GSS sequence, clone 043C17aB8.	0.16	CELC27A12_8	Caenorhabditis elegans cosmid C27A12; Partial CDS; this gene begins in the neighboring clone; coded for by C; elegans cDNA yk127f1;3; coded for by C; elegans cDNA yk127f1;5	1.30E-07

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
210	U92852	Rhoiptelea chiliantha maturase (matK) gene, chloroplast gene encoding chloroplast protein, complete cds.	0.15	SEU40259_5	Staphylococcus epidermidis trimethoprim resistance plasmid pSK639; Orf53	0.95
211	X62620	B.mori Abd-A gene homeobox.	0.15	ATAP22_36	Arabidopsis thaliana DNA chromosome 4, ESSA 1 AP2 contig fragment No; 2; Hypothetical protein; Similarity to NADH dehydrogenase, Chondrus crispus; MNOS.S59107	0.75
212	J02079	epstein-barr virus simple repeat array (ir3).	0.15	A38346	ultra-high-sulfur keratin 1 - mouse>GP:MUSSE1_1 Mouse serine 1 ultra high sulfur protein gene, complete cds; Putative	7.50E-05
213	M35027	Vaccinia virus, complete genome.	0.14	MTF1_FUSN U	MODIFICATION METHYLASE FNUDI (EC 2.1.1.73) (CYTOSINE-SPECIFIC METHYLTRANSFERASE FNUDI) (MFNUDI)	0.87
214	AC003058	*** SEQUENCING IN PROGRESS *** Arabidopsis thaliana 'IGF' BAC 'F27F23' genomic sequence near marker 'CIC06E08'; HTGS phase 1, 8 unordered pieces.	0.14	HEXA_DICDI	BETA-HEXOSAMINIDASE ALPHA CHAIN PRECURSOR (EC 3.2.1.52) (N-ACETYL-BETA-GLUCOSAMINIDASE) (BETA-N-ACETYLHEXOSAMINIDASE)>PIR2:A30766 beta-N-acetylhexosaminidase (EC 3.2.1.52) A precursor - slime mold (Dictyostelium	0.006

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					discoideum>GP:DDIN AGA_1 D;d	
215	AC001229	Sequence of BAC F5114 from Arabidopsis thaliana chromosome 1, complete sequence.	0.13	A49281	pol protein - simian T-cell lymphotropic virus type 1, STLV-1 (isolate Bab34) (fragment)>GP:STVB ABPOLA_1 Simian T-cell leukemia virus PCR derived (pol) gene, partial sequence BAB34POL; Bases 4779-4918 EMBL ATK numbering system; BAB34POL	0.77
216	U46067	Capra hircus beta-mannosidase mRNA, complete cds.	0.12	S70663	lectin heavy chain, N-acetylgalactosamine-specific - Entamoeba histolytica (fragment)>GP:EHU33 443_1 Entamoeba histolytica GalNAc lectin heavy subunit (hgl4) gene, partial cds; N-acetylgalactosamine adherence lectin heavy subunit	0.8
217	AC000380	*** SEQUENCING IN PROGRESS *** Human Chromosome 3 pac pDJ70i11; HTGS phase 1, 2 unordered pieces.	0.12	ATFCA8_19	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No; 8; Unnamed protein product	0.64

WO 99/33982

PCT/US98/27610

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
218	X61207	A.brasilense hisB, H, A, F and E genes for imidazole glycerolphosphate dehydratase, glutamine amidotransferase, phosphorybosilformimino-5-amino-phosphorybosil-4-imidazolecarboxamide isomerase, cyclase and phosphorybosil-AMP-cyclohydrolase.	0.12	OCCL02_1	O.circumcincta colost-2 gene; Cuticular collagen	0.0074
219	AF014259	HIV-1 Patient 1088 from Edinburgh, MA-p17 (gag) gene, partial cds.	0.11	DMU88570_1	Drosophila melanogaster CREB-binding protein homolog mRNA, complete cds; CBP	1
220	AC000636	Drosophila melanogaster (subclone 2_c11 from P1 DS07660 (D44)) DNA sequence, complete sequence.	0.11	A64829	hypothetical protein in dmsC 3' region - Escherichia coli (strain K-12)>GP:ECAE000192_1 Escherichia coli, ycaD, ycaK, pflA, pflB, focA genes from bases 944908 to 955952 (section 82 of 400) of the complete genome; Hypothetical protein in dmsC	0.051
221	AC002428	Human BAC clone GS039E22 from 5q31, complete sequence.	0.11	HISNMYC2_1	Human N-myc gene exon 2; Put; N-myc protein (aa 1-263) (953 is 1st base in codon)	0.00014
222	L40949	Homo sapiens (clone AT7-Seu) opioid-receptor-like protein mRNA, 5' end.	0.11	CEUNC93_2	C.elegans unc-93 gene; Protein 2	1.20E-13

WO 99/33982

PCT/US98/27610

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
223	AL008636	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 722E9; HTGS phase 1.	0.1	XELCOL2A1_A_1	Xenopus laevis alpha-1 collagen type II' mRNA, complete cds; Alpha-1 type II' collagen	2.60E-06
224	D86993	Human (lambda) DNA for immunoglobulin light chain.	0.1	CELM02B7_2	Caenorhabditis elegans cosmid M02B7	1.80E-09
225	AC002539	Homo sapiens chromosome 17, clone 195620, complete sequence.	0.098	MTCY7D11_17	Mycobacterium tuberculosis cosmid Y7D11; Unknown; MTCY07D11;17c; unknown, len: 186 aa, FASTA best: Q10390 Y009_MYCTU hypothetical 31;0 KD protein MTCY190;09C (299 aa) opt: 355 z-score: 316;8	0.026
226	M88165	Human inter-alpha-trypsin inhibitor light chain (ITI) gene, exon 1.	0.096	A54161	ryanodine-binding protein alpha form - bullfrog>GP:D21070_1 Rana catesbeiana mRNA for bullfrog skeletal muscle calcium release channel (ryanodine receptor) alpha isoform(RyR1), complete cds; Ryanodine receptor alpha isoform	1
227	Z92851	Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y39G8; HTGS phase 1.	0.082	CYA7_BOVIN	ADENYLATE CYCLASE, TYPE VII (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYL-LY CYCLASE)	0.3

WO 99/33982

PCT/US98/27610

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			P VALUE	Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION			ACCESSION	DESCRIPTION	P VALUE
228	L00638	Arabidopsis thaliana ubiquitin conjugating enzyme exons 2-4.	0.072	NUCM_TRYBB	NADH-UBIQUINONE OXIDOREDUCTASE 49 KD SUBUNIT HOMOLOG (EC 1.6.5.3) (NADH DEHYDROGENASE SUBUNIT 7 HOMOLOG)>PIR2:A35693 NADH dehydrogenase (EC 1.6.99.3) chain 7 - Trypanosoma brucei mitochondrion (SGC6)	0.24	
229	U49169	Dictyostelium discoideum V-ATPase A subunit (vatA) mRNA, complete cds.	0.071	MMU65594_1	Mus musculus Brea2 mRNA, complete cds; Similar to human breast cancer susceptibility gene BRCA2; Allele: wild type; putative tumor suppressor	1	
230	AF001549	Homo sapiens chromosome 16 BAC clone CIT987SK-270G1 complete sequence.	0.07	PM22_HUMAN	PERIPHERAL MYELIN PROTEIN 22 (PMP-22)>PIR2:JN0503 peripheral myelin protein 22 - human>GP:HUMGAS3X_1 Human peripheral myelin protein 22 (GAS3) mRNA, complete cds>GP:HUMPMP22_1 Human peripheral myelin protein 22 mRNA, complete cds>GP:HUMPMP22	0.0078	
231	L36829	Mus musculus alphaA-crystallin-binding protein I (AlphaA-CRYBP1) gene, complete cds.	0.066	<NONE>	<NONE>	<NONE>	
232	AC000159	*** SEQUENCING IN PROGRESS *** Human BAC Clone 11q13;	0.058	CEZK863_1	Caenorhabditis elegans cosmid ZK863, complete sequence; ZK863.2; Similar to collagen	1	

WO 99/33982

PCT/US98/27610

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		HTGS phase 1, 10 unordered pieces.				
233	AC000159	*** SEQUENCING IN PROGRESS *** Human BAC Clone 11q13; HTGS phase 1, 10 unordered pieces.	0.058	CAC2_HAEC O	CUTICLE COLLAGEN 2C (FRAGMENT)>GP:H AECOL2C_1 H;contortus collagen 2C mRNA, 3'end	1.20E-08
234	Z23908	H. sapiens (D5S630) DNA segment containing (CA) repeat; clone AFM268zd9; single read.	0.057	VEU34999_1	Venezuelan equine encephalitis virus nonstructural and structural polyprotein genes, complete cds; Nonstructural polyprotein; Internal stop codon, readthrough occurs 5% of the time	0.0002
235	B21875	T3E8-Sp6 TAMU Arabidopsis thaliana genomic clone T3E8.	0.055	YRR2_CAEE L	HYPOTHETICAL 91.1 KD PROTEIN R144.2 IN CHROMOSOME III>GP:CELR144_7 Caenorhabditis elegans cosmid R144; Coded for by C; elegans cDNA CEESP84R; coded for by C; elegans cDNA yk23c4;5; coded for by C; elegans cDNA yk44f9;5; coded for by C; eleg	0.68
236	Z98303	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 140H19; HTGS phase 1.	0.048	AC002330_3	Arabidopsis thaliana BAC T10P11, complete sequence; Putative zinc-finger protein; C2H2 Zn-finger signature from position 80 to 100 [CEICNKGFFORDQNL QLHRRGH]	0.99

WO 99/33982

PCT/US98/27610

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
237	D49911	Thermus thermophilus UvrA gene, complete cds.	0.044	APP1_MOUSE	AMYLOID-LIKE PROTEIN 1 PRECURSOR (APLP)>PIR2:A46362 amyloid precursor-like protein - mouse>GP:MUSAPLP_1 Mouse amyloid precursor-like protein mRNA, complete cds	8.90E-06
238	D49911	Thermus thermophilus UvrA gene, complete cds.	0.044	MMCOL18A1_2	Mus musculus alpha-1(XVIII) collagen (COL18A1) gene, exons 40-43, complete cds	1.60E-06
239	X78119	P.amygdalus, Batsch (Texas) prul mRNA.	0.042	CA44_HUMAN	COLLAGEN ALPHA 4(IV) CHAIN PRECURSOR>PIR1:CGHU1B collagen alpha 4(IV) chain precursor - human>GP:HSCOL4A4_1 H;sapiens mRNA for collagen type IV alpha 4 chain; Type IV collagen alpha 4 chain	2.00E-06
240	U72877	Rana catesbeiana L-epinephrine transporter mRNA, complete cds.	0.041	YRR6_MYCA	HYPOTHETICAL 33.0 KD PROTEIN IN LICA 3'REGION (ORF R6)>PIR2:S42125 hypothetical protein 3 - Mycoplasma capricolum (SGC3)>GP:MYCRP MH_6 M; capricolum rpmH, rpmA and licA gene; Orf R6	0.0008
241	L39891	Homo sapiens polycystic kidney disease-associated protein (PKD1) gene, complete cds.	0.04	MUC2_HUMAN	MUCIN 2 (INTESTINAL MUCIN 2) (FRAGMENTS)	5.90E-05
242	L40390	Candida glabrata ERG3 gene, complete cds.	0.039	G01763	atrophin-1 - human>GP:HSU23851_1 Human atrophin-1 mRNA, complete cds	9.00E-07

WO 99/33982

PCT/US98/27610

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
243	B28113	T2L16TRB TAMU Arabidopsis thaliana genomic clone T2L16.	0.038	CELZK1248_14	Caenorhabditis elegans cosmid ZK1248	1.60E-18
244	AC000030	00175, complete sequence.	0.033	ATFCA8_40	Arabidopsis thaliana DNA chromosome 4, ESSA 1 contig fragment No; 8; Glycerol-3-phosphate permease homolog; Similarity to glycerol-3-phosphate permease - Haemophilus influenzae	0.63
245	B10738	F13G15-Sp6 IGF Arabidopsis thaliana genomic clone F13G15.	0.032	D87521_1	Mus musculus DNA-PKcs mRNA, complete cds	0.21
246	AF024503	Caenorhabditis elegans cosmid F31F4.	0.03	I38344	titin - human	1
247	Z49888	Caenorhabditis elegans cosmid F47A4, complete sequence.	0.027	KSU52064_1	Kaposi's sarcoma-associated herpes-like virus ORF73 homolog gene, complete cds; Herpesvirus saimiri ORF73 homolog>GP:KSU756 98_78 Kaposi's sarcoma-associated herpesvirus long unique region, 80 putative ORFs and kaposin gene, complete cds; OR	3.40E-10
248	Z83822	Human DNA sequence from PAC 306D1 on chromosome X contains ESTs.	0.025	GRSB_BACBR	GRAMICIDIN S SYNTHETASE II (GRAMICIDIN S BIOSYNTHESIS GRSB PROTEIN) (EC 6.-.-.-)	1
249	Z94161	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone N102C10; HTGS	0.025	S16323	hypothetical protein - Arabidopsis thaliana>GP:ATHB1_1 A;thaliana homeobox gene Athb-1 mRNA; Open reading frame	0.0079

WO 99/33982

PCT/US98/27610

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		phase 1.				
250	AC002094	Genomic sequence from Human 17, complete sequence.	0.021	S57447	HPBR11-7 protein - human>GP:HSHPBRII 4_1 H;sapiens HPBR11-4 mRNA>GP:HSHPBRII 7_1 H;sapiens HPBR11-7 gene	8.20E-08
251	D79994	Human mRNA for KIAA0172 gene, partial cds.	0.021	CER10H10_1	Caenorhabditis elegans cosmid R10H10, complete sequence; R11A8;7; Protein predicted using Genefinder; Similarity to Mouse ankyrin (PIR Acc; No; S37771); cDNA EST CEESX25F comes from this gene;	7.00E-16
252	Z97635	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 438L4; HTGS phase 1.	0.017	CELW05H7_4	Caenorhabditis elegans cosmid W05H7	0.24
253	X84996	X.laevis mRNA for selenocysteine tRNA acting factor (Staf).	0.017	JN0786	integrin beta-4 chain precursor - mouse	0.088
254	AC002543	Human BAC clone RG300C03 from 7q31.2, complete sequence.	0.013	MZLMTCT BT_1	Mendocellus isis mitochondrial NADH dehydrogenase, and cytochrome b genes, 3' end, and transfer RNA-Ser gene; This codes for the last 43 amino acids of NADH dehydrogenase subunit 1 followed	0.044

WO 99/33982

PCT/US98/27610

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
255	U10401	Caenorhabditis elegans cosmid T20B12.	0.012	MMMHC29N_7_2	Mus musculus major histocompatibility locus class III region:butyrophilin-like protein gene, partial cds; Notch4, PBX2. RAGE, lysophatidic acid acyl transferase-alpha, palmitoyl-	0.069
256	L14593	Saccharomyces cerevisiae protein phosphatase (PTC1) gene, complete cds.	0.011	D86995_1	Human (gene 1) DNA for phosphatase 2C motif, partial cds	2.20E-14
257	U62317	Chromosome 22q13 BAC Clone CIT987SK-384D8 complete sequence.	0.0093	P2Y8_XENL_A	P2Y PURINOCEPTOR 8 (P2Y8)>GP:XL P2Y8_1 X;laevis mRNA for P2Y8 nucleotide receptor	0.89
258	D29655	Pig mRNA for UMP-CMP kinase, complete cds.	0.0075	AF004858_1	Mus musculus platelet activating factor receptor mRNA, partial cds; PAF-receptor	1
259	AF002992	Homo sapiens cosmid from Xq28, complete sequence.	0.0054	FBNI_BOVIN	FIBRILLIN 1 PRECURSOR>PIR2:A 55567 fibrillin 1 - bovine>GP:BOVXAA AA_1 Bos taurus mRNA, complete cds; Putative	0.0004
260	B20752	T19M2-T7 TAMU Arabidopsis thaliana genomic clone T19M2.	0.0043	HSV1IEP_1	Feline herpesvirus type 1 gene for immediate early protein, complete cds; Feline herpesvirus type 1 immediate early protein	3.90E-05

WO 99/33982

PCT/US98/27610

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
261	AB006699	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDJ22.	0.0037	YHV5_YEAS T	HYPOTHETICAL 143.6 KD PROTEIN IN SPO16-REC104 INTERGENIC REGION>PIR2:S4675 4 hypothetical protein YHR155w - yeast (Saccharomyces cerevisiae)>GPN:YSC H9666_15 Saccharomyces cerevisiae chromosome VIII cosmid 9666; Yhr155wp; Similar to Sip3p (Snf	0.077
262	Z99128	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 422H11; HTGS phase I.	0.0032	ALU1_HUMAN	!!!! ALU SUBFAMILY J WARNING ENTRY !!!!	0.0087
263	B21848	T2D2-Sp6 TAMU Arabidopsis thaliana genomic clone T2D2.	0.0031	B31794	mdm-1 protein (clone c103) - mouse	1.00E-05
264	L33853	Human germline immunoglobulin kappa chain variable region (Vk-IV subgroup) for anti-B-amyloid autoantibodies in Alzheimer's disease.	0.0027	B45550	cytochrome b homolog - Plasmodium yoelii	0.99
265	B36863	HS-1042-A1-F01-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 824 Col=1 Row=K.	0.0027	YQK4_CAEE L	HYPOTHETICAL 64.3 KD PROTEIN C56G2.4 IN CHROMOSOME III>GP:CELC56G2_2 Caenorhabditis elegans cosmid C56G2	0.81

WO 99/33982

PCT/US98/27610

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
266	AC003041	*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 17, clone HCIT307A16; HTGS phase 1, 10 unordered pieces.	0.0024	GLB4_LAMSP	GIANT HEMOGLOBIN AIV CHAIN (FRAGMENT)>PIR2: S01810 hemoglobin AIV - tube worm (Lamellibrachia sp.) (fragment)	0.94
267	AC002315	Mouse BAC-146N21 Chromosome X contains iduronate-2-sulfatase gene; complete sequence.	0.0022	MG42_TARMA	SRV-RELATED PROTEIN MG42 (FRAGMENT)>PIR3:I 51369 Sry-related sequence - Tarentola mauritanica (fragment)>GP:TELM G42DNA_1 Gecko MG42 gene, partial cds; Sry-related sequence	0.99
268	AF016674	Caenorhabditis elegans cosmid C03H5.	0.0015	SCYJL204C_1	S.cerevisiae chromosome X reading frame ORF YJL204c	1
269	AF016674	Caenorhabditis elegans cosmid C03H5.	0.0015	CEM199_3	Caenorhabditis elegans cosmid M199, complete sequence; M199g; Protein predicted using Genefinder; preliminary prediction	0.97
270	AF016674	Caenorhabditis elegans cosmid C03H5.	0.0015	CEM199_3	Caenorhabditis elegans cosmid M199, complete sequence; M199g; Protein predicted using Genefinder; preliminary prediction	0.97
271	Z54199	L.esculentum DNA Ailsa craig encoding l-aminocyclopropane-1-carboxylic acid oxidase.	0.0015	CEL20A1_5	Caenorhabditis elegans cosmid F20A1; Coded for by C; elegans cDNA yk9g1.3; coded for by C; elegans cDNA yk9g1.5; coded for by C; elegans cDNA CEESU55F;	0.11

WO 99/33982

PCT/US98/27610

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					weak similarity to putative	
272	Z99943	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 313L4; HTGS phase 1.	0.0014	CEK08F8_5	Caenorhabditis elegans cosmid K08F8, complete sequence; K08F8;5b	0.93
273	S81083	beta - ADD=adducin beta subunit 63 kda isoform/membrane skeleton protein, beta - ADD=adducin beta subunit 63 kda isoform/membrane skeleton protein {alternatively spliced, exon 10 to 13 region} [human, Genomic, 1851 nt, segment 3 of 3].	0.0013	MTCY277_7	Mycobacterium tuberculosis cosmid Y277; Unknown; MTCY277:07c, unknown, len: 302	0.0001
274	Z82174	Human DNA sequence from cosmid B20F6 on chromosome 22q11.2-qter.	0.001	FBLA_HUMAN	FIBULIN-1, ISOFORM A PRECURSOR>GP:HS FIBUA_1 H;sapiens mRNA for fibulin-1 A	0.00063
275	Z82215	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 6802; HTGS phase 1.	0.00079	BFR1_SCHPO	BREFELDIN A RESISTANCE PROTEIN>PIR2:S52239 hba2 protein - fission yeast (Schizosaccharomyces pombe)>GP:SPHBA2 GEN_1 S;pombe hba2 gene	0.15

WO 99/33982

PCT/US98/27610

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
276	U28153	Caenorhabditis elegans UNC-76 (unc-76) gene, complete cds.	0.00071	CX2_HEMHA	CYTOTOXIN 2 (TOXIN 12A)	0.32
277	Z82204	Human DNA sequence from clone J362G171.	0.00054	DMU34925_2	Drosophila melanogaster DNA repair protein (mei-41) gene, complete cds, and TH1 gene, partial cds	0.045
278	AC002530	Human BAC clone RG341D10 from 7p15-p21, complete sequence.	0.00053	CELT28F2_2	Caenorhabditis elegans cosmid T28F2; Weak similarity to HSP90	0.037
279	U91322	Human chromosome 16p13 BAC clone CIT987SK-276F8 complete sequence.	0.00051	CEW08D2_2	Caenorhabditis elegans cosmid W08D2, complete sequence; W08D2;3; Protein predicted using Genefinder>GP:CEW08D2_2 Caenorhabditis elegans cosmid W08D2; W08D2;3; Protein predicted using Genefinder	0.26
280	D16986	Human HepG2 partial cDNA, clone hmd2b09m5.	0.00037	POLG_PPVN A	GENOME POLYPROTEIN (CONTAINS: N-TERMINAL PROTEIN; HELPER COMPONENT PROTEINASE (EC 3.4.22.-) (HC-PRO); 42-50 KD PROTEIN; CYTOPLASMIC INCLUSION PROTEIN (CI); 6 KD PROTEIN; NUCLEAR INCLUSION PROTEIN A (NI- A) (EC 3.4.22.-) (49K PROTEINASE) (49	0.48
281	U91318	Human chromosome 16p13 BAC clone CIT987SK-962B4 complete	0.00031	<NONE>	<NONE>	<NONE>

WO 99/33982

PCT/US98/27610

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		sequence.				
282	M93406	Human dispersed Alu repeats and dispersed L1 repeat.	0.0003	VG8_SPV4	GENE 8 PROTEIN>PIR1:G8BP SV gene 8 protein - spiroplasma virus 4 (SGC3)	0.23
283	AC002398	Human DNA from chromosome 19-specific cosmid F25965, genomic sequence, complete sequence.	0.00021	HMCA_DROME	HOMEOTIC CAUDAL PROTEIN>PIR2:A263 57 homeotic protein Cad - fruit fly (Drosophila melanogaster)>GP:DR OCADA2_1 D;melanogaster caudal gene (cad) encoding a maternal and zygotic transcript, exon 2; Caudal protein>TFD:TFDP001 59 - Polypeptides en	0.021
284	AC002530	Human BAC clone RG341D10 from 7p15-p21, complete sequence.	0.0002	PL0009	complement C3d/Epstein-Barr virus receptor precursor - human	0.7
285	X01871	Yeast mitochondrial ori(o) repeat unit of petite mutant 5 (petite strain s-10/7/2).	0.00015	RVZMTCYBT_1	Reventazonia sp; mitochondrial NADH dehydrogenase, and cytochrome b genes, 3' end, and transfer RNA- Ser gene; This codes for the last 43 amino acids of NADH dehydrogenase subunit 1 followed	0.73
286	U89984	Acanthamoeba castellanii transformation-sensitive protein homolog mRNA, complete cds.	0.00015	ACU89984_1	Acanthamoeba castellanii transformation-sensitive protein homolog mRNA, complete cds; Similar to human transformation-	4.20E-13

WO 99/33982

PCT/US98/27610

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					sensitive protein: SwissProt Accession Number P31948	
287	AC002365	Homo sapiens chromosome X clone U177G4, U152H5, U168D5, 174A6, U172D6, and U186B3 from Xp22, complete sequence.	0.00011	S10340	DNA-directed RNA polymerase (EC 2.7.7.6) - yeast (<i>Kluyveromyces marxianus</i> var. <i>lactis</i>)	0.00062
288	AC002390	Human DNA from overlapping chromosome 19-specific cosmids R30072 and R28588, genomic sequence, complete sequence.	9.90E-05	D86603_1	Mouse mRNA for Bach protein 1, complete cds; Bach1	1
289	AC002980	Homo sapiens; HTGS phase 1, 34 unordered pieces.	9.20E-05	TRBKPCYB_1	<i>Trypanosoma brucei</i> kinetoplast apocytochrome b gene, complete cds	0.52
290	M99412	Human interleukin-8 receptor (IL8RB) gene, complete cds.	4.50E-05	S28832	microtubule-associated protein H1 (clone KS3.1) - longfin squid (fragment)	0.88
291	AC000120	Human BAC clone RG161K23 from 7q21, complete sequence.	4.00E-05	SXSCRBA_1	<i>S. xylosus</i> scrB and scrR genes; Sucrose repressor	0.99

WO 99/33982

PCT/US98/27610

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
292	AC003037	Homo sapiens; HTGS phase 1, 66 unordered pieces.	3.40E-05	S13569	hypothetical protein 5 - Lactococcus lactis subsp. lactis insertion sequence 1076>GP:LLTLE_1 Lactococcus lactis DNA for the transposon-like element on the lactose plasmid; ORF5 (AA 1 - 43)	0.018
293	Z81512	Caenorhabditis elegans cosmid F25C8, complete sequence.	2.40E-05	MUSDBPRC_1	Mus musculus DNA-binding protein Rc mRNA, complete cds; DNA binding protein Rc	1
294	B16681	343C3.TVB CIT978SKA1 Homo sapiens genomic clone A-343C03.	1.10E-05	COPP_YEAS_T	COATOMER BETA' SUBUNIT (BETA'-COAT PROTEIN) (BETA'-COP)>PIR2:B55123 coatomer complex beta' chain - yeast (Saccharomyces cerevisiae)>GPN:SCY GL137W_1 S;cerevisiae chromosome VII reading frame ORF YGL137w>GP:SCU11 237_1 Saccharomyces cerevisiae	0.081
295	Z16523	H. sapiens (D9S158) DNA segment containing (CA) repeat; clone AFM073yb11; single read.	1.00E-05	MMSEMF_1	M.musculus mRNA for semaphorin F; Smaphorin F	0.78
296	Z49704	S.cerevisiae chromosome XIII cosmid 8021.	5.60E-06	<NONE>	<NONE>	<NONE>
297	AC003071	Human BAC clone BK085E05 from 22q12.1-qter, complete sequence.	3.00E-06	HSRCAER_1	H;sapiens mRNA for red cell anion exchanger (EPB3, AE1, Band 3) 3' non-coding region	0.21

WO 99/33982

PCT/US98/27610

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
298	U20428	Human SNC19 mRNA sequence.	1.40E-06	HUMMUC2A_1	Human mucin-2 gene, partial cds	4.40E-06
299	U51903	Human RasGAP-related protein (IQGAP2) mRNA, complete cds.	6.60E-07	IQGA_HUMAN	RAS GTPASE-ACTIVATING-LIKE PROTEIN IQGAP1 (P195)>PIR2:A54854 Ras GTPase activating-related protein - human>GP:HUMIQGA_1 Homo sapiens ras GTPase-activating-like protein (IQGAP1) mRNA, complete cds; Amino acid feature: IQ calmodulin-binding do	1.60E-14
300	AL000805	F.rubripes GSS sequence, clone 021G08aA1.	4.70E-07	MT13_MYTED	METALLOTHIONEIN 10-III (MT-10-III)>PIR2:S39418 metallothionein 10-III - blue mussel	2.20E-10
301	AC003016	Human BAC clone RG134C19 from 8q21, complete sequence.	4.30E-07	SPC57A10_5	S.pombe chromosome I cosmid c57A10; Unknown; SPAC57A10;05;c, unknown, len:606aa, similar to A; nidulans Q00659, sulfur metabolite repression control, (678aa), fasta scores, opt:1355,	0.00041
302	AC003089	Human BAC clone RG180F08A, complete sequence.	3.80E-07	HPBPREFCK_1	Hepatitis B virus type 11 precore protein (pre-C region, C) gene, 5' end	0.41
303	AC002074	Human BAC clone GS056H18 from 7q31-q32, complete sequence.	2.40E-07	A47021_1	Sequence 23 from Patent WO9527787; Unnamed protein product; Author-given protein sequence is in conflict with the conceptual translation>GP:A51260_1 Sequence 23 from Patent WO9614416; Unnamed protein product; Author-given	0.0016

WO 99/33982

PCT/US98/27610

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					protein sequence is i	
304	U04980	Rattus norvegicus fetal troponin T 3 (fetal TnT3) mRNA, partial cds.	2.20E-07	HUMFSDH_1	Human facioscapulohumeral muscular dystrophy (FSDH) gene region, D4Z4 tandem repeat unit; ORF	3.30E-08
305	U68704	Human chromosome 21q22.3 P1-clone 3804 subclone 4-52.	2.00E-07	HHV6AGNM_96	Human herpesvirus-6 (HHV-6) U1102, variant A, complete virion genome; U88; Cys repeats; this loci is open in all six reading frames, part of IE-A	2.70E-05
306	U51583	Rattus norvegicus zinc finger homeodomain enhancer-binding protein-1 (Zfhep-1) mRNA, partial cds.	8.70E-08	AF005370_67	Alcelaphine herpesvirus 1 L-DNA, complete sequence; Putative immediate early protein; ORF73; similar to H; saimiri and KSHV ORF73	6.10E-07
307	M80206	Mus domesticus poliovirus receptor homolog (MPH) mRNA, complete cds.	8.10E-08	I53960	PRR2 alpha - human	1.70E-28
308	M60854	Human ribosomal protein S16 mRNA, complete cds.	5.70E-08	OLVPOL_1	Caprine arthritis encephalitis virus (isolate OVLV-N1) pol protein gene, 3' end of cds; Nt 2497-2695 from CAEV Co	0.27
309	U82828	Homo sapiens ataxia telangiectasia (ATM) gene, complete cds.	1.50E-08	C40201	artifact-warning sequence (translated ALU class C) - human	0.00044

WO 99/33982

PCT/US98/27610

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
310	Z83836	Human DNA sequence from PAC 111J24 on chromosome 22q12-qter contains ESTs.	1.40E-08	HSU64473_1	Human rheumatoid arthritis synovium immunoglobulin heavy chain variable region mRNA, partial cds>GP:HSU64498_1 Human rheumatoid arthritis synovium immunoglobulin heavy chain variable region mRNA, partial cds	0.34
311	Z50029	Caenorhabditis elegans cosmid ZC504, complete sequence.	1.40E-08	MMU88984_1	Mus musculus NIK mRNA, complete cds	1.70E-50
312	AC002351	Homo sapiens; HTGS phase 1, 17 unordered pieces.	1.20E-08	D41132	collagen-related protein 4 - Hydra magnipapillata (fragment)>PIR2:S21932 mini-collagen - Hydra sp.>GP:HSNCOL4_1 Hydra N-COL 4 mRNA for mini-collagen; No start codon	0.02
313	B65763	CIT-HSP-2023A12.TR CIT-HSP Homo sapiens genomic clone 2023A12.	3.60E-09	S18106	type II site-specific deoxyribonuclease (EC 3.1.21.4) A brl - Azospirillum brasilense	0.045
314	Z93021	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 516C23; HTGS phase 1.	2.00E-09	AB001684_134	Chlorella vulgaris C-27 chloroplast DNA, complete sequence; RNA polymerase gamma subunit	0.6
315	D88035	Rat mRNA for glycoprotein specific UDP-glucuronyltransferase, complete cds.	1.50E-09	D88035_1	Rat mRNA for glycoprotein specific UDP-glucuronyltransferase, complete cds	1.00E-33

WO 99/33982

PCT/US98/27610

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
316	U85193	Human nuclear factor I-B2 (NFIB2) mRNA, complete cds.	1.30E-10	VGFI_IBVB	F1 PROTEIN>PIR1:VFII B1 F1 protein - avian infectious bronchitis virus (strain Beaudette)>GP:IBACG B_1 Avian infectious bronchitis virus pol protein, spike protein, small virion-associated protein, membrane protein, and nucleocapsid protein gen	1
317	B04719	cSRL-42G12-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-42G12.	7.90E-11	JC5238	galactosylceramide-like protein, GCP - human	0.31
318	M73506	Mouse Tcp-10c (t allele) gene.	2.80E-11	A39487	T-complex protein 10a (allele 129) - mouse	4.10E-16
319	U71148	Human Xq28 cosmids U225B5 and U236A12, complete sequence.	1.20E-11	A56547	sex-peptide precursor - Drosophila suzukii	0.4
320	Z95116	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 57G9; HTGS phase 1.	9.90E-13	ALU2_HUMAN	!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!	0.0017
321	M64795	Rat MHC class I antigen gene (RT1-u haplotype), complete cds.	1.70E-14	STC_DROME	SHUTTLE CRAFT PROTEIN>GP:DMU0 9306_1 Drosophila melanogaster shuttle craft protein (stc) mRNA, complete cds; C-terminal 222 amino acids encode a novel single- stranded DNA binding domain	1.40E-13

WO 99/33982

PCT/US98/27610

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
322	Y09036	H.sapiens NTRK1 gene, exon 17.	4.20E-15	AF010403_1	Homo sapiens ALR mRNA, complete cds; Alternatively spliced; similarity to ALL-1 and Drosophila trithorax	1
323	U12523	Rattus norvegicus ultraviolet B radiation-activated UV98 mRNA, partial sequence.	2.90E-15	SPBC30D10_4	S.pombe chromosome II cosmid c30D10; Hypothetical protein; SPBC30D10;04, unknown, len:148aa	2.40E-09
324	Z98755	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 76C18; HTGS phase 1.	2.20E-15	RPON_HAL MA	DNA-DIRECTED RNA POLYMERASE SUBUNIT N (EC 2.7.7.6)>PIR2:D41715 DNA-directed RNA polymerase II chain RPB10 homolog - Haloarcula marismortui>GP:HAL HMAENOA_4 H;marismortui tRNA-Leu, HL29, HmaL13, HmaS9, OrfMMV, OrfMNA, 2-phosphoglycerate dehydr	0.019
325	M86917	Human oxysterol-binding protein (OSBP) mRNA, complete cds.	1.60E-15	CEF14H8_2	Caenorhabditis elegans cosmid F14H8, complete sequence; F14H8;1; Similarity to Human oxysterol-binding protein (S.W:OXYB_HUMAN)	2.10E-18
326	AC001231	Genomic sequence from Human 17, complete sequence.	1.30E-15	AC002397_3	Mouse BAC284H12 Chromosome 6, complete sequence; DRPLA	0.0016
327	AL008626	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1114G22; HTGS phase 1.	5.30E-16	TAU48227_1	Triticum aestivum soluble starch synthase mRNA, partial cds	5.90E-05

WO 99/33982

PCT/US98/27610

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
328	L04483	Human ribosomal protein S21 (RPS21) mRNA, complete cds.	7.60E-17	RS21_HUMAN	40S RIBOSOMAL PROTEIN S21>PIR2:S34108 ribosomal protein S21 - human>GP:SSZ84015_1 S.scrofa mRNA; expressed sequence tag (3'; clone c11g10); 40S ribosomal protein S21; Similar to human 40S ribosomal protein S21>GP:HUMRPS21X_1 Human ribosomal	1.40E-09
329	AB001899	Homo sapiens PACE4 gene, exon 2.	6.70E-17	LRP1_HUMAN	LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 1 PRECURSOR (LRP) (ALPHA-2-MACROGLOBULIN RECEPTOR) (A2MR) (APOLIPOPROTEIN E RECEPTOR) (APOER)>PIR2:S0239_2 LDL receptor-related protein precursor - human>GP:HSLDLRR L_1 Human mRNA for LDL-recept	1
330	Z98755	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 76C18; HTGS phase 1.	4.40E-17	U97553_59	Murine herpesvirus 68 strain WUMS, complete genome; Ribonucleotide reductase large	0.06
331	AF017187	Homo sapiens LTR HERV-K repetitive element fragment ltr_19_9a sequence.	3.90E-18	D84255_1	Ovophis okinavensis mitochondrial DNA for NADH dehydrogenase subunit 1, partial cds, Ile-tRNA, Pro-tRNA, Phe-tRNA, Gln-tRNA, Met-tRNA and control region (D-loop region); This cds	0.007

WO 99/33982

PCT/US98/27610

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			ACCESSION	Nearest Neighbor (BlastX vs. Non-Redundant Proteins)	
	ACCESSION	DESCRIPTION	P VALUE		DESCRIPTION	P VALUE
332	B36252	HS-1038-A2-G01-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 820 Col=2 Row=M.	3.10E-18	PGBM_MOUSE	BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN PRECURSOR (HSPG) (PERLECAN) (PLC)-PIR2:S18252 heparan sulfate proteoglycan - mouse>GP:MUSPERP A_1 Mouse perlecan mRNA, complete cds	0.00015
333	D78255	Mouse mRNA for PAP-1, complete cds.	2.70E-18	MUSPAP1_1	Mouse mRNA for PAP-1, complete cds	3.50E-18
334	AC003046	Human Xp22 PACs RPC11-263P4 and RPC11-164K3 complete sequence.	1.40E-18	CEC34F6_1	Caenorhabditis elegans cosmid C34F6; C34F6;1; CDNA EST yk46b12;5 comes from this gene; cDNA EST yk44c4;5 comes from this gene; cDNA EST yk46b12;3 comes from this gene	0.0015
335	AC003002	Human DNA from overlapping chromosome 19-specific cosmid R29515 and R28253, genomic sequence, complete sequence.	1.40E-18	MUSZFP0_1	Mouse mRNA for zinc finger protein, partial sequence	1.30E-19
336	Y15054	Rattus norvegicus mRNA for 70 kDa tumor specific antigen, partial.	3.40E-19	HS4U2IR2_1	Epstein-Barr virus (AG876 isolate) U2-IR2 domain encoding nuclear protein EBNA2, complete cds; Nuclear antigen 2	2.00E-06
337	Z97876	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 295C6; HTGS	1.30E-19	AF003535_1	Homo sapiens L1 element ORF2-like protein gene, partial cds	7.00E-05

WO 99/33982

PCT/US98/27610

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		phase 1.				
338	M97159	Mouse (clone pIL2) B1 dispersed repeat unit.	1.10E-19	A26882	pIL2 hypothetical protein - rat (fragment)>GP:RATT DR_1 Rat growth and transformation-dependent mRNA, 3' end; Growth and transformation dependent protein	0.2
339	U30817	Bos taurus very-long-chain acyl-CoA dehydrogenase mRNA, nuclear gene encoding mitochondrial protein, complete cds.	4.70E-20	ACDV_RAT	ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC PRECURSOR (EC 1.3.99.-) (VLCAD)>PIR2:A548 72 acyl-CoA dehydrogenase (EC 1.3.99.-) very-long-chain-specific precursor - rat>GP:RATVLCAD_1 Rat mRNA for very-long-chain Acyl-CoA dehydrogenase, compl	8.10E-25
340	Y11535	H.sapiens mRNA for SHOXb protein.	2.80E-20	ALU1_HUMAN	!!!! ALU SUBFAMILY J WARNING ENTRY !!!!	0.00027
341	AL008730	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 487J7; HTGS phase 1.	7.10E-21	C40201	artifact-warning sequence (translated ALU class C) - human	0.001
342	U96629	Human chromosome 8 BAC clone CIT987SK-2A8 complete sequence.	5.30E-23	ALU1_HUMAN	!!!! ALU SUBFAMILY J WARNING ENTRY !!!!	3.80E-10

WO 99/33982

PCT/US98/27610

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
343	U95743	Homo sapiens chromosome 16 BAC clone CIT987-SK65D3, complete sequence.	2.10E-24	UROM_HUMAN	UROMODULIN PRECURSOR (TAMM-HORSFALL URINARY GLYCOPROTEIN) (THP)>PIR2:A30452 uromodulin precursor - human>GP:HUMUMOD_1 Human uromodulin (Tamm-Horsfall glycoprotein) mRNA, complete cds; Uromodulin precursor	1
344	U15972	Mus musculus homeobox (Hoxa7) gene, complete cds.	4.00E-25	S20790	extensin - almond>GP:PAEXTS_1 P;amygdalus mRNA for extensin	0.34
345	U15972	Mus musculus homeobox (Hoxa7) gene, complete cds.	4.00E-25	CA24_CAEL	COLLAGEN ALPHA 2(IV) CHAIN PRECURSOR>GP:CECOLA2IV_2 C;elegans a2(IV) collagen gene; Alternatively spliced transcript	0.1
346	Z66242	H.sapiens CpG island DNA genomic MseI fragment, clone 84a4, reverse read cpg84a4.rt1a.	4.80E-26	CEC35A5_8	Caenorhabditis elegans cosmid C35A5, complete sequence; C35A5.8; CDNA EST yk31f6;5 comes from this gene; cDNA EST yk38h1;3 comes from this gene; cDNA EST yk38h1;5 comes from this gene;	7.70E-19
347	L25331	Rattus norvegicus lysyl hydroxylase mRNA, complete cds.	3.90E-26	LYSH_CHICK	PROCOLLAGEN-LYSINE,2-OXOGLUTARATE 5-DIOXYGENASE PRECURSOR (EC 1.14.11.4) (LYSYL HYDROXYLASE)>PIR2:A23742 procollagen-lysine 5-dioxygenase (EC 1.14.11.4) precursor - chicken>GP:CHKLYH_1 Chicken lysyl	1.10E-43

WO 99/33982

PCT/US98/27610

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					hydroxylase mRNA, complete cds	
348	L81569	Drosophila melanogaster (subclone 2_d7 from P1 DS04260 (D68)) DNA sequence, complete sequence.	3.30E-26	CELC52B9_2	Caenorhabditis elegans cosmid C52B9; Coded for by C; elegans cDNA cm11d6; weakly similar to S; cervisiae PTM1 precursor (SP:P32857)	8.40E-29
349	U78082	Human RNA polymerase transcriptional regulation mediator (h-MED6) mRNA, complete cds.	2.30E-26	HSU78082_1	Human RNA polymerase transcriptional regulation mediator (h-MED6) mRNA, complete cds; H-Med6p	1.50E-16
350	U43381	Human Down Syndrome region of chromosome 21 DNA.	2.10E-28	HSMRNBAB_1	H;sapiens genomic DNA, integration site for Epstein-Barr virus; Hypothetical protein	0.18
351	D50416	Mouse mRNA for AREC3, complete cds.	2.50E-29	A29947	prostaglandin-endoperoxide synthase (EC 1.14.99.1) precursor - sheep>GP:SHPCOXA_1 Sheep prostaglandin endoperoxide synthetase (cyclooxygenase), complete cds; Cyclooxygenase precursor (EC 1;14;99;1)	0.81

WO 99/33982

PCT/US98/27610

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
352	U85193	Human nuclear factor I-B2 (NFIB2) mRNA, complete cds.	2.20E-29	CFU30222_1	Crithidia fasciculata fully edited ATPase subunit 6 (MURF4) mRNA, partial cds; Cryptogene	0.53
353	Z92826	Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone C18D11; HTGS phase 1.	1.10E-30	SPAC1B3_5	S.pombe chromosome I cosmid c1B3; Hypothetical protein; SPAC1B3;05, probable transcriptional regulator, len:630aa, similar eg; to Y1L038C, NOT3_YEAST, P06102, general negative regulator,	3.20E-35
354	L09604	Homo sapiens differentiation-dependent A4 protein mRNA, complete cds.	3.70E-32	PVU72769_1	Phaseolus vulgaris PvPRP-12 (Pvprp1-12) mRNA, partial cds; Similar to cell wall proline rich protein>GP:PVU72769_1 Phaseolus vulgaris PvPRP-12 (Pvprp1-12) mRNA, partial cds; Similar to cell wall proline rich protein	0.00049
355	B42455	HS-1055-B2-G03-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 777 Col=6 Row=N.	1.30E-32	CELT05H4_8	Caenorhabditis elegans cosmid T05H4; Similar to the beta transducin family; coded for by C; elegans cDNA yk156e11;3; coded for by C; elegans cDNA yk14c8;3; coded for by C; elegans cDNA	6.90E-14
356	AF001905	Homo sapiens cosmids E079, B0920 and A8 from Xq25 X-linked lymphoproliferative disease gene candidate region, complete sequence.	1.80E-33	I38344	titin - human	1

WO 99/33982

PCT/US98/27610

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
357	E03743	DNA sequence including male hormone dependent gene derived from hamster frankorgan.	1.10E-34	CELC03A7_2	Caenorhabditis elegans cosmid C03A7; Weak similarity to serotonin receptors	0.59
358	U31199	Human laminin gamma2 chain gene (LAMC2), exon 22 and flanking sequences.	1.20E-35	B44018	laminin B2t chain - human>GP:HSLAMB2 TB_1 H;sapiens mRNA for laminin	1.20E-14
359	D14678	Human mRNA for kinesin-related protein, partial cds.	2.00E-36	D49544_1	Mouse mRNA for KIFC1, complete cds	1.20E-23
360	AB000425	Porcine DNA for endopeptidase 24.16, exon 16 and complete cds.	8.20E-38	POL4_DROM E	RETROVIRUS-RELATED POLYPROTEIN (PROTEASE (EC 3.4.23.-); REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE) (TRANSPOSON 412)>PIR1:GNFF42 retrovirus-related pol polyprotein - fruit fly (Drosophila melanogaster) transposon 412>GP:DMRT412G_4	0.65
361	U39875	Rattus norvegicus EF-hand Ca2+-binding protein p22 mRNA, complete cds.	8.80E-42	I56333	apolipoprotein B - rat (fragment)>GP:RATA POLPB_1 Rattus norvegicus (clone rb9E) apolipoprotein B apoB mRNA, 3' end	0.23

WO 99/33982

PCT/US98/27610

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
362	L09647	Rattus norvegicus hepatocyte nuclear factor 3a (HNF-3 beta) mRNA, complete cds.	6.60E-42	HN3B_RAT	HEPATOCTYTE NUCLEAR FACTOR 3-BETA (HNF-3B)>GP:RATHNF3B_1 Rattus norvegicus hepatocyte nuclear factor 3a (HNF-3 beta) mRNA, complete cds>TFD:TFDP01611 - Polypeptides entry for factor HNF-3 (beta)	8.10E-25
363	D25538	Human mRNA for KIAA0037 gene, complete cds.	4.10E-43	CELC34D4_1 2	Caenorhabditis elegans cosmid C34D4	0.018
364	Z56764	H.sapiens CpG island DNA genomic MseI fragment, clone 13f7, reverse read cpg13f7.r1a.	1.40E-43	S75263	hypothetical protein - Synechocystis sp. (PCC 6803)>GP:D90904_29 Synechocystis sp; PCC6803 complete genome, 6/27, 630555-781448; Hypothetical protein; ORF_ID:sll0983	0.0028
365	AC002636	*** SEQUENCING IN PROGRESS *** Drosophila melanogaster (subclone 2_g4 from P1 DS03323 (D127)) DNA sequence; HTGS phase 2.	8.40E-44	DMU95760_1	Drosophila melanogaster strawberry notch (sno) mRNA, complete cds; Notch pathway component; nuclear protein	3.40E-51
366	J05499	Rattus norvegicus L-glutamine amidohydrolase mRNA, complete cds.	8.00E-44	GLSL_RAT	GLUTAMINASE, LIVER ISOFORM PRECURSOR (EC 3.5.1.2) (GLS)>GP:RATGAH_1 Rattus norvegicus L-glutamine amidohydrolase mRNA, complete cds	8.00E-29

WO 99/33982

PCT/US98/27610

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
367	U95760	Drosophila melanogaster strawberry notch (sno) mRNA, complete cds.	5.00E-45	DMU95760_1	Drosophila melanogaster strawberry notch (sno) mRNA, complete cds; Notch pathway component; nuclear protein	4.80E-45
368	L10106	Mus musculus protein tyrosine phosphate mRNA, complete cds.	4.10E-45	PTPK_HUMAN	PROTEIN-TYROSINE PHOSPHATASE KAPPA PRECURSOR (EC 3.1.3.48) (R-PTP-KAPPA)>GP:HSPTKAP_1 H:sapiens mRNA for phosphotyrosine phosphatase kappa; Human phosphotyrosine phosphatase kappa	4.70E-16
369	D17218	Human HepG2 3' region Mbol cDNA, clone hmd3g02m3.	9.40E-47	MMU53563_1	Mus musculus Brg1 mRNA, partial cds; N-terminal region of the protein	0.00012
370	U78310	Homo sapiens pescadillo mRNA, complete cds.	8.10E-48	HSU78310_1	Homo sapiens pescadillo mRNA, complete cds	1.10E-21
371	AC000399	Genomic sequence from Mouse 9, complete sequence.	7.40E-48	KIP2_YEAST	KINESIN-LIKE PROTEIN KIP2>PIR1:C42640 kinesin-related protein KIP2 - yeast (Saccharomyces cerevisiae)>GP:SCKIP2XVI_2 S:cerevisiae PEP4 and KIP2 genes encoding PEP4 proteinase (partial) and kinesin-related protein KIP2>GP:SCLACHXVI_17 S:cerev	0.14
372	AC002327	*** SEQUENCING IN PROGRESS *** Genomic sequence from Mouse 7; HTGS phase 1, 3	1.40E-48	CHKC1A205_1	Chicken alpha-2 type-I collagen; amino acids - 16 to 3; Precollagen alpha-2	0.024

WO 99/33982

PCT/US98/27610

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		unordered pieces.				
373	X67016	H.sapiens mRNA for amphiglycan.	9.00E-49	CED2085_2	Caenorhabditis elegans cosmid D2085, complete sequence; D2085;1; Similar to glutamine-dependent carbamoyl-phosphate synthase, aspartate carbamoyltransferase, dihydroorotase; cDNA EST cm16f3>GP:CED2085_2 Caenorhabditis elegans cosmid D2085; D	0.14
374	L10409	Mouse fork head related protein (HNF-3beta) mRNA, complete cds.	1.50E-49	MMU04197_1	Mus musculus HNF3 beta transcription factor (HNF3b) mRNA, partial cds; Sequence of this partial cDNA begins in the first third of the conserved HNF3/forkhead DNA binding domain	1.20E-30
375	U01139	Mus musculus B6D2F1 clone 2C11B mRNA.	1.20E-49	SPBC3D5_14	S.pombe chromosome II cosmid c3D5; Unknown; SPBC3D5;14c, unknown; partial; serine rich, len:309aa, similar eg; to YNL283C, YN23_YEAST, P53832, hypothetical 52;3 kd protein, (503aa),	0.00091
376	Z82170	Human DNA sequence from PAC 326L13 containing brain-4 mRNA ESTs and polymorphic CA repeat.	9.00E-50	BSU55043_3	Bacillus subtilis plasmid pPOD2000 Rep, RapAB, RapA, ParA, ParB, and ParC genes, complete cds; ORF3	0.025

WO 99/33982

PCT/US98/27610

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
377	Z99289	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 142L7; HTGS phase 1.	7.70E-50	A64431	hypothetical protein MJ1050 - Methanococcus jannaschii>GP: MJU67548_2 Methanococcus jannaschii from bases 986219 to 996377 (section 90 of 150) of the complete genome; M; jannaschii predicted coding region MJ1050; Identified by GeneMark; putativ	5.60E-05
378	X98260	H.sapiens mRNA for M-phase phosphoprotein, mpp11.	6.20E-50	ZRF1_MOUSE	ZUOTIN RELATED FACTOR>GP:MMU53208_1 Mus musculus zuotin related factor (ZRF1) mRNA, complete cds; Similar to DnaJ encoded by GenBank Accession Number L16953	3.90E-30
379	M18981	Human prolactin receptor-associated protein (PRA) gene, complete cds.	9.00E-52	S106_HUMAN	CALCYCLIN (PROLACTIN RECEPTOR ASSOCIATED PROTEIN) (PRA) (GROWTH FACTOR-INDUCIBLE PROTEIN 2A9) (S100 CALCIUM-BINDING PROTEIN A6)>PIR1:BCHUY calcyclin - human>GP:HUMCAC Y_1 Human calcyclin gene, complete cds>GP:HUMCAC Y_1 Human prolactin recept	8.80E-24
380	AB006622	Homo sapiens mRNA for KIAA0284 gene, partial cds.	1.60E-53	S33015	hypothetical protein - human herpesvirus 4	0.00088

WO 99/33982

PCT/US98/27610

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
381	U53225	Human sorting nexin 1 (SNX1) mRNA, complete cds.	1.80E-55	G02522	sorting nexin 1 - human>GP:HSU53225_1 Human sorting nexin 1 (SNX1) mRNA, complete cds	9.20E-50
382	Z92844	Human DNA sequence from PAC 435C23 on chromosome X. Contains ESTs.	6.50E-56	D14487_1	Lentivirus edodes Le:MFB1 mRNA, complete cds	1
383	D87450	Human mRNA for KIAA0261 gene, partial cds.	4.30E-56	D87450_1	Human mRNA for KIAA0261 gene, partial cds; Similar to D:melanogaster parallel sister chromatids protein	4.30E-30
384	AC002301	*** SEQUENCING IN PROGRESS *** Human chromosome +16p11.2 BAC clone CIT987SK-A-328A3; HTGS phase 2, 1 ordered pieces.	9.80E-57	S62328	kinesin-like DNA binding protein KID - human>GP:HUMKID_1 Human mRNA for Kid (kinesin-like DNA binding protein), complete cds	2.60E-27
385	L29766	Homo sapiens epoxide hydrolase (EPHX) gene, complete cds.	7.30E-57	HSBCTCF4_1	Homo sapiens mRNA for hTCF-4	2.30E-05
386	U58884	Mus musculus SH3-containing protein SH3P7 mRNA, complete cds, similar to Human Drebrin.	3.30E-58	MMU58884_1	Mus musculus SH3-containing protein SH3P7 mRNA, complete cds; similar to Human Drebrin; SH3-containing protein; similar to human drebrin	6.00E-43
387	Y15054	Rattus norvegicus mRNA for 70 kDa tumor specific antigen, partial.	9.50E-59	RNY15054_1	Rattus norvegicus mRNA for 70 kDa tumor specific antigen, partial; 70 kD tumor-specific antigen	4.70E-45

WO 99/33982

PCT/US98/27610

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
388	AC000406	*** SEQUENCING IN PROGRESS *** Human Chromosome 11 overlapping pacs pDJ235k10 and pDJ239b22; HTGS phase 1, 17 unordered pieces.	7.40E-59	<NONE>	<NONE>	<NONE>
389	L42612	Homo sapiens keratin 6 isoform K6f (KRT6F) mRNA, complete cds.	3.60E-59	KRHUEA	keratin, type II cytoskeletal - human (fragment)>GP:HSKE RA_1 Human messenger fragment encoding cytoskeletal keratin (type II); mRNA from cultured epidermal cells from human foreskin>GP:HUMKE R56K_1 Human 56k cytoskeletal type II keratin mRNA	7.60E-30
390	L29766	Homo sapiens epoxide hydrolase (EPHX) gene, complete cds.	2.70E-60	EGR2_HUMAN	EARLY GROWTH RESPONSE PROTEIN 2 (EGR-2) (KROX-20 PROTEIN) (AT591)>GP:HUMEG R2A_1 Human early growth response 2 protein (EGR2) mRNA, complete cds>TFD:TFDP00485 - Polypeptides entry for factor Egr-2	7.80E-06
391	L08758	Mus musculus homeobox protein (Hox A10) gene, 5' end of cds.	1.40E-60	PAALGYGE N_1	Paeruginosa algY gene; Alginate lyase	0.00031
392	I29058	Sequence 3 from patent US 5576423.	4.20E-61	JC5106	stromal cell-derived factor 2 - human>GP:D50645_1 Human mRNA for SDF2, complete cds; Stroma cell-derived	1.50E-32

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					factor-2	
393	I29058	Sequence 3 from patent US 5576423.	4.20E-61	JC5106	stromal cell-derived factor 2 - human>GP:D50645_1 Human mRNA for SDF2, complete cds; Stroma cell-derived factor-2	1.50E-32
394	U46067	Capra hircus beta-mannosidase mRNA, complete cds.	1.90E-62	CHU46067_1	Capra hircus beta-mannosidase mRNA, complete cds	2.70E-39
395	U40747	Mus musculus formin binding protein 11 mRNA, partial cds.	6.90E-63	S64713	formin binding protein 11 - mouse (fragment)>GP:MMU40747_1 Mus musculus formin binding protein 11 mRNA, partial cds; FBP 11; Formin binding protein 11; tandem WWP/WW domains separated by 15 amino acid linker	3.00E-46
396	M36164	Human glyceraldehyde-3-phosphate dehydrogenase mRNA, 3' flank.	1.10E-63	BHT1UL_12	Bovine herpesvirus type 1 UL22-35 genes; UL26;5>GP:BHU31809_2 Bovine herpesvirus 1 maturational proteinase (UL26) gene, complete cds, and scaffold protein (UL26;5) gene, complete cds	0.003
397	Y09036	H.sapiens NTRK1 gene, exon 17.	7.30E-65	MMU39060_1	Mus musculus glucocorticoid receptor interacting protein 1 (GRIP1) mRNA, complete cds; Hormone-dependent interaction with hormone binding domains of steroid receptors;	0.0054

WO 99/33982

PCT/US98/27610

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					transactivation	
398	U17901	Rattus norvegicus phospholipase A-2-activating protein (plap) mRNA, complete cds.	2.70E-70	JC4239	phospholipase A2-activating protein - rat	8.40E-17
399	D12646	Mouse kif4 mRNA for microtubule-based motor protein KIF4, complete cds.	1.70E-74	KIF4_MOUSE	KINESIN-LIKE PROTEIN KIF4>PIR2:A54803 microtubule-associated motor KIF4 - mouse>GP:MUSKIF4_1 Mouse kif4 mRNA for microtubule-based motor protein KIF4, complete cds; ATP-binding site: base980-1037, motor domain: base732-1781, alpha-helical co	1.10E-44
400	AF007860	Xenopus laevis xl-Mago mRNA, complete cds.	4.60E-75	AF007862_1	Mus musculus mm-Mago mRNA, complete cds; Similar to Drosophila melanogaster Mago protein	6.50E-68
401	I45565	Sequence 15 from patent US 5637463.	2.30E-82	RNU57391_1	Rattus norvegicus FceRI gamma-chain interacting protein SH2-B (SH2-B) mRNA, complete cds; Putative FceRI gamma ITAM interacting protein; SH2 domain-containing protein B; Method: conceptual	9.90E-42

WO 99/33982

PCT/US98/27610

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
402	U29156	Mus musculus eps15R mRNA, complete cds.	1.00E-85	MMU29156_1	Mus musculus eps15R mRNA, complete cds; Involved in signaling by the epidermal growth factor receptor; Method: conceptual translation supplied by author	4.90E-62
403	U70139	Mus musculus putative CCR4 protein mRNA, partial cds.	1.00E-85	MMU70139_1	Mus musculus putative CCR4 protein mRNA, partial cds; Similar to yeast transcription factor CCR4; transcriptional readthrough occurs with transcription being initiated at the IAP and continues	7.20E-66
404	U82626	Rattus norvegicus basement membrane-associated chondroitin proteoglycan Bamacan mRNA, complete cds.	7.60E-96	RNU82626_1	Rattus norvegicus basement membrane-associated chondroitin proteoglycan Bamacan mRNA, complete cds; Chondroitin sulfate proteoglycan; CSPG	8.20E-58

WO 99/33982

PCT/US98/27610

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
405	L09604	Homo sapiens differentiation-dependent A4 protein mRNA, complete cds.	2.00E-35	<NONE>	<NONE>	<NONE>
406	AB000516	Homo sapiens mRNA for DSIF p160, complete cds	0.41	POLG_TUMVQ	GENOME POLYPROTEIN (CONTAINS: N-TERMINAL PROTEIN; HELPER COMPONENT PROTEINASE (EC 3.4.22.-) (HC-PRO); 42-50 KD PROTEIN; CYTOPLASMIC INCLUSION PROTEIN (CI); 6 KD PROTEIN; VPG PROTEIN; NUCLEAR INCLUSION PROTEIN A (NI-A)	2.9
407	Z94753	Human DNA sequence from PAC 465G10 on chromosome X contains Menkes Disease (ATP7A) putative Cu ⁺⁺ -transporting P-type ATPase exons 22, 23 and STS	0.004	<NONE>	<NONE>	<NONE>
408	AB011123	Homo sapiens mRNA for KIAA0551 protein, partial cds	0	MI15_CAEEL	Q23356 caenorhabditis elegans, serine/threonine-protein kinase mig-15 (cc 2.7.1.-). 11/98	2.00E-51
409	D17218	Human HepG2 3' region Mbol cDNA, clone hmd3g02m3	e-123	NARG_BACSU	NITRATE REDUCTASE ALPHA CHAIN (EC 1.7.99.4)	9.9
410	M95098	Bos taurus lysozyme gene (cow 2), complete cds	1.1	HAIR_MOUSE	HAIRLESS PROTEIN	8.00E-10

WO 99/33982

PCT/US98/27610

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
411	Z60048	H.sapiens CpG DNA, clone 187a9, reverse read cpg187a9.rt1a.	4.00E-54	HN3B_MOUSE	HEPATOCYTE NUCLEAR FACTOR 3-BETA (HNF-3B)	4.00E-21
412	Z48975	P.magnus gene for protein urPAB	0.014	YPT2_CAEEL	HYPOTHETICAL 21.6 KD PROTEIN F37A4.2 IN CHROMOSOME III	2.00E-12
413	AJ001296	Notophthalmus viridescens mRNA for cytokeratin 8	0.37	YA53_SCHPO	24.2 KD PROTEIN C13A11.03 IN CHROMOSOME I	5.00E-21
414	J03831	Xenopus laevis (clone pXEC1.3) C protein mRNA, complete cds.	0.37	PDR5_YEAST	SUPPRESSOR OF TOXICITY OF SPORIDESMIN	3.3
415	AB007157	Homo sapiens gene for ribosomal protein S21, partial cds	e-142	RS21_HUMAN	40S RIBOSOMAL PROTEIN S21	0.002
416	X86340	H.sapiens C7 gene, exon 13	3.3	STC_DROME	SHUTTLE CRAFT PROTEIN	4.3
417	U12404	Human Csa-19 mRNA, complete cds.	0	R10A_PIG	60S RIBOSOMAL PROTEIN L10A (CSA-19) (FRAGMENT)	9.00E-37
418	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	8.00E-08	<NONE>	<NONE>	<NONE>
419	M80198	Human FKBP-12 pseudogene, clone lambda-512, 5' flank and complete cds.	5.00E-14	RCO1_NEUCR	TRANSCRIPTIONAL REPRESSOR RCO-1	0.008
420	AF052573	Homo sapiens DNA polymerase eta (POLH) mRNA, complete cds	0	<NONE>	<NONE>	<NONE>
421	AF035940	Homo sapiens MAGOH mRNA, complete cds	e-131	MGN_DROME	MAGO NASHI PROTEIN	4.00E-39
422	AF054994	Homo sapiens clone 23832 mRNA sequence	0.12	<NONE>	<NONE>	<NONE>

WO 99/33982

PCT/US98/27610

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
423	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	6.00E-05	<NONE>	<NONE>	<NONE>
424	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	7.00E-07	<NONE>	<NONE>	<NONE>
425	D43952	Mouse gene for reticulocalbin, exon1 and promoter region	0.36	<NONE>	<NONE>	<NONE>
426	X68553	C.elegans repetitive DNA sequence	0.4	TCB1_RABIT	T-CELL RECEPTOR BETA CHAIN PRECURSOR (ANA 11)	0.11
427	M83314	Tomato phenylalanine ammonia lyase (pal) gene, complete cds and promoter region.	3.3	SMB2_HUMAN	DNA-BINDING PROTEIN SMUBP-2 (GLIAL FACTOR-1) (GF-1)	0.65
428	AF070636	Homo sapiens clone 24686 mRNA sequence	5.00E-23	<NONE>	<NONE>	<NONE>
429	<NONE>	<NONE>	<NONE>	IQGA_HUMAN	RAS GTPASE-ACTIVATING-LIKE PROTEIN IQGAP1 (P195)	2.00E-06
430	AF068627	Mus musculus DNA cytosine-5 methyltransferase 3B2 (Dnmt3b) mRNA, alternatively spliced, complete cds	5.00E-04	LOX1_LENCU	LIPXYGENASE (EC 1.13.11.12)	9.9
431	AF020043	Homo sapiens chromosome-associated polypeptide	0	YJH4_YEAST	HYPOTHETICAL 141.3 KD PROTEIN IN SCP160-MRPL8 INTERGENIC REGION	4.00E-16
432	K00046	ross river virus 26s subgenomic rna and junction region.	0.12	CUL2_HUMAN	CULLIN HOMOLOG 2 (CUL-2)	7.4

WO 99/33982

PCT/US98/27610

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
433	AF005664	Homo sapiens properdin (PFC) gene, complete cds	0.005	UL88_HCMVA	PROTEIN UL88	5.8
434	Z70705	H.sapiens mRNA (fetal brain cDNA com5)	2.00E-05	PH87_YEAST	INORGANIC PHOSPHATE TRANSPORTER PHO87	1.5
435	U29156	Mus musculus eps15R mRNA, complete cds.	e-125	EP15_HUMAN	EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE 15 (PROTEIN EPS15) (AF-1P PROTEIN)	1.00E-13
436	AE000750	Aquifex aeolicus section 82 of 109 of the complete genome	0.37	<NONE>	<NONE>	<NONE>
437	U49169	Dictyostelium discoideum V-ATPase A subunit (vatA) mRNA, complete cds	0.12	VCAP_HSV6U	MAJOR CAPSID PROTEIN (MCP)	5.6
438	AF032871	Homo sapiens uncoupling protein 3 (UCP3) gene, exon 1 and partial exon 2	0.13	WEE1_SCHPO	MITOSIS INHIBITOR PROTEIN KINASE WEE1 (EC 2.7.1.-)	3.7
439	AB000425	Porcine DNA for endopeptidase 24.16, exon 16 and complete cds	4.00E-32	<NONE>	<NONE>	<NONE>
440	U51037	Mus musculus 11-zinc-finger transcription factor	0.04	<NONE>	<NONE>	<NONE>
441	AF032456	Homo sapiens ubiquitin conjugating enzyme G2	e-110	<NONE>	<NONE>	<NONE>
442	AF009288	Homo sapiens clone HEB8 Cri-du-chat region mRNA	2.00E-14	LMG1_HUMAN	LAMININ GAMMA-1 CHAIN PRECURSOR (LAMININ B2 CHAIN)	8.1

WO 99/33982

PCT/US98/27610

Table 2

Nearest Neighbor (BlastN vs. Genbank)				Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
443	AF024578	Homo sapiens type-1 protein phosphatase skeletal muscle glycogen targeting subunit (PPP1R3) gene, exon 4, and complete cds	1.1	<NONE>	<NONE>	<NONE>
444	M24486	Human prollyl 4-hydroxylase alpha subunit mRNA, complete cds, clone PA-11.	0	DACHA	<NONE>	4.00E-58
445	X96400	P.tetraulalia alpha-51D gene	0.37	<NONE>	<NONE>	<NONE>
446	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
447	X84996	X.laevis mRNA for selenocysteine tRNA acting factor (Staf)	0.12	POL_MLVRD	POL POLYPROTEIN (PROTEASE (EC 3.4.23.-); REVERSE TRANSCRIPTASE (EC 2.7.7.49); RIBONUCLEASE H (EC 3.1.26.4))	2.00E-08
448	AF019980	Dictyostelium discoideum ZipA (zipA) gene, partial cds	3.4	HMDL_BRAFL	HOMEOBOX PROTEIN DLL HOMOLOG	0.23
449	X78424	D.carota (Queen Anne's Lace) Inv*De2 gene, 3432bp	0.38	<NONE>	<NONE>	<NONE>
450	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
451	X89886	P.patens mRNA for 5-aminolevulinate dehydratase	1.1	CKR6_HUMAN	C-C CHEMOKINE RECEPTOR TYPE 6 (C-C CKR-6) (CCR6)	9.9
452	U67471	Methanococcus jannaschii section 13 of 150 of the complete genome	0.12	YR72_ECOLI	HYPOTHETICAL 53.2 KD PROTEIN (ORF2) (RETROIN EC67)	5.8
453	AF060246	Mus musculus strain C57BL/6 zinc finger protein 106 (Zip106) mRNA, H3a-a allele, complete cds	1.00E-62	YOJ8_CAEL	HYPOTHETICAL 51.6 KD PROTEIN ZK353.8 IN CHROMOSOME III	1.7

WO 99/33982

PCT/US98/27610

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
454	U70667	Human Fas-ligand associated factor 1 mRNA, partial cds	0	YKB2_YEAST	HYPOTHETICAL 69.1 KD PROTEIN IN PUT3-CCE1 INTERGENIC REGION	3.00E-09
455	M95858	Bos taurus recoverin mRNA, complete cds.	0.35	GIDA_MYCGE	GLUCOSE INHIBITED DIVISION PROTEIN A	1.4
456	U67594	Methanococcus jannaschii section 136 of 150 of the complete genome	0.36	<NONE>	<NONE>	<NONE>
457	X06747	Human hnRNP core protein A1	3.00E-31	<NONE>	<NONE>	<NONE>
458	Z65575	H.sapiens CpG DNA, clone 47c5, reverse read cpg47c5.r11a.	1.3	<NONE>	<NONE>	<NONE>
459	X88893	C.jacchus intron 4 of visual pigment gene	5.00E-15	<NONE>	<NONE>	<NONE>
460	M57426	Maize stripe virus RNA 3 nonstructural protein	0.33	DSC2_MOUSE	DESMOCOLLIN 2A/2B PRECURSOR (EPITHELIAL TYPE 2 DESMOCOLLIN)	6.5
461	X01638	Yeast TEF1 gene for elongation factor EF-1 alpha	1.1	PPOL_DROME	POLY (ADP-RIBOSE) POLYMERASE (EC 2.4.2.30) (PARP)	3.5
462	M60064	S.typhimurium glutamate 1-semialdehyde aminotransferase (hemL) gene, complete cds.	1.1	EPB4_MOUSE	EPHRIN TYPE-B RECEPTOR 4 PRECURSOR (EC 2.7.1.112) KINASE 2) (TYROSINE KINASE MYK- 1)	2.5
463	X51508	Rabbit mRNA for aminopeptidase N (partial)	0.36	ACHG_XENLA	ACETYLCHOLINE RECEPTOR PROTEIN, GAMMA CHAIN PRECURSOR	1.5
464	L10106	Mus musculus protein tyrosine phosphate mRNA, complete cds.	2.00E-58	VG13_BPML5	GENE 13 PROTEIN (GP13)	2.5

WO 99/33982

PCT/US98/27610

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
465	M77235	Human cardiac tetrodotoxin-insensitive voltage-dependent sodium channel alpha subunit (HH1) mRNA, complete cds.	3.8	ZPBOC1	<NONE>	6.9
466	M58330	C.maltosa autonomously replicating sequence.	0.004	EPB4_MOUSE	EPHRIN TYPE-B RECEPTOR 4 PRECURSOR (EC 2.7.1.112) KINASE 2) (TYROSINE KINASE MYK- 1)	2.4
467	X51508	Rabbit mRNA for aminopeptidase N (partial)	0.35	ACHG_XENLA	ACETYLCHOLINE RECEPTOR PROTEIN, GAMMA CHAIN PRECURSOR	2.4
468	L10106	Mus musculus protein tyrosine phosphate mRNA, complete cds.	7.00E-59	VGLI_PVRVI	GLYCOPROTEIN GP63 PRECURSOR	4.3
469	U65939	Azotobacter vinelandii GTPase (ftsA) gene, partial cds, and ATP binding protein (ftsZ) gene, complete cds	1.1	TRUA_BACSP	Q45557 bacillus sp. (strain ksm-64). trna pseudouridine synthase a (ec 4.2.1.70) (pseudouridylate synthase i) (pseudouridine synthase i) (uracil hydrolyase). 11/98	0.001
470	U51037	Mus musculus 11-zinc-finger transcription factor	0.041	<NONE>	<NONE>	<NONE>
471	M32685	Human platelet glycoprotein IIIa, exon 14.	3.6	<NONE>	<NONE>	<NONE>

WO 99/33982

PCT/US98/27610

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
472	U82691	Phrynocephalus raddei CAS 179770 NADH dehydrogenase subunit 1 (ND1), partial cds, tRNA-Gln, tRNA-Ile and tRNA-Met, NADH dehydrogenase subunit 2 tRNA-Cys and tRNA-Tyr and c...	1.1	<NONE>	<NONE>	<NONE>
473	D85430	Mouse Murr1 mRNA, exon	0.12	EPA5_CHICK	EPHRIN TYPE-A RECEPTOR 5 PRECURSOR (EC 2.7.1.112)	2.5
474	U20661	Dictyostelium discoideum unknown internal repeat protein gene, complete cds, and unknown orf1, orf2 and orf3 genes, partial cds	0.36	YHL1_EBV	HYPOTHETICAL BHLF1 PROTEIN	4.00E-04
475	X56537	Human novel homeobox mRNA for a DNA binding protein	0.04	FA5_HUMAN	COAGULATION FACTOR V PRECURSOR (ACTIVATED PROTEIN C COFACTOR)	9.5
476	U32843	Haemophilus influenzae Rd section 158 of 163 of the complete genome	5	<NONE>	<NONE>	<NONE>
477	U67554	Methanococcus jannaschii section 96 of 150 of the complete genome	0.36	<NONE>	<NONE>	<NONE>
478	AB004244	Narke japonica mRNA for Nj-synaphin 1b, complete cds	1.1	NIA1_ORYSA	NITRATE REDUCTASE 1 (EC 1.6.6.1) (NR1)	1.00E-07
479	AF075079	Homo sapiens full length insert cDNA YQ80A08	1.00E-12	<NONE>	<NONE>	<NONE>

WO 99/33982

PCT/US98/27610

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
480	AE000723	Aquifex aeolicus section 55 of 109 of the complete genome	1	YKK0_YEAST	HYPOTHETICAL 67.5 KD PROTEIN IN APE1/LAP4-CWP1 INTERGENIC REGION	9.1
481	X73902	H.sapiens mRNA for nicein B2 chain	0	LMG2_HUMAN	LAMININ GAMMA-2 CHAIN PRECURSOR	3.00E-93
482	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	3.00E-10	P53_CRIGR	CELLULAR TUMOR ANTIGEN P53	5.7
483	AL010240	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-64, complete sequence	1.2	<NONE>	<NONE>	<NONE>
484	U49919	Arabidopsis thaliana lupeol synthase mRNA, complete cds	0.54	YA53_SCHPO	HYPOTHETICAL 24.2 KD PROTEIN C13A11.03 IN CHROMOSOME I	6.00E-10
485	AF077618	Homo sapiens p73 gene, exon 3	0.39	MYOD_MOUSE	MYOBLAST DETERMINATION PROTEIN 1	2.1
486	AF054994	Homo sapiens clone 23832 mRNA sequence	0.13	<NONE>	<NONE>	<NONE>
487	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3.00E-10	<NONE>	<NONE>	<NONE>
488	AF068627	Mus musculus DNA cytosine-5 methyltransferase 3B2 (Dnm3b) mRNA, alternatively spliced, complete cds	5.00E-04	ACE2_YEAST	METALLOTHIONE IN EXPRESSION ACTIVATOR	1.5
489	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3.00E-07	RINI_PIG	RIBONUCLEASE INHIBITOR	0.19

WO 99/33982

PCT/US98/27610

Table 2

Nearest Neighbor (BlastN vs. Genbank)				Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
490	L77886	Human protein tyrosine phosphatase mRNA, complete cds	1.00E-21	VS48_TBRVS	SATELLITE RNA 48 KD PROTEIN	1.6
491	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	5.00E-04	CRP3_LIMPO	C-REACTIVE PROTEIN 3.3 PRECURSOR	3.5
492	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	8.00E-08	EPA5_CHICK	EPHRIN TYPE-A RECEPTOR 5 PRECURSOR (EC 2.7.1.112)	2.7
493	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	3.00E-09	<NONE>	<NONE>	<NONE>
494	U28153	Caenorhabditis elegans UNC-76 (unc-76) gene, complete cds.	0.37	<NONE>	<NONE>	<NONE>
495	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	0.37	NCPR_YEAST	NADPH-CYTOCHROME P450 REDUCTASE (EC 1.6.2.4) (CPR)	7.00E-05
496	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.013	YMB3_CAEEL	PROBABLE INTEGRIN ALPHA CHAIN F54G8.3 PRECURSOR	3.3
497	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	7.00E-07	<NONE>	<NONE>	<NONE>
498	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1.00E-10	<NONE>	<NONE>	<NONE>
499	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2.00E-07	VGLY_LYCVW	GLYCOPROTEIN POLYPROTEIN PRECURSOR (CONTAINS: GLYCOPROTEINS G1 AND G2)	3.2

WO 99/33982

PCT/US98/27610

Table 2

Nearest Neighbor (BlastN vs. Genbank)				Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
500	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	8.00E-06	HR78_DROME	NUCLEAR HORMONE RECEPTOR HR78 (DHR78) (NUCLEAR RECEPTOR XR78E/F)	2.5
501	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	9.00E-10	MYSH_BOVIN	MYOSIN I HEAVY CHAIN-LIKE PROTEIN (MIHC) (BRUSH BORDER MYOSIN I) (BBMI)	4.00E-04
502	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2.00E-04	BAL_HUMAN	BILE-SALT-ACTIVATED LIPASE PRECURSOR (EC 3.1.1.3) (EC 3.1.1.13) (BAL) (BILE-SALT-STIMULATED LIPASE) (BSSL) (ESTERASE) (PANCREATIC LYSOPHOSPHOLIPASE)	2.6
503	AF080399	Drosophila melanogaster mitotic checkpoint control protein kinase BUB1 (Bub1) mRNA, complete cds	1.1	NAT1_YEAST	N-TERMINAL ACETYLTRANSFERASE 1 (EC 2.3.1.88)	2.00E-23
504	U59706	Gallus gallus alternatively spliced AMPA glutamate receptor, isoform GluR2 flop, (GluR2) mRNA, partial cds.	0.014	<NONE>	<NONE>	<NONE>
505	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2.00E-05	<NONE>	<NONE>	<NONE>
506	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	2.00E-04	<NONE>	<NONE>	<NONE>

WO 99/33982

PCT/US98/27610

Table 2

Nearest Neighbor (BlastN vs. Genbank)				Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
507	AF100661	Caenorhabditis elegans cosmid H20E11	0.38	<NONE>	<NONE>	<NONE>
508	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3.00E-11	CA1A_HUMAN	COLLAGEN ALPHA 1(X) CHAIN PRECURSOR	0.024
509	U47322	Cloning vector DNA, complete sequence.	2.00E-38	COA1_SV40	COAT PROTEIN VP1	6.2
510	AF031924	Homo sapiens homeobox transcription factor barx2	e-156	CCMA_HAEIN	HEME EXPORTER PROTEIN A (CYTOCHROME C-TYPE BIOGENESIS ATP-BINDING PROTEIN CCMA)	3.5
511	AF010484	Homo sapiens ICI YAC 91A12, right end sequence	3.00E-10	<NONE>	<NONE>	<NONE>
512	Z63829	H.sapiens CpG DNA, clone 90h2, forward read cpg90h2.ft1a .	5.00E-22	NFIR_MESAU	NUCLEAR FACTOR 1 CLONE PNFI/RED1 (NF-1) (CCAAT-BOX BINDING TRANSCRIPTION FACTOR) (CTF) (TGGCA-BINDING PROTEIN)	2.4
513	Z35094	H.sapiens mRNA for SURF-2	5.00E-97	SUR2_HUMAN	SURFEIT LOCUS PROTEIN 2	1.00E-46
514	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	7.00E-06	<NONE>	<NONE>	<NONE>
515	D38417	Mouse mRNA for arylhydrocarbon receptor, complete cds	e-154	TEGU_EBV	LARGE TEGUMENT PROTEIN	3.4
516	L10911	Homo sapiens splicing factor (CC1.4) mRNA, complete cds.	e-117	<NONE>	<NONE>	<NONE>

WO 99/33982

PCT/US98/27610

Table 2

Nearest Neighbor (BlastN vs. Genbank)				Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
517	X17093	Human HLA-F gene for human leukocyte antigen F	0.009	YEN1_SCHPO	O13695 schizosaccharomyces pombe (fission yeast), hypothetical 52.9 kd serine-rich protein c11g7.01 in chromosome i. 11/98	5.4
518	AB017026	Mus musculus mRNA for oxysterol-binding protein, complete cds	0	OXYB_HUMAN	OXYSTEROL-BINDING PROTEIN	1.00E-40
519	X55038	Mouse mCENP-B gene for centromere autoantigen B	0.001	YNW7_YEAST	HYPOTHETICAL 68.8 KD PROTEIN IN URE2-SSU72 INTERGENIC REGION	3.00E-04
520	AB018323	Homo sapiens mRNA for KIAA0780 protein, partial cds	3.00E-41	LBR_CHICK	LAMIN B RECEPTOR	2.3
521	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1.00E-10	CA25_HUMAN	PROCOLLAGEN ALPHA 2(V) CHAIN PRECURSOR	0.002
522	X03558	Human mRNA for elongation factor 1 alpha subunit	0	EF11_HUMAN	ELONGATION FACTOR 1-ALPHA 1 (EF-1-ALPHA-1)	e-110
523	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3.00E-11	YMT8_YEAST	HYPOTHETICAL 36.4 KD PROTEIN IN NUP116-FAR3 INTERGENIC REGION	8.00E-07
524	AB014591	Homo sapiens mRNA for KIAA0691 protein, complete cds	0	NOT2_YEAST	GENERAL NEGATIVE REGULATOR OF TRANSCRIPTION SUBUNIT 2	8.00E-05
525	AB019488	Homo sapiens DNA for TRKA, exon 17 and complete cds	0	TRKA_HUMAN	HIGH AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR PROTEIN (P140-TRKA)	2.00E-27

WO 99/33982

PCT/US98/27610

Table 2

Nearest Neighbor (BlastN vs. Genbank)				Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
526	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	5.00E-15	CNG4_BOVIN	240K PROTEIN OF ROD PHOTORECEPTOR CNG-CHANNEL CYCLIC-NUCLEOTIDE-GATED CATION CHANNEL 4 (CNG CHANNEL 4) MODULATORY SUBUNIT))	0.018
527	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2.00E-06	HMZ1_DROME	ZERKNUELLT PROTEIN 1 (ZEN-1)	0.88
528	J03750	Mouse single stranded DNA binding protein p9 mRNA, complete cds.	e-135	P15_HUMAN	ACTIVATED RNA POLYMERASE II TRANSCRIPTIONAL COACTIVATOR P15 (PC4) (P14)	3.00E-21
529	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1.00E-12	RS5_DROME	40S RIBOSOMAL PROTEIN S5	0.42
530	Z57610	H.sapiens CpG DNA, clone 187a10, reverse read cpg187a10.r11a .	8.00E-61	HN3B_MOUSE	HEPATOCYTE NUCLEAR FACTOR 3-BETA (HNF-3B)	4.00E-15
531	U95760	Drosophila melanogaster strawberry notch (sno) mRNA, complete cds	3.00E-60	<NONE>	<NONE>	<NONE>
532	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	4.00E-11	<NONE>	<NONE>	<NONE>
533	U50535	Human BRCA2 region, mRNA sequence CG006	4.00E-12	ALU1_HUMAN	!!!! ALU SUBFAMILY J WARNING ENTRY !!!!	1.1
534	X92841	H.sapiens MICA gene	1.00E-55	LIN1_HUMAN	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG	6.00E-09

Table 2

Nearest Neighbor (BlastN vs. Genbank)				Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
535	U60337	Homo sapiens beta-mannosidase mRNA, complete cds	0	NODC_BRAEL	N-ACETYLGLUCOSAMINYLTRANSFERASE (EC 2.4.1.-)	1.4
536	M21731	Human lipocortin-V mRNA, complete cds.	e-169	ANX5_HUMAN	ANNEXIN V (LIPOCORTIN V) (ENDONEXIN II) (CALPHOBINDIN I) (CBP-I) (PLACENTAL ANTICOAGULANT PROTEIN I) (PAP-I) ANTICOAGULANT-ALPHA) (VAC-ALPHA) (ANCHORIN CII)	1.00E-05
537	Y08013	S.salar DNA segment containing GT repeat	0.006	<NONE>	<NONE>	<NONE>
538	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
539	M98502	Mus musculus protein encoding twelve zinc finger proteins (pMLZ-4) mRNA, complete cds.	2.00E-17	DYNA_CHICK	DYNACTIN, 117 KD ISOFORM	7.4
540	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	6.00E-05	HXA3_HAEIN	HEME:HEMOPEXIN-BINDING PROTEIN PRECURSOR	2.6
541	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1.00E-13	AMO_KLEAE	AMINE OXIDASE PRECURSOR (EC 1.4.3.6) (MONAMINE OXIDASE) (TYRAMINE OXIDASE)	1.5
542	AF083322	Homo sapiens centriole associated protein CEP110 mRNA, complete cds	e-133	CA34_HUMAN	PROCOLLAGEN ALPHA 3(IV) CHAIN PRECURSOR	1.5
543	J03746	Human glutathione S-transferase mRNA, complete cds.	e-170	GTMI_HUMAN	GLUTATHIONE S-TRANSFERASE, MICROSOMAL (EC 2.5.1.18)	5.00E-39

WO 99/33982

PCT/US98/27610

Table 2

Nearest Neighbor (BlastN vs. Genbank)				Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
544	U67522	Methanococcus jannaschii section 64 of 150 of the complete genome	0.37	A1AA_HUMAN	ALPHA-1A ADRENERGIC RECEPTOR	4.3
545	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2.00E-07	<NONE>	<NONE>	<NONE>
546	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
547	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
548	D87001	Human (lambda) DNA for immunoglobulin light chain	0.35	VAL3_TYLCU	AL3 PROTEIN (C3 PROTEIN)	3.2
549	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	3.00E-08	TEGU_HSV11	LARGE TEGUMENT PROTEIN (VIRION PROTEIN UL36)	0.004
550	D16991	Human HepG2 partial cDNA, clone hmd2d01m5	8.00E-09	PTM1_YEAST	PROTEIN PTM1 PRECURSOR	0.033
551	M34025	Human fetal Ig heavy chain variable region	3.2	<NONE>	<NONE>	<NONE>
552	M98502	Mus musculus protein encoding twelve zinc finger proteins (pMLZ-4) mRNA, complete cds.	5.00E-14	<NONE>	<NONE>	<NONE>
553	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	0.002	<NONE>	<NONE>	<NONE>
554	Z78730	H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA15C3	3.00E-20	ALU1_HUMAN	!!!! ALU SUBFAMILY J WARNING ENTRY !!!!	5.00E-06
555	U74496	Human chromosome 4q35 subtelomeric sequence	8.00E-08	ICP4_VZVD	TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP4	0.39

WO 99/33982

PCT/US98/27610

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
556	U39875	Rattus norvegicus EF-hand Ca2+-binding protein p22 mRNA, complete cds.	2.00E-56	YHFK_ECOLI	HYPOTHETICAL 79.5 KD PROTEIN IN CRP-ARGD INTERGENIC REGION (O696)	9.8
557	U65416	Human MHC class I molecule (MICB) gene, complete cds	0.12	<NONE>	<NONE>	<NONE>
558	AG000037	Homo sapiens genomic DNA, 21q region, clone: 9H11A22	5.00E-25	<NONE>	<NONE>	<NONE>
559	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	5.00E-05	<NONE>	<NONE>	<NONE>
560	AB007918	Homo sapiens mRNA for KIAA0449 protein, partial cds	0.015	VGLE_HSV11	GLYCOPROTEIN PRECURSOR	2.2
561	U58884	Mus musculus SH3-containing protein SH3P7 mRNA, complete cds. similar to Human Drebrin	1.00E-73	YCV2_YEAST	HYPOTHETICAL 13.8 KD PROTEIN IN PWP2-SUP61 INTERGENIC REGION	2.6
562	AB007878	Homo sapiens KIAA0418 mRNA, complete cds	e-110	GLU2_MAIZE	GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)	0.72
563	AF065482	Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds	0	YJD6_YEAST	HYPOTHETICAL 49.0 KD PROTEIN IN NSP1-KAR2 INTERGENIC REGION	1.4
564	U27873	Stealth virus 1 clone 3B11 T7	0.002	SYN1_HUMAN	SYNAPSINS 1A AND 1B (BRAIN PROTEIN 4.1)	1.6
565	L38951	Homo sapiens importin beta subunit mRNA, complete cds	2.00E-68	VP2_BRD	STRUCTURAL CORE PROTEIN VP2	1.1
566	AF007155	Homo sapiens clone 23763 unknown mRNA, partial cds	e-165	YOH1_AZOVI	HYPOTHETICAL 33.2 KD PROTEIN IN IBPB 5'REGION	7.5

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
567	Z56295	H.sapiens CpG DNA, clone 10c2, forward read cpg10c2.fl1a .	0.12	A1AB_CANFA	ALPHA-1B ADRENERGIC RECEPTOR (FRAGMENT)	0.85
568	Z83792	G.gallus microsatellite DNA (LEI0222	0.12	<NONE>	<NONE>	<NONE>
569	U11820	Feline immunodeficiency virus USIL2489_7B gag polyprotein (gag) gene, complete cds, polymerase polyprotein (pol) gene, partial cds, vif protein (vif), complete cds, and envelope glycoprotein (env), complete cds, complete g...	1.1	<NONE>	<NONE>	<NONE>
570	M18065	Mouse 18S and 28S ribosomal DNA, 5' hypervariable (Vr) region, clone M1.	6.00E-04	CC40_YEAST	CELL DIVISION CONTROL PROTEIN 40	3.7
571	AF053645	Homo sapiens cellular apoptosis susceptibility protein (CSE1) gene, exons 3 through 10	2.00E-07	YMQ4_CAEEL	HYPOTHETICAL 25.8 KD PROTEIN K02D10.4 IN CHROMOSOME III	4.3
572	X04588	Human 2.5 kb mRNA for cytoskeletal tropomyosin TM30(nm)	0	<NONE>	<NONE>	<NONE>
573	AC001159	Homo sapiens (subclone 1_h9 from PAC H92) DNA sequence	5.00E-04	XYND_CELFI	ENDO-1,4-BETA-XYLANASE D PRECURSOR (EC 3.2.1.8)	7.3
574	Z60625	H.sapiens CpG DNA, clone 2c10, forward read cpg2c10.fl1aa .	4.00E-13	<NONE>	<NONE>	<NONE>
575	AF070640	Homo sapiens clone 24781	e-164	<NONE>	<NONE>	<NONE>

Table 2

Nearest Neighbor (BlastN vs. Genbank)				Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		mRNA sequence				
576	Y11306	Homo sapiens mRNA for hTCF-4	2.00E-48	TCF1_HUMAN	T-CELL-SPECIFIC TRANSCRIPTION FACTOR 1 (TCF-1)	2.00E-15
577	X65279	pWE15 cosmid vector DNA	7.00E-69	OCN_POTTR	Q28793 potorous tridactylus (potoroo). occludin. 11/98	0.71
578	M10296	Mouse DNA with homology to EBV IR3 repeat, segment 1, clone Mu2.	0.001	LMB1_HYDAT	LAMININ BETA-I CHAIN PRECURSOR (FRAGMENTS)	1.9
579	X53744	Canine mRNA for 68kDA subunit of signal recognition particle (SRP68)	e-162	SR68_CANFA	SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68)	5.00E-16
580	AF086438	Homo sapiens full length insert cDNA clone ZD80G11	2.00E-04	<NONE>	<NONE>	<NONE>
581	U15140	Mycobacterium bovis ribosomal proteins IF-1 complete cds, and S4 (rpsD) gene, partial cds	1.3	<NONE>	<NONE>	<NONE>
582	D13292	Human mRNA for ryudocan core protein	e-166	RSP4_ARATH	40S RIBOSOMAL PROTEIN SA (P40) (LAMININ RECEPTOR HOMOLOG)	1.4
583	S71022	neoplasm-related C140 product [human, thyroid carcinoma cells, mRNA, 670 nt]	9.00E-30	RL6_HUMAN	60S RIBOSOMAL PROTEIN L6 (TAX-RESPONSIVE ENHANCER ELEMENT BINDING PROTEIN 107) (TAXREB107)	5.6
584	L20934	Anopheles gambiae complete mitochondrial genome	0.014	<NONE>	<NONE>	<NONE>
585	Z49269	H.sapiens gene for chemokine HCC-1.	1.1	AMY1_DICTH	ALPHA-AMYLASE 1 (EC 3.2.1.1) (1,4-ALPHA-D-GLUCAN GLUCANOHYDROLASE)	2.5

WO 99/33982

PCT/US98/27610

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
586	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	2.00E-04	<NONE>	<NONE>	<NONE>
587	AF029893	Homo sapiens i-beta-1,3-N-acetylglucosaminyltransferase mRNA, complete cds	0.13	HEMO_PIG	HEMOPEXIN PRECURSOR (HYALURONIDASE) (EC 3.2.1.35)	3.5
588	J05109	T.thermophila calcium-binding 25 kDa (TCBP 25) protein gene, complete cds.	0.014	<NONE>	<NONE>	<NONE>
589	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	6.00E-04	<NONE>	<NONE>	<NONE>
590	AF060246	Mus musculus strain C57BL/6 zinc finger protein 106 (Zfp106) mRNA, H3a-a allele, complete cds	1.00E-83	SCRB_PEDPE	SUCROSE-6-PHOSPHATE HYDROLASE (EC 3.2.1.26) (SUCRASE)	10
591	Y11966	B.aphidicola (host T.suberi) plasmid pBTs1 genes leuA, hspA, repA2, repA1, leuB, leuC, leuD, leuA	0.37	<NONE>	<NONE>	<NONE>
592	U20428	Human SNC19 mRNA sequence	1.00E-64	YY22_MYCTU	HYPOTHETICAL 30.8 KD PROTEIN CY49.22	0.29
593	AF043084	Lycopersicon esculentum ethylene receptor homolog (ETR1) mRNA, complete cds	0.37	KNIR_DROME	ZYGOTIC GAP PROTEIN KNIRPS	9.9
594	X65279	pWE15 cosmid vector DNA	5.00E-66	COA1_SV40	COAT PROTEIN VP1	0.001
595	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial	0.041	UL88_HSV7J	PROTEIN U59	5.8

WO 99/33982

PCT/US98/27610

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		cds				
596	M91452	Sus scrofa ryanodine receptor (RyR1) gene, complete cds.	3.2	<NONE>	<NONE>	<NONE>
597	U77327	Human Ki-1/57 intracellular antigen mRNA, partial cds	e-158	GAT1_CHICK	ERYTHROID TRANSCRIPTION FACTOR (GATA-1) (ERYF1)	1.2
598	U77327	Human Ki-1/57 intracellular antigen mRNA, partial cds	0	RPB7_ARATH	DNA-DIRECTED RNA POLYMERASE II 19 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE II SUBUNIT 5)	6.2
599	Y16964	Saccharomyces sp. mitochondrial DNA for OL11 gene, strain CID1	0.37	NMD5_YEAST	NONSENSE-MEDIATED MRNA DECAY PROTEIN 5	1.9
600	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	6.00E-06	<NONE>	<NONE>	<NONE>
601	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	8.00E-08	<NONE>	<NONE>	<NONE>
602	AF091046	Brugia pahangi nuclear hormone receptor (bhr-1) gene, partial cds	1.1	INVO_PONPY	INVOLUCRIN	0.23
603	M87339	Human replication factor C, 37-kDa subunit mRNA, complete cds	0	AC12_HUMAN	ACTIVATOR 1 37 KD SUBUNIT (REPLICATION FACTOR C 37 KD SUBUNIT) (A1 37 KD SUBUNIT) (RFC- C 37 KD SUBUNIT) (RFC37)	1.00E-38
604	D28116	Human genes for collagen type IV alpha 5 and 6, exon 1 and exon	0.39	<NONE>	<NONE>	<NONE>

WO 99/33982

PCT/US98/27610

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		1'				
605	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2.00E-06	<NONE>	<NONE>	<NONE>
606	AE001149	Borrelia burgdorferi (section 35 of 70) of the complete genome	0.13	<NONE>	<NONE>	<NONE>
607	X14168	Human pLC46 with DNA replication origin	6.00E-16	Z136_HUMAN	ZINC FINGER PROTEIN 136	0.31
608	Z57610	H.sapiens CpG DNA, clone 187a10, reverse read cpg187a10.rtl.a.	7.00E-90	HN3B_RAT	HEPATOCYTE NUCLEAR FACTOR 3-BETA (HNF-3B)	1.00E-19
609	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	0.043	PGCV_MOUSE	VERSICAN CORE PROTEIN PRECURSOR (LARGE FIBROBLAST PROTEOGLYCAN) (CHONDROITIN SULFATE PROTEOGLYCAN CORE PROTEIN 2) (PG-M)	3.5
610	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	7.00E-07	CA11_CHICK	PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR	0.4
611	AB007956	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487	e-106	RRPB_CVMA5	RNA-DIRECTED RNA POLYMERASE (EC 2.7.7.48) (ORF1B)	9.7
612	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.005	<NONE>	<NONE>	<NONE>

WO 99/33982

PCT/US98/27610

Table 2

Nearest Neighbor (BlastN vs. Genbank)				Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
613	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	6.00E-05	UL52_EBV	HELICASE/PRIMA SE COMPLEX PROTEIN (PROBABLE DNA REPLICATION PROTEIN BSLF1)	5.9
614	U95760	Drosophila melanogaster strawberry notch (sno) mRNA, complete cds	3.00E-71	POLG_PVYHU	GENOME POLYPROTEIN (CONTAINS: N- TERMINAL PROTEIN; HELPER COMPONENT PROTEINASE (EC 3.4.22.-) (HC-PRO); 42-50 KD PROTEIN; CYTOPLASMIC INCLUSION PROTEIN (CI); 6 KD PROTEIN; NUCLEAR INCLUSION PROTEIN A (NI- A) (EC 3.4.22.-) (49K PROTEINASE) (49	4.3
615	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	9.00E-09	VP3_ROTPO	INNER CORE PROTEIN VP3	7.7
616	J05499	Rattus norvegicus L-glutamine amidohydrolase mRNA, complete cds	e-143	GLSL_RAT	GLUTAMINASE, LIVER ISOFORM PRECURSOR (EC 3.5.1.2) (GLS)	7.00E-67
617	M19262	Rat clathrin light chain (LCB3) mRNA, complete cds.	0.37	Y642_METJA	HYPOTHETICAL PROTEIN MJ0642	5.8
618	M21191	Human aldolase pseudogene mRNA, complete cds.	1.00E-32	LINE1_NYCCO	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG	6.00E-17
619	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1.00E-11	NUCM_BOVIN	NADH- UBIQUINONE OXIDOREDUCTAS E 49 KD SUBUNIT (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I- 49KD) (CI-49KD)	0.044

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
620	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	0.005	HEMZ_RHOCA	FERROCHELATASE (EC 4.99.1.1) (PROTOHEME FERRO-LYASE)	4.4
621	AF041428	Homo sapiens ribosomal protein s4 X isoform gene, complete cds	0.002	<NONE>	<NONE>	<NONE>
622	X07158	Chironomus thummi DNA for Cla repetitive element	0.13	<NONE>	<NONE>	<NONE>
623	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	8.00E-04	<NONE>	<NONE>	<NONE>
624	AF100470	Rattus norvegicus ribosome attached membrane protein 4 (RAMP4) mRNA, complete cds	1.00E-53	<NONE>	<NONE>	<NONE>
625	U85193	Human nuclear factor I-B2 (NFIB2) mRNA, complete cds	2.00E-38	<NONE>	<NONE>	<NONE>
626	M13452	Human lamin A mRNA, 3'end.	6.00E-16	<NONE>	<NONE>	<NONE>
627	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	0.014	ACDV_RAT	ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC PRECURSOR (EC 1.3.99.-) (VLCAD)	4.00E-20
628	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	3.00E-10	<NONE>	<NONE>	<NONE>
629	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
630	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2.00E-05	<NONE>	<NONE>	<NONE>

WO 99/33982

PCT/US98/27610

Table 2

Nearest Neighbor (BlastN vs. Genbank)				Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
631	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	6.00E-05	<NONE>	<NONE>	<NONE>
632	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	6.00E-05	YS83_CAEEL	HYPOTHETICAL 86.9 KD PROTEIN ZK945.3 IN CHROMOSOME II	0.65
633	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3.00E-09	NRP_MOUSE	NEUROPILIN PRECURSOR (A5 PROTEIN)	2.7
634	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	2.00E-05	Y4JN_RHISN	HYPOTHETICAL 16.3 KD PROTEIN Y4JN	5.9
635	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	6.00E-05	<NONE>	<NONE>	<NONE>
636	X64707	H.sapiens BBC1 mRNA	e-179	RLI3_HUMAN	60S RIBOSOMAL PROTEIN L13 (BREAST BASIC CONSERVED PROTEIN I)	5.00E-40
637	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3.00E-08	<NONE>	<NONE>	<NONE>
638	X14168	Human pLC46 with DNA replication origin	5.00E-14	SP3_HUMAN	TRANSCRIPTION FACTOR SP3 (SPR-2) (FRAGMENT)	0.19
639	X90999	H.sapiens mRNA for Glyoxalase II	9.00E-20	GLO2_HUMAN	HYDROXYACYLG LUTATHIONE HYDROLASE (EC 3.1.2.6)	0.007
640	AF083322	Homo sapiens centriole associated protein CEP110 mRNA, complete cds	9.00E-51	KIF4_MOUSE	KINESIN-LIKE PROTEIN KIF4	0.005

WO 99/33982

PCT/US98/27610

Table 2

Nearest Neighbor (BlastN vs. Genbank)				Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
641	Z12002	M.musculus Pvt-1 mRNA.	0.36	CP5F_CANTR	CYTOCHROME P450 L1A6 (ALKANE-INDUCIBLE) (EC 1.14.14.1) (P450-ALK3)	5.6
642	M10206	R.sphaeroides reaction center L subunit (complete cds) and M subunit (5' end) genes.	1.1	YGR1_YEAST	HYPOTHETICAL 34.8 KD PROTEIN IN SUT1-RCK1 INTERGENIC REGION	0.006
643	K02668	E. coli ddl gene encoding D-alanine:D-alanine ligase and ftsQ and ftsA genes, complete cds, and ftsZ gene, 5' end.	3.3	ANKB_HUMAN	ANKYRIN, BRAIN VARIANT 1 (ANKYRIN B) (ANKYRIN, NONERYTHROID)	7.00E-07
644	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
645	X53616	C.domesticus calnexin (pp90) mRNA	1.1	<NONE>	<NONE>	<NONE>
646	X57010	Human COL2A1 gene for collagen II alpha 1 chain, exons E2-E15	3.3	PRIO_PIG	MAJOR PRION PROTEIN PRECURSOR (PRP)	1.9
647	U95097	Xenopus laevis mitotic phosphoprotein 43 mRNA, partial cds	1.1	UL07_HSV2H	PROTEIN UL7	7.3
648	X52956	Human CAM1-psi3 calmodulin retroseudogene	0.37	PRTP_EBV	PROBABLE PROCESSING AND TRANSPORT PROTEIN	7.5
649	M93425	Human protein tyrosine phosphatase (PTP-PEST) mRNA, complete cds.	0	PTNC_HUMAN	PROTEIN-TYROSINE PHOSPHATASE G1 (EC 3.1.3.48) (PTPG1)	e-107
650	L47615	Mus musculus DNA-binding protein (Fli-1) gene, 5' end of cds.	0.13	YA53_SCHPO	HYPOTHETICAL 24.2 KD PROTEIN C13A11.03 IN CHROMOSOME 1	2.00E-07
651	U60337	Homo sapiens beta-mannosidase mRNA, complete	0	GIL1_ENTHI	GALACTOSE-INHIBITABLE LECTIN 170 KD	0.22

WO 99/33982

PCT/US98/27610

Table 2

Nearest Neighbor (BlastN vs. Genbank)				Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		cds			SUBUNIT	
652	U08813	Oryctolagus cuniculus Na+/glucose cotransporter-related protein mRNA, complete cds.	1.00E-22	NAG1_HUMAN	SODIUM/GLUCOSE COTRANSPORTER 1 (NA(+)/GLUCOSE COTRANSPORTER 1) (HIGH AFFINITY SODIUM-GLUCOSE COTRANSPORTER)	0.1
653	Y00282	Human mRNA for ribophorin II	2.00E-78	RIB2_HUMAN	DOLICHYL-DIPHOSPHOOLIGOSACCHARIDE--PROTEIN GLYCOSYLTRANSFERASE 63 KD SUBUNIT PRECURSOR (EC 2.4.1.119) (RIBOPHORIN II)	5.00E-19
654	D10051	Human gene for 92-kDa type IV collagenase, 5'-flanking region	0.014	TAGB_DICDI	PRESTALK-SPECIFIC PROTEIN TAGB PRECURSOR (EC 3.4.21.-)	7.6
655	M29930	Human insulin receptor (allele 2) gene, exons 14, 15, 16 and 17.	8.00E-08	<NONE>	<NONE>	<NONE>
656	U78310	Homo sapiens pescadillo mRNA, complete cds	0	YG2S_YEAST	HYPOTHETICAL 69.9 KD PROTEIN IN MIC1-SRB5 INTERGENIC REGION	0.002
657	X68792	S.coelicolor A3(2) promoter sequence pth270	3.2	YBS0_YEAST	HYPOTHETICAL 27.0 KD PROTEIN IN VAL1-HSP26 INTERGENIC REGION	0.073
658	U50535	Human BRCA2 region, mRNA sequence CG006	4.00E-12	ALU1_HUMAN	!!!! ALU SUBFAMILY J WARNING ENTRY !!!!	1.2

WO 99/33982

PCT/US98/27610

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
659	U15522	Sus scrofa clone pvg1a Ig heavy chain variable VDJ region mRNA, partial cds.	3.2	Z165_HUMAN	ZINC FINGER PROTEIN 165	3.2
660	M20918	C.thummi piger haemoglobin (Hb) gene DNA, complete cds.	0.12	YT25_CAEEL	HYPOTHETICAL 59.9 KD PROTEIN B0304.5 IN CHROMOSOME II	0.033
661	U60337	Homo sapiens beta-mannosidase mRNA, complete cds	0	<NONE>	<NONE>	<NONE>
662	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	0.001	ENV_MLVFP	ENV POLYPROTEIN PRECURSOR (CONTAINS: KNOB PROTEIN GP70; SPIKE PROTEIN P15E; R PROTEIN)	3.3
663	M97287	Human MAR/SAR DNA binding protein (SATB1) mRNA, complete cds. > :: gb 58691 58691 Sequence 1 from patent US 5652340	0	SAT1_HUMAN	DNA-BINDING PROTEIN SATB1 (SPECIAL AT-RICH SEQUENCE BINDING PROTEIN 1)	2.00E-20
664	L42612	Homo sapiens keratin 6 isoform K6f (KRT6F) mRNA, complete cds	e-168	K2C4_BOVIN	KERATIN, TYPE II CYTOSKELETAL 59 KD, COMPONENT IV	4.00E-10
665	U17901	Rattus norvegicus phospholipase A-2-activating protein (plap) mRNA, complete cds.	e-152	PLAP_MOUSE	PHOSPHOLIPASE A-2-ACTIVATING PROTEIN (PLAP)	4.00E-13
666	M73047	Homo sapiens tripeptidyl peptidase II mRNA, complete cds.	0	MERT_STRLI	MERCURIC TRANSPORT PROTEIN (MERCURY ION TRANSPORT PROTEIN)	4.4

WO 99/33982

PCT/US98/27610

Table 2

Nearest Neighbor (BlastN vs. Genbank)				Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
667	U09954	Human ribosomal protein L9 gene, 5' region and complete cds.	0	RL9_HUMAN	60S RIBOSOMAL PROTEIN L9	2.00E-11
668	X98330	H.sapiens mRNA for ryanodine receptor 2	1.1	HS74_MOUSE	HEAT SHOCK 70 KD PROTEIN AGP-2	0.034
669	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	0.002	RPC2_DROME	DNA-DIRECTED RNA POLYMERASE III 128 KD POLYPEPTIDE	1.1
670	AF069250	Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds	7.00E-80	LEGB_PEA	LEGUMIN B (FRAGMENT)	0.011
671	Z71419	S.cerevisiae chromosome XIV reading frame ORF YNL143c	1.1	FOCD_ECOLI	OUTER MEMBRANE USHER PROTEIN FOCD PRECURSOR	9.7
672	AF044965	Homo sapiens polio virus related protein 2 gene, alpha isoform, exon 6 and partial cds	e-167	PVR_MOUSE	POLIOVIRUS RECEPTOR HOMOLOG PRECURSOR	1.00E-12
673	X65319	Cloning vector pCAT-Enhancer	2.00E-80	S106_HUMAN	CALCYCLIN (PROLACTIN RECEPTOR ASSOCIATED PROTEIN) CALCIUM-BINDING PROTEIN A6)	3.00E-15
674	D29655	Pig mRNA for UMP-CMP kinase, complete cds	e-103	V319_ASFB7	J319 PROTEIN	4.3
675	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	8.00E-08	VEGR_RAT	VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR 1 PRECURSOR RECEPTOR FLT) (FLT-1)	3.3

WO 99/33982

PCT/US98/27610

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
676	D90217	S. cerevisiae gene for YmL33, mitochondrial ribosomal proteins of large subunit	2.00E-07	MALY_ECOLI	MALY PROTEIN (EC 2.6.1.-)	5.6
677	AF038952	Homo sapiens cofactor A protein mRNA, complete cds	e-160	T1CA_MOUSE	TCPI-CHAPERONIN COFACTOR A	4.00E-19
678	Z96950	Gorilla gorilla DNA sequence orthologous to the human Xp:Yp telomere-junction region	5.00E-14	YHBZ_ECOLI	HYPOTHETICAL 43.3 KD GTP-BINDING PROTEIN IN DACB-RPMA INTERGENIC REGION (F390)	3.3
679	D50418	Mouse mRNA for AREC3, partial cds	2.00E-79	CYGX_RAT	OLFACTORY GUANYLYL CYCLASE GC-D PRECURSOR (EC 4.6.1.2)	1.1
680	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	8.00E-08	P2C2_SCHPO	PROTEIN PHOSPHATASE 2C HOMOLOG 2 (EC 3.1.3.16)	1.00E-04
681	AL010280	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-106, complete sequence	0.12	<NONE>	<NONE>	<NONE>
682	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	5.00E-04	VSM2_TRYBB	VARIANT SURFACE GLYCOPROTEIN MITAT 1.2 PRECURSOR (VSG 221)	4.3
683	U00238	Homo sapiens glutamine PRPP amidotransferase (GPAT) mRNA, complete cds	0	<NONE>	<NONE>	<NONE>
684	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.005	PRPR_SALTY	PROPIONATE CATABOLISM OPERON REGULATORY PROTEIN	1.5

WO 99/33982

PCT/US98/27610

Table 2

Nearest Neighbor (BlastN vs. Genbank)				Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
685	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	7.00E-07	YAND_SCHPO	HYPOTHETICAL 30.4 KD PROTEIN C3H1.13 IN CHROMOSOME I	0.38
686	D25538	Human mRNA for KIAA0037 gene, complete cds	0	<NONE>	<NONE>	<NONE>
687	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2.00E-07	A1AA_RAT	ALPHA-1A ADRENERGIC RECEPTOR (RA42)	4.4
688	L26956	Mesocricetus auratus stearyl-CoA desaturase sequence including male hormone dependent gene derived from hamster frankorgan	4.00E-33	<NONE>	<NONE>	<NONE>
689	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3.00E-10	<NONE>	<NONE>	<NONE>
690	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3.00E-09	YO93_CAEEL	HYPOTHETICAL 58.5 KD PROTEIN T20B12.3 IN CHROMOSOME III	2.00E-08
691	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	8.00E-09	<NONE>	<NONE>	<NONE>
692	AB017026	Mus musculus mRNA for oxysterol-binding protein, complete cds	0	OXYB_RABIT	OXYSTEROL-BINDING PROTEIN	1.00E-34
693	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	6.00E-04	UFO2_MAIZE	FLAVONOL 3-O-GLUCOSYLTRANSFERASE (EC 2.4.1.91)	3.1

WO 99/33982

PCT/US98/27610

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
694	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	5.00E-04	<NONE>	<NONE>	<NONE>
695	U34954	Caenorhabditis elegans cyclophilin isoform 10	5.00E-24	CYPA_CAEEL	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE 10 (EC 5.2.1.8)	2.00E-29
696	AB011167	Homo sapiens mRNA for KIAA0595 protein, partial cds	0	RFX5_HUMAN	BINDING REGULATORY FACTOR	2.1
697	U03886	Human GS2 mRNA, complete cds.	2.00E-28	SKD1_MOUSE	SKD1 PROTEIN	4.00E-17
698	AF086275	Homo sapiens full length insert cDNA clone ZD45C02	3.00E-41	SPT7_YEAST	TRANSCRIPTIONAL ACTIVATOR SPT7	0.82
699	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3.00E-10	CA1E_HUMAN	COLLAGEN ALPHA 1(XV) CHAIN PRECURSOR	1.1
700	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	4.00E-11	E434_ADECC	Q65962 canine adenovirus type 1 (strain cll). early e4 31 kd protein. 11/98	4.4
701	L17340	Drosophila melanogaster germline transcription factor gene, complete cds.	3.3	CISY_TETTH	CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR (EC 4.1.3.7) (14 NM FILAMENT-FORMING PROTEIN)	9.7
702	X58170	M.musculus mRNA for t-Complex Tcp-10a gene	2.00E-45	PME2_LYCES	PECTINESTERASE 2 PRECURSOR (EC 3.1.1.11) (PECTIN METHYLESTERASE) (PE 2)	7.4
703	Z96207	H.sapiens telomeric DNA sequence, clone 12PTEL049, read 12PTELOO049.se	8.00E-08	<NONE>	<NONE>	<NONE>

WO 99/33982

PCT/US98/27610

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		q				
704	X58430	Human Hox1.8 gene	e-146	HXAA_HUMAN	HOMEBOX PROTEIN HOX-A10 (HOX-1H) (HOX-1.8) (PL)	4.00E-05
705	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	6.00E-06	YN39_SYNP7	HYPOTHETICAL 9.2 KD PROTEIN IN CYST-CYSR INTERGENIC REGION (ORF 81)	0.89
706	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1.00E-11	MYSH_BOVIN	MYOSIN I HEAVY CHAIN-LIKE PROTEIN (MIHC) (BRUSH BORDER MYOSIN I) (BBMI)	0.001
707	M19961	Human cytochrome c oxidase subunit Vb (coxVb) mRNA, complete cds.	e-123	OTHU5B	<NONE>	3.00E-30
708	X68380	M.musculus gene for cathepsin D, exon 3	5.00E-04	42_MOUSE	ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2 (P4.2) (PALLIDIN)	9.9
709	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	1.00E-11	TCPA_DROME	T-COMPLEX PROTEIN 1, ALPHA SUBUNIT (TCP-1-ALPHA)	4.3
710	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3.00E-10	<NONE>	<NONE>	<NONE>
711	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	4.00E-12	<NONE>	<NONE>	<NONE>
712	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.002	<NONE>	<NONE>	<NONE>

WO 99/33982

PCT/US98/27610

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
713	AB018323	Homo sapiens mRNA for KIAA0780 protein, partial cds	3.00E-41	LBR_CHICK	LAMIN B RECEPTOR	3.4
714	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	6.00E-06	YM8L_YEAST	HYPOTHETICAL 71.1 KD PROTEIN IN DSK2-CAT8 INTERGENIC REGION	3.00E-08
715	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	4.00E-13	PSC_DROME	POSTERIOR SEX COMBS PROTEIN	0.6
716	L28101	Homo sapiens kallistatin (PI4) gene, exons 1-4, complete cds	7.00E-07	IRKX_RAT	INWARD RECTIFIER POTASSIUM CHANNEL BIR9 (KIR5.1)	5.4
717	AC001038	Homo sapiens (subclone 2_h2 from P1 H49) DNA sequence	8.00E-09	MGMT_YEAST	METHYLATED-DNA--PROTEIN-CYSTEINE METHYLTRANSFERASE	0.48
718	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1.00E-11	YWDE_BACSU	HYPOTHETICAL 19.9 KD PROTEIN IN SACA-UNG INTERGENIC REGION PRECURSOR	1.8
719	U01139	Mus musculus B6D2F1 clone 2C11B mRNA.	e-110	GSC_DROME	HOMEBOX PROTEIN GOOSECOID	7.2
720	AB017430	Homo sapiens mRNA for kinesin-like DNA binding protein, complete cds	0	YBAV_ECOLI	HYPOTHETICAL 12.7 KD PROTEIN IN HUPB-COF INTERGENIC REGION	0.17
721	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	0.001	CPCF_SYNP2	PHYCOCYANOBILIN LYASE BETA SUBUNIT (EC 4.---)	2.4
722	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	9.00E-10	<NONE>	<NONE>	<NONE>

WO 99/33982

PCT/US98/27610

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
723	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.04	YKK7_CAEEL	HYPOTHETICAL 54.9 KD PROTEIN C02F5.7 IN CHROMOSOME III	0.057
724	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	8.00E-08	H5_CAIMO	HISTONE H5	0.39
725	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	3.00E-09	DED1_YEAST	PUTATIVE ATP-DEPENDENT RNA HELICASE DED1	0.5
726	J04617	Human elongation factor EF-1-alpha gene, complete cds. > :: dbj E02629 E02629 DNA of human polypeptide chain elongation factor-1 alpha	5.00E-36	ALU7_HUMAN	!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!	0.84
727	X54859	Porcine TNF-alpha and TNF-beta genes for tumour necrosis factors alpha and beta, respectively.	3.3	Z165_HUMAN	ZINC FINGER PROTEIN 165	5.6
728	D49911	Thermus thermophilus UvrA gene, complete cds	0.014	CC48_CAPAN	CELL DIVISION CYCLE PROTEIN 48 HOMOLOG	9.9
729	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	2.00E-06	CA25_HUMAN	PROCOLLAGEN ALPHA 2(V) CHAIN PRECURSOR	0.011
730	D15057	Human mRNA for DAD-1, complete cds	0	DAD1_HUMAN	DEFENDER AGAINST CELL DEATH 1 (DAD-1)	8.00E-16
731	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	6.00E-06	ANFD_RHOCA	NITROGENASE IRON-IRON PROTEIN ALPHA CHAIN (EC 1.18.6.1) (NITROGENASE COMPONENT 1) (DINITROGENASE	9.6

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
)	
732	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	7.00E-07	EFTU_CHLVI	ELONGATION FACTOR TU (EFTU)	2.5
733	AB018335	Homo sapiens mRNA for KIAA0792 protein, complete cds	0	TRYM_RAT	MAST CELL TRYPTASE PRECURSOR (EC 3.4.21.59)	5.6
734	X98743	H.sapiens mRNA for RNA helicase (Myc-regulated dead box protein)	0.04	<NONE>	<NONE>	<NONE>
735	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	2.00E-07	<NONE>	<NONE>	<NONE>
736	Z49314	S.cerevisiae chromosome X reading frame ORF YJL039c	3.2	<NONE>	<NONE>	<NONE>
737	D12646	Mouse kif4 mRNA for microtubule-based motor protein KIF4, complete cds	0	KIF4_MOUSE	KINESIN-LIKE PROTEIN KIF4	2.00E-76
738	J04038	Human glyceraldehyde-3-phosphate dehydrogenase	2.00E-47	SDC1_HUMAN	SYNDECAN-1 PRECURSOR (SYND1) (CD138)	3.5
739	AF010238	Homo sapiens von Hippel-Lindau tumor suppressor	1.00E-09	LIN1_HUMAN	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG	0.001
740	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2.00E-06	YQJX_BACSU	HYPOTHETICAL 13.2 KD PROTEIN IN GLNQ-ANSR INTERGENIC REGION	9.9

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
741	L21186	Human lysyl oxidase-like protein mRNA, complete cds.	e-145	OXRTL	<NONE>	1.00E-34
742	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2.00E-05	CC48_SOYBN	CELL DIVISION CYCLE PROTEIN 48 HOMOLOG (VALOSIN CONTAINING PROTEIN HOMOLOG) (VCP)	7.6
743	AF009203	Homo sapiens YAC clone 377A1 unknown mRNA, 3' untranslated region	3.3	<NONE>	<NONE>	<NONE>
744	Z74894	S.cerevisiae chromosome XV reading frame ORF YOL152w	0.12	CD14_RABIT	Q28680 oryctolagus cuniculus (rabbit). monocyte differentiation antigen cd14 precursor. 11/98	1.9
745	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	9.00E-10	KIN3_YEAST	SERINE/THREONINE-PROTEIN KINASE KIN3 (EC 2.7.1.-)	2.5
746	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2.00E-05	YA53_SCHPO	HYPOTHETICAL 24.2 KD PROTEIN C13A11.03 IN CHROMOSOME 1	7.00E-17
747	S61044	ALDH3=aldehyde dehydrogenase isozyme 3 [human, stomach, mRNA Partial, 1362 nt]	0	DHAP_HUMAN	ALDEHYDE DEHYDROGENASE, DIMERIC NADP-PREFERRING (EC 1.2.1.5) (CLASS 3)	2.00E-71
748	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2.00E-08	CA1E_CHICK	COLLAGEN ALPHA 1(XIV) CHAIN PRECURSOR (UNDULIN)	0.36
749	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	7.00E-06	<NONE>	<NONE>	<NONE>

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
750	L14815	Entamoeba histolytica HM-1:IMSS galactose-specific adhesin 170kD subunit (hgl3) gene, complete cds.	0.12	<NONE>	<NONE>	<NONE>
751	X63785	T.thermophila gene for snRNA U2-2	1.1	<NONE>	<NONE>	<NONE>
752	M83756	Mytilus edulis mitochondrial NADH dehydrogenase subunit 5 (ND5) gene, 3' end; NADH dehydrogenase subunit 6 (ND6) gene, complete cds; and cytochrome b (cyt b), 5' end.	0.042	DSC1_HUMAN	DESMOCOLLIN 1A/1B PRECURSOR (DESMOSOMAL GLYCOPROTEIN 2/3) (DG2 / DG3)	2.6
753	AB001066	Brown trout microsatellite DNA sequence	0.38	IMB3_HUMAN	IMPORTIN BETA-3 SUBUNIT (KARYOPHERIN BETA-3 SUBUNIT)	1.2
754	AF064787	Lotus japonicus rac GTPase activating protein 1 mRNA, complete cds	0.51	<NONE>	<NONE>	<NONE>
755	U20608	Dictyostelium discoideum unknown spore germination-specific protein-like protein, orf1, orf2 and orf3 genes, complete cds	0.043	<NONE>	<NONE>	<NONE>
756	M77812	Rabbit myosin heavy chain mRNA, complete cds.	1.2	RBL1_HUMAN	RETINOBLASTOM A-LIKE PROTEIN 1 (107 KD RETINOBLASTOM A-ASSOCIATED PROTEIN) (PRB1) (P107)	4.9

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
757	X63789	T.thermophila genes for snRNA U5-1, snRNA U5-2	0.058	<NONE>	<NONE>	<NONE>
758	D50646	Mouse mRNA for SDF2, complete cds	2.00E-27	PMT3_YEAST	DOLICHYL-PHOSPHATE-MANNOSE--PROTEIN MANNOSYLTRANSFERASE 3 (EC 2.4.1.109)	0.002
759	L81583	Homo sapiens (subclone 3_g2 from P1 H11) DNA sequence	3.00E-19	ALU5_HUMAN	!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!	0.86
760	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2.00E-06	SYFA_YEAST	PHENYLALANYL-TRNA SYNTHETASE ALPHA CHAIN CYTOPLASMIC	5.7
761	AF000370	Homo sapiens polymorphic CA dinucleotide repeat flanking region	6.00E-89	APPI_MOUSE	AMYLOID-LIKE PROTEIN 1 PRECURSOR (APLP)	5.7
762	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	0.002	<NONE>	<NONE>	<NONE>
763	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	7.00E-06	PSF_HUMAN	PTB-ASSOCIATED SPLICING FACTOR (PSF)	0.72
764	AB018288	Homo sapiens mRNA for KIAA0745 protein, partial cds	0	TC2A_CAEBR	TRANSPOSABLE ELEMENT TCB2 TRANSPOSASE	1.5
765	AF020282	Dictyostelium discoideum DG2033 gene, partial cds	0.38	PMT2_YEAST	DOLICHYL-PHOSPHATE-MANNOSE--PROTEIN MANNOSYLTRANSFERASE 2 (EC 2.4.1.109)	0.18

WO 99/33982

PCT/US98/27610

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
766	AF017357	Oryza sativa low molecular early light-inducible protein mRNA, complete cds	0.38	RGS3_HUMAN	REGULATOR OF G-PROTEIN SIGNALLING 3 (RGS3) (RGP3)	0.23
767	U67599	Methanococcus jannaschii section 141 of 150 of the complete genome	0.13	<NONE>	<NONE>	<NONE>
768	X74178	B.taurus microsatellite DNA INRA153	0.13	FAG1_SYNY3	P73574 synechocystis sp. (strain pcc 6803). 3-oxoacyl-[acyl-carrier protein] reductase 1 (ec 1.1.1.100) (3-ketoacyl- acyl carrier protein reductase 1). 11/98	5.00E-16
769	AF041858	Mus musculus synaptojanin 2 isoform delta mRNA, partial cds	0.043	CA44_HUMAN	COLLAGEN ALPHA 4(IV) CHAIN PRECURSOR	0.24
770	J01404	Drosophila melanogaster mitochondrial cytochrome c oxidase subunits, ATPase6, 7 tRNAs (Trp, Cys, Tyr, Leu(UUR), Lys, Asp, Gly) genes, and unidentified reading frames A61, 2 and 3.	0.021	NUIM_CITLA	NADH-UBIQUINONE OXIDOREDUCTAS E CHAIN I (EC 1.6.5.3)	7.2
771	AL022317	Human DNA sequence from clone 140L1 on chromosome 22q13.1-13.31, complete sequence [Homo sapiens]	3.00E-41	ALU7_HUMAN	!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!	4.00E-08
772	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1.00E-09	<NONE>	<NONE>	<NONE>

WO 99/33982

PCT/US98/27610

Table 2

Nearest Neighbor (BlastN vs. Genbank)				Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
773	AF095927	Rattus norvegicus protein phosphatase 2C mRNA, complete cds	0	P2C_PARTE	PROTEIN PHOSPHATASE 2C (EC 3.1.3.16) (PP2C)	1.00E-16
774	X87212	H.sapiens mRNA for cathepsin C	0	CATC_HUMAN	DIPEPTIDYL-PEPTIDASE I PRECURSOR (EC 3.4.14.1)	2.00E-46
775	X05283	Drosophila melanogaster PKCG7 gene exons 7-14 for protein kinase C	4.5	<NONE>	<NONE>	<NONE>
776	X03558	Human mRNA for elongation factor 1 alpha subunit	0	EF11_HUMAN	ELONGATION FACTOR 1-ALPHA 1 (EF-1-ALPHA-1)	1.00E-83
777	X06960	Aspergillus nidulans mitochondrial DNA for cytochrome oxidase subunit 3, tRNA-Tyr	0.23	<NONE>	<NONE>	<NONE>
778	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3.00E-09	YMT8_YEAST	HYPOTHETICAL 36.4 KD PROTEIN IN NUP116-FAR3 INTERGENIC REGION	5.00E-07
779	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2.00E-07	NAT1_YEAST	N-TERMINAL ACETYLTRANSFERASE 1 (EC 2.3.1.88)	5.00E-23
780	U59706	Gallus gallus alternatively spliced AMPA glutamate receptor, isoform GluR2 flop, (GluR2) mRNA, partial cds.	0.014	PPOL_SARPE	POLY (ADP-RIBOSE) POLYMERASE (EC 2.4.2.30) (PARP)	0.021
781	U57391	Rattus norvegicus FceR1 gamma-chain interacting protein SH2-B (SH2-B) mRNA, complete cds	1.00E-84	<NONE>	<NONE>	<NONE>

WO 99/33982

PCT/US98/27610

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
782	AB014591	Homo sapiens mRNA for KIAA0691 protein, complete cds	7.00E-57	SSGP_VOLCA	SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185)	5.3
783	AJ008065	Chrysolina bankii 16S rRNA gene, mitotype B2	0.043	<NONE>	<NONE>	<NONE>
784	AF067212	Caenorhabditis elegans cosmid F37F2	0.005	MEK1_RAT	MAPK/ERK KINASE KINASE 1 (EC 2.7.1.-) (MEK KINASE 1)	4.5
785	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	0.042	<NONE>	<NONE>	<NONE>
786	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	9.00E-09	<NONE>	<NONE>	<NONE>
787	Y13401	Homo sapiens CD3 delta gene, enhancer sequence	8.00E-08	<NONE>	<NONE>	<NONE>
788	AE001038	Archaeoglobus fulgidus section 69 of 172 of the complete genome	0.13	<NONE>	<NONE>	<NONE>
789	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2.00E-06	<NONE>	<NONE>	<NONE>
790	AF041463	Manihot esculenta elongation factor 1-alpha	1.4	<NONE>	<NONE>	<NONE>
791	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.002	HXA3_HAEIN	HEME:HEMOPEXIN-BINDING PROTEIN PRECURSOR	2.7
792	Z12112	pWE15A cosmid vector DNA	3.00E-29	PKWA_THECU	PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-)	2.00E-04

WO 99/33982

PCT/US98/27610

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
793	U85193	Human nuclear factor I-B2 (NFIB2) mRNA, complete cds	4.00E-44	<NONE>	<NONE>	<NONE>
794	U89331	Human pseudoautosomal homeodomain-containing protein (PHOG) mRNA, complete cds	7.00E-06	NRL_HUMAN	NEURAL RETINA-SPECIFIC LEUCINE ZIPPER PROTEIN (NRL)	6.3
795	AF055666	Mus musculus kinesin light chain 2 (Klc2) mRNA, complete cds	0.52	PSPD_BOVIN	PULMONARY SURFACTANT-ASSOCIATED PROTEIN D PRECURSOR	0.33
796	L13321	Homo sapiens iduronate-2-sulfatase (IDS) gene, exon 1, incomplete 5' end.	0.14	YRP2_YEAST	HYPOTHETICAL 84.4 KD PROTEIN IN RPC2/RET1 3'REGION	0.27
797	AL010270	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-96, complete sequence	0.37	YTH3_CAEEL	HYPOTHETICAL 75.5 KD PROTEIN C14A4.3 IN CHROMOSOME II	2
798	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	0.015	IMB3_HUMAN	IMPORTIN BETA-3 SUBUNIT (KARYOPHERIN BETA-3 SUBUNIT)	0.063
799	U70139	Mus musculus putative CCR4 protein mRNA, partial cds	0	CCR4_YEAST	GLUCOSE-REPRESSIBLE ALCOHOL DEHYDROGENASE TRANSCRIPTIONAL EFFECTOR (CARBON CATABOLITE REPRESSOR PROTEIN 4)	5.00E-11
800	L26507	Mouse myocyte nuclear factor (MNF) mRNA, complete cds.	3.00E-41	MNF_MOUSE	MYOCYTE NUCLEAR FACTOR (MNF)	4.00E-18

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
801	U20527	Mus musculus chemokine KC gene, 5' region.	0	GRO_MOUSE	GROWTH REGULATED PROTEIN PRECURSOR (PLATELET-DERIVED GROWTH FACTOR-INDUCIBLE PROTEIN KC) (SECRETORY PROTEIN N51)	1.00E-28
802	AF065482	Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds	0	MYSA_DROME	MYOSIN HEAVY CHAIN, MUSCLE	0.089
803	U05823	Mus musculus pericentrin mRNA, complete cds.	1.00E-94	M84D_DROME	MALE SPECIFIC SPERM PROTEIN MST84DD	0.099
804	U67468	Methanococcus jannaschii section 10 of 150 of the complete genome	0.4	<NONE>	<NONE>	<NONE>
805	U14178	Human type II IL-1 receptor gene, exon 1B	1.00E-19	AMPH_HUMAN	AMPHIPHYSIN	2.9
806	L40411	Homo sapiens thyroid receptor interactor	0	TRI8_HUMAN	THYROID RECEPTOR INTERACTING PROTEIN 8 (TRIP8)	4.00E-86
807	D17218	Human HepG2 3' region Mbol cDNA, clone hmd3g02m3	e-136	CA1A_HUMAN	COLLAGEN ALPHA 1(X) CHAIN PRECURSOR	3.00E-04
808	Z57610	H.sapiens CpG DNA, clone 187a10, reverse read cpg187a10.rt1a.	e-102	HN3B_MOUSE	HEPATOCYTE NUCLEAR FACTOR 3-BETA (HNF-3B)	1.00E-24
809	D14678	Human mRNA for kinesin-related protein, partial cds	0	NCD_DROME	CLARET SEGREGATIONAL PROTEIN	1.00E-70

WO 99/33982

PCT/US98/27610

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
810	X56317	Xiphophorus maculatus Xmrk(proto-oncogene) gene for receptor tyrosine kinase.	0.49	WN1B_MOUSE	WNT-10B PROTEIN PRECURSOR (WNT-12)	7.2
811	M36200	Human synaptobrevin 1 (SYB1) gene, exon 5.	0.2	VE2_HPVI4	REGULATORY PROTEIN E2	3.1
812	M18157	Human glandular kallikrein gene, complete cds.	1.5	EKLF_MOUSE	ERYTHROID KRUEPPEL-LIKE TRANSCRIPTION FACTOR (EKLF)	1.1
813	D25215	Human mRNA for KIAA0032 gene, complete cds	1.9	YXIS_SACER	HYPOTHETICAL 28.9 KD PROTEIN IN XIS 5'REGION (ORF1)	1.3
814	M96628	Human gene sequence, 5' end.	2.00E-06	AGRI_DISOM	AGRIN (FRAGMENT)	9.5
815	Z57610	H.sapiens CpG DNA, clone 187a10, reverse read cpg187a10.rt1a.	e-102	HN3B_MOUSE	HEPATOCYTE NUCLEAR FACTOR 3-BETA (HNF-3B)	1.00E-19
816	X14168	Human pLC46 with DNA replication origin	5.00E-16	ZN44_HUMAN	ZINC FINGER PROTEIN 44 (ZINC FINGER PROTEIN KOX7)	1.6
817	M19262	Rat clathrin light chain (LCB3) mRNA, complete cds.	0.28	LMA_DROME	LAMININ ALPHA CHAIN PRECURSOR	4.7
818	AF058055	Mus musculus monocarboxylate transporter 1	0.2	<NONE>	<NONE>	<NONE>
819	AB014570	Homo sapiens mRNA for KIAA0670 protein, partial cds	0.16	YGR1_YEAST	HYPOTHETICAL 34.8 KD PROTEIN IN SUT1-RCK1 INTERGENIC REGION	4.00E-06
820	M19262	Rat clathrin light chain (LCB3) mRNA, complete cds.	0.27	LMA_DROME	LAMININ ALPHA CHAIN PRECURSOR	4.5

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
821	Z54367	H.sapiens gene for plectin	0.29	YO93_CAEEL	HYPOTHETICAL 58.5 KD PROTEIN T20B12.3 IN CHROMOSOME III	1.00E-14
822	AB017026	Mus musculus mRNA for oxysterol-binding protein, complete cds	0	OXYB_HUMAN	OXYSTEROL-BINDING PROTEIN	2.00E-49
823	X58170	M.musculus mRNA for t-Complex Tcp-10a gene	1.00E-20	UL52_HSV11	DNA HELICASE/PRIMASE COMPLEX PROTEIN (DNA REPLICATION PROTEIN UL52)	5.3
824	X58430	Human Hox1.8 gene	0	HXAA_HUMAN	HOMEODOMAIN PROTEIN HOX-A 10 (HOX-1H) (HOX-1.8) (PL)	1.00E-44
825	X53754	Porcine sarcoplasmic/endoplasmic reticulum Ca(2+) pump gene 2 3'-end region	1.3	<NONE>	<NONE>	<NONE>
826	AB005786	Arabidopsis thaliana tRNA-Glu gene	0.46	<NONE>	<NONE>	<NONE>
827	AB012130	Homo sapiens SBC2 mRNA for sodium bicarbonate cotransporter2, complete cds	1.9	<NONE>	<NONE>	<NONE>
828	AB017430	Homo sapiens mRNA for kinesin-like DNA binding protein, complete cds	0	YBAV_ECOLI	HYPOTHETICAL 12.7 KD PROTEIN IN HUPB-COF INTERGENIC REGION	0.063
829	AB007886	Homo sapiens KIAA0426 mRNA, complete cds	0.042	YDF3_SCHPO	PROBABLE EUKARYOTIC INITIATION FACTOR C17C9.03	0.52
830	AB018335	Homo sapiens mRNA for KIAA0792 protein, complete cds	e-172	UROT_BOVIN	TISSUE PLASMINOGEN ACTIVATOR PRECURSOR (EC 3.4.21.68)	0.86

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
831	D12646	Mouse kif4 mRNA for microtubule-based motor protein KIF4, complete cds	0	KIF4_MOUSE	KINESIN-LIKE PROTEIN KIF4	9.00E-96
832	U38376	Rattus norvegicus cytosolic phospholipase A2 mRNA, complete cds	0.048	<NONE>	<NONE>	<NONE>
833	L40411	Homo sapiens thyroid receptor interactor	0	TR18_HUMAN	THYROID RECEPTOR INTERACTING PROTEIN 8 (TRIP8)	4.00E-86
834	U08110	Mus musculus RNA1 homolog (Fug1) mRNA, complete cds.	8.00E-04	YNW7_YEAST	HYPOTHETICAL 68.8 KD PROTEIN IN URE2-SSU72 INTERGENIC REGION	0.02
835	D50646	Mouse mRNA for SDF2, complete cds	1.00E-40	YB64_YEAST	HYPOTHETICAL 57.2 KD PROTEIN IN MET8-HPC2 INTERGENIC REGION	4.9
836	D50646	Mouse mRNA for SDF2, complete cds	1.00E-40	YB64_YEAST	HYPOTHETICAL 57.2 KD PROTEIN IN MET8-HPC2 INTERGENIC REGION	4.9
837	U67459	Methanococcus jannaschii section 1 of 150 of the complete genome	5.00E-05	GCS1_HUMAN	MANNOSYL-OLIGOSACCHARIDE GLUCOSIDASE (EC 3.2.1.106)	9.2
838	U18657	Haemophilus influenzae LeuA (leuA) gene, partial cds, DprA (dprA+), orf272 and orf193 genes, complete cds, and PfkA (pfkA) gene, partial cds.	0.01	STE6_YEAST	MATING FACTOR A SECRETION PROTEIN STE6 (MULTIPLE DRUG RESISTANCE PROTEIN HOMOLOG) (P-GLYCOPROTEIN)	7

WO 99/33982

PCT/US98/27610

Table 2

Nearest Neighbor (BlastN vs. Genbank)				Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
839	U12523	Rattus norvegicus ultraviolet B radiation-activated UV98 mRNA, partial sequence.	1.00E-10	YMT8_YEAST	HYPOTHETICAL 36.4 KD PROTEIN IN NUP116-FAR3 INTERGENIC REGION	2.00E-06
840	D78255	Mouse mRNA for PAP-1, complete cds	e-175	<NONE>	<NONE>	<NONE>
841	D17263	Human HepG2 3' region Mbol cDNA, clone hmd5f07m3	1.00E-58	<NONE>	<NONE>	<NONE>
842	AF006751	Homo sapiens ES/130 mRNA, complete cds	0.061	YRP2_YEAST	HYPOTHETICAL 84.4 KD PROTEIN IN RPC2/RET1 3'REGION	2.00E-07
843	U67459	Methanococcus jannaschii section 1 of 150 of the complete genome	6.00E-05	YC14_METJA	HYPOTHETICAL PROTEIN MJ1214	8.1
844	D88689	Mus musculus mRNA for flt-1, complete cds	0.084	ICP0_HSV2H	TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (VMW118 PROTEIN)	0.014

WO 99/33982

PCT/US98/27610

Table 5 All Differential Data for Libs 1-4 and 8-9

Clone Name	Cluster ID	Clones in Lib1	Clones in Lib2	Clones in Lib3	Clones in Lib4	Clones in Lib8	Clones in Lib9
M00001340B:A06	17062	3	0	0	0	0	0
M00001340D:F10	11589	2	2	1	3	3	8
M00001341A:E12	4443	10	6	2	6	3	11
M00001342B:E06	39805	2	0	0	0	1	0
M00001343C:F10	2790	7	15	13	14	6	0
M00001343D:H07	23255	3	0	1	1	0	0
M00001345A:E01	6420	8	0	2	0	1	0
M00001346A:F09	5007	4	8	3	6	2	6
M00001346D:E03	6806	5	2	1	2	0	3
M00001346D:G06	5779	5	4	3	4	0	0
M00001346D:G06	5779	5	4	3	4	0	0
M00001347A:B10	13576	5	0	0	0	12	11
M00001348B:B04	16927	4	0	0	2	0	0
M00001348B:G06	16985	4	0	0	0	0	0
M00001349B:B08	3584	5	11	5	0	0	2
M00001350A:H01	7187	5	3	1	0	1	0
M00001351B:A08	3162	10	14	1	6	6	5
M00001351B:A08	3162	10	14	1	6	6	5
M00001352A:E02	16245	4	0	0	0	0	0
M00001353A:G12	8078	4	3	1	0	1	0
M00001353D:D10	14929	4	0	0	1	23	16
M00001355B:G10	14391	3	1	0	0	0	0
M00001357D:D11	4059	8	6	8	16	0	1
M00001361A:A05	4141	5	2	10	16	4	27
M00001361D:F08	2379	26	13	4	2	2	3
M00001362B:D10	5622	7	4	2	13	1	2
M00001362C:H11	945	9	21	2	1	0	0
M00001365C:C10	40132	2	0	0	0	3	0
M00001370A:C09	6867	7	3	0	0	0	0
M00001371C:E09	7172	3	5	1	2	0	1
M00001376B:G06	17732	1	3	5	0	1	4
M00001378B:B02	39833	2	0	0	0	0	0
M00001379A:A05	1334	27	38	35	28	3	0
M00001380D:B09	39886	2	0	0	0	0	0
M00001382C:A02	22979	2	1	0	0	0	0
M00001383A:C03	39648	2	0	0	0	0	0
M00001383A:C03	39648	2	0	0	0	0	0
M00001386C:B12	5178	5	5	4	2	5	2
M00001387A:C05	2464	5	19	25	16	1	0
M00001387B:G03	7587	6	2	1	0	0	0
M00001388D:G05	5832	10	3	0	1	5	0
M00001389A:C08	16269	3	0	0	0	1	1
M00001394A:F01	6583	2	7	3	2	0	0
M00001395A:C03	4016	5	14	0	6	0	0
M00001396A:C03	4009	6	4	13	5	4	10
M00001402A:E08	39563	2	0	0	0	0	0

WO 99/33982

PCT/US98/27610

Table 5 All Differential Data for Libs 1-4 and 8-9

Clone Name	Cluster ID	Clones in Lib1	Clones in Lib2	Clones in Lib3	Clones in Lib4	Clones in Lib8	Clones in Lib9
M00001407B:D11	5556	8	1	5	0	2	0
M00001409C:D12	9577	5	2	0	1	11	12
M00001410A:D07	7005	8	2	0	0	0	0
M00001412B:B10	8551	4	4	0	3	0	0
M00001415A:H06	13538	5	0	0	0	9	1
M00001416A:H01	7674	5	2	0	5	0	0
M00001416B:H11	8847	4	1	3	0	6	1
M00001417A:E02	36393	2	0	0	1	0	0
M00001418B:F03	9952	4	2	1	1	0	0
M00001418D:B06	8526	3	2	1	5	1	0
M00001421C:F01	9577	5	2	0	1	11	12
M00001423B:E07	15066	4	0	0	0	0	0
M00001424B:G09	10470	5	1	0	2	0	1
M00001425B:H08	22195	3	0	0	0	0	0
M00001426D:C08	4261	4	9	7	9	12	15
M00001428A:H10	84182	1	0	0	0	0	0
M00001429A:H04	2797	15	11	18	16	1	14
M00001429B:A11	4635	7	9	2	0	0	0
M00001429D:D07	40392	2	0	1	8	12	16
M00001439C:F08	40054	1	0	0	0	0	0
M00001442C:D07	16731	3	1	0	0	0	0
M00001445A:F05	13532	3	2	1	0	1	2
M00001446A:F05	7801	5	2	4	6	1	0
M00001447A:G03	10717	7	2	0	5	8	0
M00001448D:C09	8	1850	2127	1703	3133	1355	122
M00001448D:H01	36313	2	0	0	0	1	30
M00001449A:A12	5857	6	2	3	4	0	0
M00001449A:B12	41633	1	1	0	0	0	0
M00001449A:D12	3681	12	5	10	1	2	5
M00001449A:G10	36535	2	0	0	0	0	0
M00001449C:D06	86110	1	0	0	0	0	0
M00001450A:A02	39304	2	0	0	0	0	0
M00001450A:A11	32663	1	1	0	0	0	0
M00001450A:B12	82498	1	0	0	0	0	0
M00001450A:D08	27250	2	0	0	0	0	0
M00001452A:B04	84328	1	0	0	0	0	0
M00001452A:B12	86859	1	0	0	0	0	0
M00001452A:D08	1120	44	41	5	11	5	0
M00001452A:F05	85064	1	0	0	0	0	0
M00001452C:B06	16970	4	0	0	0	3	4
M00001453A:E11	16130	3	1	0	0	0	1
M00001453C:F06	16653	3	1	0	0	0	0
M00001454A:A09	83103	1	0	0	0	0	0
M00001454B:C12	7005	8	2	0	0	0	0
M00001454D:G03	689	58	95	17	36	66	95
M00001455A:E09	13238	4	1	0	0	0	0
M00001455B:E12	13072	4	1	0	0	0	0
M00001455D:F09	9283	4	1	0	1	0	1

WO 99/33982

PCT/US98/27610

Table 5 All Differential Data for Libs 1-4 and 8-9

Clone Name	Cluster ID	Clones in Lib1	Clones in Lib2	Clones in Lib3	Clones in Lib4	Clones in Lib8	Clones in Lib9
M00001455D:F09	9283	4	1	0	1	0	1
M00001460A:F06	2448	23	22	2	3	3	1
M00001460A:F12	39498	2	0	0	0	0	0
M00001461A:D06	1531	20	23	32	17	14	14
M00001463C:B11	19	1415	1203	1364	525	479	774
M00001465A:B11	10145	2	0	2	0	0	0
M00001466A:E07	4275	11	2	5	0	4	2
M00001467A:B07	38759	2	0	0	0	1	1
M00001467A:D04	39508	2	0	0	0	0	0
M00001467A:D08	16283	3	0	0	0	0	0
M00001467A:D08	16283	3	0	0	0	0	0
M00001467A:E10	39442	2	0	0	0	0	0
M00001468A:F05	7589	6	2	1	1	1	0
M00001469A:C10	12081	4	0	0	0	0	0
M00001469A:H12	19105	2	0	2	0	1	0
M00001470A:B10	1037	53	48	4	22	0	0
M00001470A:C04	39425	2	0	0	0	0	0
M00001471A:B01	39478	2	0	0	0	0	0
M00001481D:A05	7985	3	1	4	0	1	0
M00001490B:C04	18699	2	1	0	0	0	3
M00001494D:F06	7206	4	3	3	1	2	0
M00001497A:G02	2623	12	4	31	4	6	1
M00001499B:A11	10539	2	1	1	0	1	0
M00001500A:C05	5336	9	2	4	8	3	15
M00001500A:E11	2623	12	4	31	4	6	1
M00001500C:E04	9443	4	2	1	1	0	0
M00001501D:C02	9685	3	2	0	7	2	3
M00001504C:A07	10185	5	1	0	0	2	4
M00001504C:H06	6974	7	3	0	1	0	0
M00001504D:G06	6420	8	0	2	0	1	0
M00001507A:H05	39168	2	0	0	0	0	0
M00001511A:H06	39412	2	0	0	0	0	0
M00001512A:A09	39186	2	0	0	0	0	0
M00001512D:G09	3956	9	9	5	2	0	0
M00001513A:B06	4568	10	4	0	9	2	0
M00001513C:E08	14364	1	0	0	0	0	0
M00001514C:D11	40044	2	0	0	0	0	0
M00001517A:B07	4313	13	6	1	0	1	0
M00001518C:B11	8952	3	4	0	4	2	0
M00001528A:C04	7337	4	4	3	16	12	21
M00001528A:F09	18957	3	0	0	0	0	0
M00001528B:H04	8358	3	3	2	0	0	0
M00001531A:D01	38085	2	0	0	0	0	0
M00001532B:A06	3990	6	12	4	1	3	1
M00001533A:C11	2428	14	14	13	9	2	19
M00001534A:C04	16921	4	0	0	1	2	1
M00001534A:D09	5097	6	5	1	1	3	2
M00001534A:F09	5321	11	7	1	5	10	26

WO 99/33982

PCT/US98/27610

Table 5 All Differential Data for Libs 1-4 and 8-9

Clone Name	Cluster ID	Clones in Lib1	Clones in Lib2	Clones in Lib3	Clones in Lib4	Clones in Lib8	Clones in Lib9
M00001534C:A01	4119	9	4	2	2	5	3
M00001535A:B01	7665	3	1	5	0	0	0
M00001535A:C06	20212	2	0	1	1	0	0
M00001535A:F10	39423	2	0	0	0	0	0
M00001536A:B07	2696	23	11	9	18	10	21
M00001536A:C08	39392	2	0	0	0	0	0
M00001537A:F12	39420	2	0	0	0	0	0
M00001537B:G07	3389	4	11	13	2	0	0
M00001540A:D06	8286	6	1	0	3	4	0
M00001541A:D02	3765	19	6	0	0	0	0
M00001541A:F07	22085	3	0	0	0	0	1
M00001541A:H03	39174	2	0	0	0	0	0
M00001542A:A09	22113	3	0	0	0	0	0
M00001542A:E06	39453	2	0	0	0	0	0
M00001544A:E03	12170	2	1	2	0	0	0
M00001544A:G02	19829	2	0	1	0	0	0
M00001544B:B07	6974	7	3	0	1	0	0
M00001545A:C03	19255	2	0	0	0	0	0
M00001545A:D08	13864	3	0	2	1	2	4
M00001546A:G11	1267	43	55	5	0	0	0
M00001548A:E10	5892	5	1	4	4	1	3
M00001548A:H09	1058	40	44	37	47	39	59
M00001549A:B02	4015	10	5	8	15	2	0
M00001549A:D08	10944	3	0	3	1	0	7
M00001549B:F06	4193	12	7	2	2	0	1
M00001549C:E06	16347	4	0	0	0	0	0
M00001550A:A03	7239	5	2	1	0	2	0
M00001550A:G01	5175	8	1	3	2	0	0
M00001551A:B10	6268	6	4	3	18	5	0
M00001551A:F05	39180	2	0	0	0	0	0
M00001551A:G06	22390	2	1	0	0	0	1
M00001551C:G09	3266	12	14	0	1	0	6
M00001552A:B12	307	73	60	196	75	79	27
M00001552A:D11	39458	2	0	0	0	0	0
M00001552B:D04	5708	5	4	4	3	1	4
M00001553A:H06	8298	4	3	1	3	0	0
M00001553B:F12	4573	5	7	2	5	0	1
M00001553D:D10	22814	3	0	0	0	0	0
M00001555A:B02	39539	2	0	0	0	1	0
M00001555A:C01	39195	2	0	0	0	0	0
M00001555D:G10	4561	8	4	4	8	0	0
M00001556A:C09	9244	2	0	3	2	10	17
M00001556A:F11	1577	12	40	25	3	4	0
M00001556A:H01	15855	2	1	1	2	12	213
M00001556B:C08	4386	7	8	3	1	3	21
M00001556B:G02	11294	4	0	2	0	0	1
M00001557A:D02	7065	5	3	2	1	0	0
M00001557A:D02	7065	5	3	2	1	0	0

WO 99/33982

PCT/US98/27610

Table 5 All Differential Data for Libs 1-4 and 8-9

Clone Name	Cluster ID	Clones in Lib1	Clones in Lib2	Clones in Lib3	Clones in Lib4	Clones in Lib8	Clones in Lib9
M00001557A:F01	9635	3	0	2	1	0	0
M00001557A:F03	39490	2	0	0	0	1	0
M00001557B:H10	5192	8	5	0	5	0	0
M00001557D:D09	8761	3	4	0	1	0	1
M00001558B:H11	7514	5	3	0	0	0	0
M00001560D:F10	6558	4	3	4	0	0	5
M00001561A:C05	39486	2	0	0	0	0	0
M00001563B:F06	102	289	233	278	116	123	184
M00001564A:B12	5053	11	4	2	2	1	1
M00001571C:H06	5749	4	1	9	0	0	0
M00001578B:E04	23001	2	1	0	2	0	0
M00001579D:C03	6539	8	3	0	0	0	1
M00001583D:A10	6293	3	5	2	6	0	0
M00001586C:C05	4623	3	4	12	2	1	1
M00001587A:B11	39380	2	0	0	0	0	0
M00001594B:H04	260	189	188	27	2	15	0
M00001597C:H02	4837	6	2	10	0	3	1
M00001597D:C05	10470	5	1	0	2	0	1
M00001598A:G03	16999	4	0	0	0	0	0
M00001601A:D08	22794	2	0	0	0	0	0
M00001604A:B10	1399	49	27	19	7	10	23
M00001604A:F05	39391	2	0	0	0	0	0
M00001607A:E11	11465	5	0	0	0	0	0
M00001608A:B03	7802	5	4	0	1	0	0
M00001608B:E03	22155	3	0	0	0	0	0
M00001614C:F10	13157	4	1	0	3	1	0
M00001617C:E02	17004	4	0	1	0	1	0
M00001619C:F12	40314	2	0	0	0	1	0
M00001621C:C08	40044	2	0	0	0	0	0
M00001623D:F10	13913	2	1	2	0	0	1
M00001624A:B06	3277	10	11	8	3	5	1
M00001624C:F01	4309	4	13	3	10	0	0
M00001630B:H09	5214	10	2	2	2	4	3
M00001644C:B07	39171	2	0	0	0	0	0
M00001645A:C12	19267	2	0	0	0	0	1
M00001648C:A01	4665	5	9	0	0	0	0
M00001657D:C03	23201	3	0	0	0	3	0
M00001657D:F08	76760	1	0	2	2	0	5
M00001662C:A09	23218	3	0	0	0	0	0
M00001663A:E04	35702	2	0	0	0	0	0
M00001669B:F02	6468	4	3	3	8	1	0
M00001670C:H02	14367	3	0	0	0	0	0
M00001673C:H02	7015	6	3	1	2	1	1
M00001675A:C09	8773	4	1	4	4	4	6
M00001676B:F05	11460	4	2	0	0	0	0
M00001677C:E10	14627	1	2	1	0	1	0
M00001677D:A07	7570	5	3	0	0	0	0
M00001678D:F12	4416	9	5	2	6	1	3

WO 99/33982

PCT/US98/27610

Table 5 All Differential Data for Libs 1-4 and 8-9

Clone Name	Cluster ID	Clones in Lib1	Clones in Lib2	Clones in Lib3	Clones in Lib4	Clones in Lib8	Clones in Lib9
M00001679A:A06	6660	7	0	4	2	1	0
M00001679A:F10	26875	1	0	0	0	1	0
M00001679B:F01	6298	2	4	5	3	1	0
M00001679C:F01	78091	1	0	0	0	0	0
M00001679D:D03	10751	3	2	0	1	0	1
M00001679D:D03	10751	3	2	0	1	0	1
M00001680D:F08	10539	2	1	1	0	1	0
M00001682C:B12	17055	4	0	0	0	0	0
M00001686A:E06	4622	7	6	4	2	3	0
M00001688C:F09	5382	6	2	6	2	0	3
M00001693C:G01	4393	10	6	2	4	1	1
M00001716D:H05	67252	1	0	0	1	0	0
M00003741D:C09	40108	2	0	0	0	0	0
M00003747D:C05	11476	6	0	0	0	0	0
M00003759B:B09	697	76	52	30	72	21	30
M00003762C:B08	17076	4	0	0	0	0	0
M00003763A:F06	3108	14	11	7	5	0	1
M00003774C:A03	67907	1	0	0	0	0	0
M00003796C:A05	5619	3	5	3	3	0	4
M00003826B:A06	11350	3	3	0	0	1	0
M00003833A:E05	21877	2	1	0	0	0	1
M00003837D:A01	7899	5	4	0	2	1	0
M00003839A:D08	7798	5	2	2	0	0	1
M00003844C:B11	6539	8	3	0	0	0	1
M00003846B:D06	6874	6	3	0	0	0	0
M00003851B:D10	13595	4	0	1	0	0	1
M00003853A:D04	5619	3	5	3	3	0	4
M00003853A:F12	10515	5	1	0	1	1	2
M00003856B:C02	4622	7	6	4	2	3	0
M00003857A:G10	3389	4	11	13	2	0	0
M00003857A:H03	4718	4	5	5	2	4	6
M00003871C:E02	4573	5	7	2	5	0	1
M00003875B:F04	12977	5	0	0	0	0	0
M00003875B:F04	12977	5	0	0	0	0	0
M00003875C:G07	8479	4	3	1	1	2	4
M00003876D:E12	7798	5	2	2	0	0	1
M00003879B:C11	5345	7	1	7	4	6	27
M00003879B:D10	31587	1	1	0	0	1	0
M00003879D:A02	14507	3	1	0	0	3	1
M00003885C:A02	13576	5	0	0	0	12	11
M00003885C:A02	13576	5	0	0	0	12	11
M00003906C:E10	9285	4	3	0	0	1	2
M00003907D:A09	39809	1	0	0	0	2	1
M00003907D:H04	16317	3	0	0	0	0	0
M00003909D:C03	8672	4	4	0	0	0	0
M00003912B:D01	12532	4	1	0	1	0	1
M00003914C:F05	3900	9	6	8	1	7	13
M00003922A:E06	23255	3	0	1	1	0	0

WO 99/33982

PCT/US98/27610

Table 5 All Differential Data for Libs 1-4 and 8-9

Clone Name	Cluster ID	Clones in Lib1	Clones in Lib2	Clones in Lib3	Clones in Lib4	Clones in Lib8	Clones in Lib9
M00003958A:H02	18957	3	0	0	0	0	0
M00003958A:H02	18957	3	0	0	0	0	0
M00003958C:G10	40455	2	0	0	0	0	0
M00003958C:G10	40455	2	0	0	0	0	0
M00003968B:F06	24488	2	0	1	4	0	0
M00003970C:B09	40122	2	0	0	0	0	0
M00003974D:E07	23210	3	0	0	0	0	0
M00003974D:H02	23358	3	0	0	0	1	0
M00003975A:G11	12439	4	0	0	0	0	0
M00003978B:G05	5693	7	4	1	3	1	1
M00003981A:E10	3430	9	10	7	3	0	0
M00003982C:C02	2433	10	13	21	18	8	8
M00003983A:A05	9105	5	1	1	1	0	0
M00004028D:A06	6124	4	8	1	9	1	0
M00004028D:C05	40073	2	0	1	0	0	1
M00004031A:A12	9061	5	2	0	0	0	0
M00004031A:A12	9061	5	2	0	0	0	0
M00004035C:A07	37285	2	0	0	1	0	1
M00004035D:B06	17036	4	0	0	0	0	0
M00004059A:D06	5417	10	4	0	9	2	0
M00004068B:A01	3706	7	14	4	22	1	0
M00004072B:B05	17036	4	0	0	0	0	0
M00004081C:D10	15069	3	0	0	1	0	0
M00004081C:D12	14391	3	1	0	0	0	0
M00004086D:G06	9285	4	3	0	0	1	2
M00004087D:A01	6880	2	6	1	1	0	0
M00004093D:B12	5325	5	5	2	0	2	1
M00004093D:B12	5325	5	5	2	0	2	1
M00004105C:A04	7221	5	2	2	2	0	0
M00004108A:E06	4937	4	9	3	1	3	1
M00004111D:A08	6874	6	3	0	0	0	0
M00004114C:F11	13183	2	3	0	7	0	1
M00004138B:H02	13272	3	2	0	3	0	0
M00004146C:C11	5257	2	8	5	5	5	25
M00004151D:B08	16977	4	0	0	0	0	0
M00004157C:A09	6455	3	1	6	0	0	0
M00004169C:C12	5319	6	2	8	2	2	3
M00004171D:B03	4908	6	7	2	2	2	0
M00004172C:D08	11494	4	0	0	0	0	0
M00004183C:D07	16392	3	0	0	0	0	0
M00004185C:C03	11443	5	1	0	0	0	0
M00004197D:H01	8210	2	6	0	0	0	0
M00004203B:C12	14311	4	0	0	0	1	2
M00004212B:C07	2379	26	13	4	2	2	3
M00004214C:H05	11451	3	2	1	2	1	1
M00004223A:G10	16918	4	0	0	0	0	0
M00004223B:D09	7899	5	4	0	2	1	0
M00004223D:E04	12971	4	0	0	0	1	0

WO 99/33982

PCT/US98/27610

Table 5 All Differential Data for Libs 1-4 and 8-9

Clone Name	Cluster ID	Clones in Lib1	Clones in Lib2	Clones in Lib3	Clones in Lib4	Clones in Lib8	Clones in Lib9
M00004229B:F08	6455	3	1	6	0	0	0
M00004230B:C07	7212	3	5	2	1	3	0
M00004269D:D06	4905	7	6	3	1	3	1
M00004275C:C11	16914	3	0	0	1	0	0
M00004283B:A04	14286	3	1	0	1	1	1
M00004285B:E08	56020	1	0	0	0	0	0
M00004295D:F12	16921	4	0	0	1	2	1
M00004296C:H07	13046	4	1	0	1	0	0
M00004307C:A06	9457	2	0	5	0	3	0
M00004312A:G03	26295	2	0	0	0	0	0
M00004318C:D10	21847	2	1	0	0	0	0
M00004372A:A03	2030	13	10	32	4	0	0
M00004377C:F05	2102	12	20	23	21	6	5

WO 99/33982

PCT/US98/27610

Table 6 All Differential Data for Libs 15-20

Clone Name	Cluster ID	Clones in Lib15	Clones in Lib16b	Clones in Lib17	Clones in Lib18	Clones in Lib19	Clones in Lib20
M00001340B:A06	17062	0	0	0	0	0	0
M00001340D:F10	11589	0	0	0	0	0	0
M00001341A:E12	4443	0	0	0	1	0	0
M00001342B:E06	39805	0	0	0	0	0	0
M00001343C:F10	2790	0	0	0	0	0	0
M00001343D:H07	23255	0	0	0	0	0	0
M00001345A:E01	6420	0	0	0	0	0	0
M00001346A:F09	5007	0	0	0	0	0	0
M00001346D:E03	6806	0	0	0	0	0	0
M00001346D:G06	5779	0	0	0	0	0	0
M00001346D:G06	5779	0	0	0	0	0	0
M00001347A:B10	13576	0	0	0	0	0	0
M00001348B:B04	16927	0	0	0	0	0	0
M00001348B:G06	16985	0	0	0	0	0	0
M00001349B:B08	3584	0	0	0	0	0	0
M00001350A:H01	7187	0	0	0	0	0	0
M00001351B:A08	3162	0	1	0	0	1	0
M00001351B:A08	3162	0	1	0	0	1	0
M00001352A:E02	16245	0	0	0	0	0	0
M00001353A:G12	8078	0	0	0	0	0	0
M00001353D:D10	14929	0	3	1	0	5	0
M00001355B:G10	14391	0	0	0	0	0	0
M00001357D:D11	4059	0	0	0	0	0	0
M00001361A:A05	4141	0	0	0	0	0	0
M00001361D:F08	2379	0	0	0	0	0	0
M00001362B:D10	5622	0	0	0	0	0	0
M00001362C:H11	945	0	0	0	0	0	1
M00001365C:C10	40132	0	0	0	0	0	0
M00001370A:C09	6867	0	0	0	0	0	0
M00001371C:E09	7172	0	0	0	0	0	0
M00001376B:G06	17732	0	0	0	0	0	1
M00001378B:B02	39833	0	0	0	0	0	0
M00001379A:A05	1334	0	0	0	0	0	1
M00001380D:B09	39886	0	0	0	0	0	0
M00001382C:A02	22979	0	0	0	0	0	0
M00001383A:C03	39648	0	0	0	0	0	0
M00001383A:C03	39648	0	0	0	0	0	0
M00001386C:B12	5178	0	0	0	0	0	0
M00001387A:C05	2464	0	0	0	0	0	0
M00001387B:G03	7587	0	0	0	0	0	0
M00001388D:G05	5832	0	0	0	0	0	0
M00001389A:C08	16269	0	1	0	0	0	0
M00001394A:F01	6583	1	4	1	0	0	0
M00001395A:C03	4016	0	0	0	0	0	0
M00001396A:C03	4009	0	0	0	0	0	0
M00001402A:E08	39563	0	0	0	0	0	0
M00001407B:D11	5556	0	0	0	0	0	0
M00001409C:D12	9577	0	0	0	0	0	0

WO 99/33982

PCT/US98/27610

Table 6 All Differential Data for Libs 15-20

Clone Name	Cluster ID	Clones in Lib15	Clones in Lib16b	Clones in Lib17	Clones in Lib18	Clones in Lib19	Clones in Lib20
M00001410A:D07	7005	0	0	0	0	0	0
M00001412B:B10	8551	0	0	0	0	0	0
M00001415A:H06	13538	0	0	0	0	0	0
M00001416A:H01	7674	0	0	0	0	0	0
M00001416B:H11	8847	0	0	0	0	0	0
M00001417A:E02	36393	0	0	0	0	0	0
M00001418B:F03	9952	0	0	0	0	0	0
M00001418D:B06	8526	0	0	0	0	0	0
M00001421C:F01	9577	0	0	0	0	0	0
M00001423B:E07	15066	0	0	0	0	0	0
M00001424B:G09	10470	0	0	0	0	0	0
M00001425B:H08	22195	0	0	0	0	0	0
M00001426D:C08	4261	0	0	1	0	0	1
M00001428A:H10	84182	0	0	0	0	0	0
M00001429A:H04	2797	0	0	0	0	0	0
M00001429B:A11	4635	0	0	0	0	0	0
M00001429D:D07	40392	0	0	0	0	0	0
M00001439C:F08	40054	0	0	0	0	0	0
M00001442C:D07	16731	0	0	0	0	0	0
M00001445A:F05	13532	0	0	0	0	0	0
M00001446A:F05	7801	0	0	0	0	0	0
M00001447A:G03	10717	0	0	0	0	0	0
M00001448D:C09	8	1	6	6	1	14	1
M00001448D:H01	36313	0	3	0	0	3	0
M00001449A:A12	5857	0	0	0	0	0	0
M00001449A:B12	41633	0	0	0	0	0	0
M00001449A:D12	3681	0	0	0	0	0	0
M00001449A:G10	36535	0	0	0	0	0	0
M00001449C:D06	86110	0	0	0	0	0	0
M00001450A:A02	39304	0	0	0	0	0	0
M00001450A:A11	32663	0	0	0	0	0	0
M00001450A:B12	82498	0	0	0	0	0	0
M00001450A:D08	27250	0	0	0	0	0	0
M00001452A:B04	84328	0	0	0	0	0	0
M00001452A:B12	86859	0	0	0	0	0	0
M00001452A:D08	1120	0	0	0	0	0	0
M00001452A:F05	85064	0	0	0	0	0	0
M00001452C:B06	16970	0	0	2	0	1	0
M00001453A:E11	16130	0	0	0	0	0	0
M00001453C:F06	16653	0	0	0	0	0	0
M00001454A:A09	83103	0	0	0	0	0	0
M00001454B:C12	7005	0	0	0	0	0	0
M00001454D:G03	689	0	2	2	0	4	2
M00001455A:E09	13238	0	0	0	0	0	0
M00001455B:E12	13072	0	0	0	0	0	0
M00001455D:F09	9283	0	0	0	0	0	0
M00001455D:F09	9283	0	0	0	0	0	0
M00001460A:F06	2448	0	0	0	0	0	0
M00001460A:F12	39498	0	0	0	0	0	0

WO 99/33982

PCT/US98/27610

Table 6 All Differential Data for Libs 15-20

Clone Name	Cluster ID	Clones in Lib15	Clones in Lib16b	Clones in Lib17	Clones in Lib18	Clones in Lib19	Clones in Lib20
M00001461A:D06	1531	0	0	0	0	0	0
M00001463C:B11	19	2	13	13	0	69	10
M00001465A:B11	10145	0	0	0	0	0	0
M00001466A:E07	4275	0	0	0	0	0	0
M00001467A:B07	38759	0	0	0	0	0	0
M00001467A:D04	39508	0	0	0	0	0	0
M00001467A:D08	16283	0	0	0	0	0	0
M00001467A:D08	16283	0	0	0	0	0	0
M00001467A:E10	39442	0	0	0	0	0	0
M00001468A:F05	7589	0	0	0	0	0	0
M00001469A:C10	12081	0	0	0	0	0	0
M00001469A:H12	19105	0	0	0	0	0	0
M00001470A:B10	1037	0	0	0	0	0	0
M00001470A:C04	39425	0	0	0	0	0	0
M00001471A:B01	39478	0	0	0	0	0	0
M00001481D:A05	7985	0	0	0	0	0	0
M00001490B:C04	18699	0	0	0	0	0	0
M00001494D:F06	7206	0	0	0	0	0	0
M00001497A:G02	2623	0	0	0	0	0	0
M00001499B:A11	10539	0	0	0	0	0	0
M00001500A:C05	5336	0	0	0	0	0	0
M00001500A:E11	2623	0	0	0	0	0	0
M00001500C:E04	9443	0	0	0	0	0	0
M00001501D:C02	9685	0	0	0	0	0	0
M00001504C:A07	10185	0	0	0	0	0	0
M00001504C:H06	6974	0	0	0	0	0	0
M00001504D:G06	6420	0	0	0	0	0	0
M00001507A:H05	39168	0	0	0	0	0	0
M00001511A:H06	39412	0	0	0	0	0	0
M00001512A:A09	39186	0	0	0	0	0	0
M00001512D:G09	3956	0	0	1	0	0	0
M00001513A:B06	4568	0	0	0	0	0	0
M00001513C:E08	14364	0	0	0	0	0	0
M00001514C:D11	40044	0	1	0	0	0	0
M00001517A:B07	4313	0	0	0	0	0	0
M00001518C:B11	8952	0	0	0	0	0	0
M00001528A:C04	7337	0	0	0	0	0	0
M00001528A:F09	18957	0	0	0	0	0	0
M00001528B:H04	8358	0	0	0	0	0	0
M00001531A:D01	38085	0	0	0	0	0	0
M00001532B:A06	3990	1	1	0	0	0	0
M00001533A:C11	2428	0	0	1	0	0	0
M00001534A:C04	16921	0	0	0	0	0	0
M00001534A:D09	5097	0	0	0	0	0	0
M00001534A:F09	5321	0	1	0	0	2	0
M00001534C:A01	4119	0	0	0	0	0	0
M00001535A:B01	7665	0	0	0	0	0	0
M00001535A:C06	20212	0	0	0	0	0	0
M00001535A:F10	39423	0	0	0	0	0	0

WO 99/33982

PCT/US98/27610

Table 6 All Differential Data for Libs 15-20

Clone Name	Cluster ID	Clones in Lib15	Clones in Lib16b	Clones in Lib17	Clones in Lib18	Clones in Lib19	Clones in Lib20
M00001536A:B07	2696	0	0	0	0	3	0
M00001536A:C08	39392	0	0	0	0	0	0
M00001537A:F12	39420	0	0	0	0	0	0
M00001537B:G07	3389	0	0	0	0	0	0
M00001540A:D06	8286	0	0	0	0	0	0
M00001541A:D02	3765	0	0	0	0	0	0
M00001541A:F07	22085	0	0	0	0	0	0
M00001541A:H03	39174	0	0	0	0	0	0
M00001542A:A09	22113	0	0	0	0	0	0
M00001542A:E06	39453	0	0	0	0	0	0
M00001544A:E03	12170	0	0	0	0	0	0
M00001544A:G02	19829	0	0	0	0	0	0
M00001544B:B07	6974	0	0	0	0	0	0
M00001545A:C03	19255	0	0	0	0	0	0
M00001545A:D08	13864	0	0	0	0	0	0
M00001546A:G11	1267	1	0	0	0	7	0
M00001548A:E10	5892	0	0	0	0	0	0
M00001548A:H09	1058	0	0	1	0	0	0
M00001549A:B02	4015	0	0	0	0	0	0
M00001549A:D08	10944	0	0	0	0	0	0
M00001549B:F06	4193	0	0	0	0	0	0
M00001549C:E06	16347	0	0	0	0	0	0
M00001550A:A03	7239	0	0	0	0	0	0
M00001550A:G01	5175	0	0	0	0	0	0
M00001551A:B10	6268	0	0	0	0	0	0
M00001551A:F05	39180	0	0	0	0	0	0
M00001551A:G06	22390	0	0	0	0	0	0
M00001551C:G09	3266	0	0	1	0	0	0
M00001552A:B12	307	0	0	0	0	3	0
M00001552A:D11	39458	0	0	0	0	0	0
M00001552B:D04	5708	0	1	0	0	0	0
M00001553A:H06	8298	0	0	0	0	0	0
M00001553B:F12	4573	0	0	0	0	0	0
M00001553D:D10	22814	0	0	0	0	0	0
M00001555A:B02	39539	0	0	0	0	0	0
M00001555A:C01	39195	0	0	0	0	0	0
M00001555D:G10	4561	0	0	0	0	0	0
M00001556A:C09	9244	0	0	0	0	0	0
M00001556A:F11	1577	0	0	0	0	0	0
M00001556A:H01	15855	3	5	5	0	3	1
M00001556B:C08	4386	1	2	0	0	0	0
M00001556B:G02	11294	0	0	0	0	0	0
M00001557A:D02	7065	0	0	0	0	0	0
M00001557A:D02	7065	0	0	0	0	0	0
M00001557A:F01	9635	0	0	0	0	0	0
M00001557A:F03	39490	0	0	0	0	0	0
M00001557B:H10	5192	0	0	0	0	0	0
M00001557D:D09	8761	0	0	0	0	0	0
M00001558B:H11	7514	0	0	0	0	0	0

WO 99/33982

PCT/US98/27610

Table 6 All Differential Data for Libs 15-20

Clone Name	Cluster ID	Clones in Lib15	Clones in Lib16b	Clones in Lib17	Clones in Lib18	Clones in Lib19	Clones in Lib20
M00001560D:F10	6558	0	0	0	0	0	0
M00001561A:C05	39486	0	0	0	0	0	0
M00001563B:F06	102	22	38	65	7	43	10
M00001564A:B12	5053	0	0	1	0	0	0
M00001571C:H06	5749	0	0	0	0	0	0
M00001578B:E04	23001	0	0	0	0	0	0
M00001579D:C03	6539	0	0	0	0	0	0
M00001583D:A10	6293	0	0	0	0	0	0
M00001586C:C05	4623	0	0	0	0	1	0
M00001587A:B11	39380	0	0	0	0	0	0
M00001594B:H04	260	0	0	0	0	1	0
M00001597C:H02	4837	0	0	0	0	0	0
M00001597D:C05	10470	0	0	0	0	0	0
M00001598A:G03	16999	1	1	1	0	0	0
M00001601A:D08	22794	0	0	0	0	0	0
M00001604A:B10	1399	0	0	0	0	0	0
M00001604A:F05	39391	0	0	0	0	0	0
M00001607A:E11	11465	0	0	0	0	0	0
M00001608A:B03	7802	0	0	0	0	0	0
M00001608B:E03	22155	0	0	0	0	0	0
M00001614C:F10	13157	0	0	0	0	0	0
M00001617C:E02	17004	0	0	0	0	1	0
M00001619C:F12	40314	0	0	0	0	0	0
M00001621C:C08	40044	0	1	0	0	0	0
M00001623D:F10	13913	0	0	0	0	0	0
M00001624A:B06	3277	0	0	0	0	0	0
M00001624C:F01	4309	0	0	0	0	0	0
M00001630B:H09	5214	1	0	0	1	1	0
M00001644C:B07	39171	0	0	0	0	0	0
M00001645A:C12	19267	0	0	0	0	1	0
M00001648C:A01	4665	0	0	0	0	0	0
M00001657D:C03	23201	0	0	0	0	0	0
M00001657D:F08	76760	0	0	0	0	0	0
M00001662C:A09	23218	0	0	0	0	0	0
M00001663A:E04	35702	0	0	0	0	0	0
M00001669B:F02	6468	0	0	0	0	0	0
M00001670C:H02	14367	0	0	0	0	0	0
M00001673C:H02	7015	0	0	0	0	0	0
M00001675A:C09	8773	0	0	0	0	0	0
M00001676B:F05	11460	0	0	0	0	0	0
M00001677C:E10	14627	0	1	0	0	0	0
M00001677D:A07	7570	0	0	0	0	0	0
M00001678D:F12	4416	0	0	0	0	0	0
M00001679A:A06	6660	0	0	0	0	0	0
M00001679A:F10	26875	0	0	0	0	0	0
M00001679B:F01	6298	0	0	0	0	0	0
M00001679C:F01	78091	0	0	0	0	0	0
M00001679D:D03	10751	0	0	0	0	0	0
M00001679D:D03	10751	0	0	0	0	0	0

WO 99/33982

PCT/US98/27610

Table 6 All Differential Data for Libs 15-20

Clone Name	Cluster ID	Clones in Lib15	Clones in Lib16b	Clones in Lib17	Clones in Lib18	Clones in Lib19	Clones in Lib20
M00001680D:F08	10539	0	0	0	0	0	0
M00001682C:B12	17055	0	0	0	0	0	0
M00001686A:E06	4622	0	0	0	0	0	0
M00001688C:F09	5382	0	0	0	0	0	0
M00001693C:G01	4393	0	0	0	0	0	0
M00001716D:H05	67252	0	0	0	0	0	0
M00003741D:C09	40108	0	0	0	0	0	0
M00003747D:C05	11476	0	0	0	0	0	0
M00003759B:B09	697	0	0	0	0	1	0
M00003762C:B08	17076	0	0	0	0	0	0
M00003763A:F06	3108	0	0	0	0	0	0
M00003774C:A03	67907	0	0	0	0	0	0
M00003796C:D05	5619	0	0	0	0	0	0
M00003826B:A06	11350	0	0	0	0	0	0
M00003833A:E05	21877	0	0	0	0	0	0
M00003837D:A01	7899	0	0	0	0	0	0
M00003839A:D08	7798	0	0	0	0	0	0
M00003844C:B11	6539	0	0	0	0	0	0
M00003846B:D06	6874	0	0	1	0	0	0
M00003851B:D10	13595	0	0	0	0	0	0
M00003853A:D04	5619	0	0	0	0	0	0
M00003853A:F12	10515	0	0	0	0	0	0
M00003856B:C02	4622	0	0	0	0	0	0
M00003857A:G10	3389	0	0	0	0	0	0
M00003857A:H03	4718	0	0	0	0	0	0
M00003871C:E02	4573	0	0	0	0	0	0
M00003875B:F04	12977	0	0	0	0	0	0
M00003875B:F04	12977	0	0	0	0	0	0
M00003875C:G07	8479	0	0	0	0	0	1
M00003876D:E12	7798	0	0	0	0	0	0
M00003879B:C11	5345	0	0	0	2	0	1
M00003879B:D10	31587	0	0	0	0	0	0
M00003879D:A02	14507	0	0	0	0	0	0
M00003885C:A02	13576	0	0	0	0	0	0
M00003885C:A02	13576	0	0	0	0	0	0
M00003906C:E10	9285	0	0	0	0	0	0
M00003907D:A09	39809	0	0	0	0	0	0
M00003907D:H04	16317	0	0	0	0	0	0
M00003909D:C03	8672	0	0	0	0	0	0
M00003912B:D01	12532	0	0	0	0	0	0
M00003914C:F05	3900	0	0	0	0	1	0
M00003922A:E06	23255	0	0	0	0	0	0
M00003958A:H02	18957	0	0	0	0	0	0
M00003958A:H02	18957	0	0	0	0	0	0
M00003958C:G10	40455	0	0	0	0	0	0
M00003958C:G10	40455	0	0	0	0	0	0
M00003968B:F06	24488	0	0	0	0	0	0
M00003970C:B09	40122	0	0	0	0	0	0
M00003974D:E07	23210	0	0	0	0	0	0

WO 99/33982

PCT/US98/27610

Table 6 All Differential Data for Libs 15-20

Clone Name	Cluster ID	Clones in Lib15	Clones in Lib16b	Clones in Lib17	Clones in Lib18	Clones in Lib19	Clones in Lib20
M00003974D:H02	23358	0	0	0	0	0	0
M00003975A:G11	12439	0	0	0	0	0	0
M00003978B:G05	5693	0	0	0	0	0	0
M00003981A:E10	3430	0	0	0	0	1	0
M00003982C:C02	2433	0	0	0	0	0	0
M00003983A:A05	9105	0	0	0	0	0	0
M00004028D:A06	6124	0	0	0	0	0	0
M00004028D:C05	40073	0	0	0	0	0	0
M00004031A:A12	9061	0	0	0	0	0	0
M00004031A:A12	9061	0	0	0	0	0	0
M00004035C:A07	37285	0	0	0	0	0	0
M00004035D:B06	17036	0	0	0	0	0	0
M00004059A:D06	5417	0	0	0	0	0	0
M00004068B:A01	3706	0	0	0	0	0	0
M00004072B:B05	17036	0	0	0	0	0	0
M00004081C:D10	15069	0	0	0	0	0	0
M00004081C:D12	14391	0	0	0	0	0	0
M00004086D:G06	9285	0	0	0	0	0	0
M00004087D:A01	6880	0	0	0	0	0	0
M00004093D:B12	5325	1	1	0	1	0	1
M00004093D:B12	5325	1	1	0	1	0	1
M00004105C:A04	7221	0	0	0	0	0	0
M00004108A:E06	4937	0	0	0	0	0	0
M00004111D:A08	6874	0	0	1	0	0	0
M00004114C:F11	13183	0	0	0	0	0	0
M00004138B:H02	13272	0	0	0	0	0	0
M00004146C:C11	5257	0	1	0	0	0	0
M00004151D:B08	16977	0	0	0	0	0	0
M00004157C:A09	6455	0	0	0	0	0	0
M00004169C:C12	5319	0	0	0	0	0	0
M00004171D:B03	4908	0	0	0	0	0	0
M00004172C:D08	11494	0	0	0	0	0	0
M00004183C:D07	16392	0	0	0	0	0	0
M00004185C:C03	11443	0	0	0	0	0	0
M00004197D:H01	8210	0	0	0	0	0	0
M00004203B:C12	14311	0	0	0	0	0	0
M00004212B:C07	2379	0	0	0	0	0	0
M00004214C:H05	11451	0	0	0	0	0	0
M00004223A:G10	16918	0	0	0	0	0	0
M00004223B:D09	7899	0	0	0	0	0	0
M00004223D:E04	12971	0	0	0	0	0	0
M00004229B:F08	6455	0	0	0	0	0	0
M00004230B:C07	7212	0	0	0	0	0	0
M00004269D:D06	4905	0	0	0	0	0	0
M00004275C:C11	16914	0	0	0	0	0	0
M00004283B:A04	14286	0	0	0	0	0	0
M00004285B:E08	56020	0	0	0	0	0	0
M00004295D:F12	16921	0	0	0	0	0	0
M00004296C:H07	13046	0	0	0	0	0	0

WO 99/33982

PCT/US98/27610

Table 6 All Differential Data for Libs 15-20

Clone Name	Cluster ID	Clones in Lib15	Clones in Lib16b	Clones in Lib17	Clones in Lib18	Clones in Lib19	Clones in Lib20
M00004307C:A06	9457	0	0	0	0	0	0
M00004312A:G03	26295	0	0	0	0	0	0
M00004318C:D10	21847	0	0	0	0	0	0
M00004372A:A03	2030	0	0	0	0	0	0
M00004377C:F05	2102	0	0	0	0	0	0

WO 99/33982

PCT/US98/27610

Table 7 All Differential Data for Libs 12-14

Clone Name	Cluster ID	Clones in Lib12	Clones in Lib13	Clones in Lib14
M00001340B:A06	17062	0	0	0
M00001340D:F10	11589	0	0	0
M00001341A:E12	4443	4	2	0
M00001342B:E06	39805	0	0	0
M00001343C:F10	2790	0	0	0
M00001343D:H07	23255	0	0	0
M00001345A:E01	6420	0	0	0
M00001346A:F09	5007	0	0	0
M00001346D:E03	6806	0	1	1
M00001346D:G06	5779	0	0	0
M00001346D:G06	5779	0	0	0
M00001347A:B10	13576	0	0	0
M00001348B:B04	16927	0	0	0
M00001348B:G06	16985	0	0	0
M00001349B:B08	3584	0	0	0
M00001350A:H01	7187	0	0	0
M00001351B:A08	3162	0	0	1
M00001351B:A08	3162	0	0	1
M00001352A:E02	16245	0	0	0
M00001353A:G12	8078	0	0	0
M00001353D:D10	14929	0	1	0
M00001355B:G10	14391	0	0	0
M00001357D:D11	4059	0	0	0
M00001361A:A05	4141	1	2	1
M00001361D:F08	2379	0	0	0
M00001362B:D10	5622	0	2	1
M00001362C:H11	945	0	0	0
M00001365C:C10	40132	0	0	0
M00001370A:C09	6867	0	0	0
M00001371C:E09	7172	0	0	1
M00001376B:G06	17732	2	0	0
M00001378B:B02	39833	0	0	0
M00001379A:A05	1334	0	0	0
M00001380D:B09	39886	0	0	0
M00001382C:A02	22979	1	0	0
M00001383A:C03	39648	0	0	0
M00001383A:C03	39648	0	0	0
M00001386C:B12	5178	0	0	0
M00001387A:C05	2464	0	0	0
M00001387B:G03	7587	0	0	0
M00001388D:G05	5832	0	0	0
M00001389A:C08	16269	2	0	0
M00001394A:F01	6583	0	0	0
M00001395A:C03	4016	0	0	0
M00001396A:C03	4009	2	0	0
M00001402A:E08	39563	0	0	0
M00001407B:D11	5556	0	0	0

WO 99/33982

PCT/US98/27610

Table 7 All Differential Data for Libs 12-14

Clone Name	Cluster ID	Clones in Lib12	Clones in Lib13	Clones in Lib14
M00001409C:D12	9577	0	0	0
M00001410A:D07	7005	0	0	0
M00001412B:B10	8551	0	0	0
M00001415A:H06	13538	0	0	0
M00001416A:H01	7674	0	0	0
M00001416B:H11	8847	1	0	0
M00001417A:E02	36393	0	0	0
M00001418B:F03	9952	0	0	0
M00001418D:B06	8526	0	0	0
M00001421C:F01	9577	0	0	0
M00001423B:E07	15066	0	0	0
M00001424B:G09	10470	0	0	0
M00001425B:H08	22195	0	0	0
M00001426D:C08	4261	0	0	0
M00001428A:H10	84182	0	0	0
M00001429A:H04	2797	0	0	0
M00001429B:A11	4635	0	0	0
M00001429D:D07	40392	0	0	0
M00001439C:F08	40054	0	0	0
M00001442C:D07	16731	0	0	0
M00001445A:F05	13532	0	0	0
M00001446A:F05	7801	0	1	0
M00001447A:G03	10717	0	0	0
M00001448D:C09	8	7	6	9
M00001448D:H01	36313	1	0	0
M00001449A:A12	5857	0	0	0
M00001449A:B12	41633	0	0	0
M00001449A:D12	3681	1	0	0
M00001449A:G10	36535	0	0	0
M00001449C:D06	86110	0	0	0
M00001450A:A02	39304	0	1	0
M00001450A:A11	32663	0	0	0
M00001450A:B12	82498	0	0	0
M00001450A:D08	27250	0	0	0
M00001452A:B04	84328	0	0	0
M00001452A:B12	86859	0	0	0
M00001452A:D08	1120	0	0	0
M00001452A:F05	85064	0	0	0
M00001452C:B06	16970	1	0	0
M00001453A:E11	16130	0	0	0
M00001453C:F06	16653	0	0	0
M00001454A:A09	83103	0	0	0
M00001454B:C12	7005	0	0	0
M00001454D:G03	689	0	0	1
M00001455A:E09	13238	0	0	0
M00001455B:E12	13072	0	0	0
M00001455D:F09	9283	0	0	0
M00001455D:F09	9283	0	0	0

WO 99/33982

PCT/US98/27610

Table 7 All Differential Data for Libs 12-14

Clone Name	Cluster ID	Clones in Lib12	Clones in Lib13	Clones in Lib14
M00001460A:F06	2448	0	0	0
M00001460A:F12	39498	0	0	0
M00001461A:D06	1531	0	0	1
M00001463C:B11	19	17	32	31
M00001465A:B11	10145	0	0	0
M00001466A:E07	4275	0	0	0
M00001467A:B07	38759	0	0	0
M00001467A:D04	39508	0	0	0
M00001467A:D08	16283	0	0	0
M00001467A:D08	16283	0	0	0
M00001467A:E10	39442	0	0	0
M00001468A:F05	7589	0	0	0
M00001469A:C10	12081	0	0	0
M00001469A:H12	19105	0	0	0
M00001470A:B10	1037	0	0	0
M00001470A:C04	39425	0	0	0
M00001471A:B01	39478	0	0	0
M00001481D:A05	7985	0	0	0
M00001490B:C04	18699	0	0	0
M00001494D:F06	7206	0	0	0
M00001497A:G02	2623	1	0	0
M00001499B:A11	10539	0	1	0
M00001500A:C05	5336	0	0	0
M00001500A:E11	2623	1	0	0
M00001500C:E04	9443	0	0	0
M00001501D:C02	9685	0	0	0
M00001504C:A07	10185	0	0	0
M00001504C:H06	6974	0	0	0
M00001504D:G06	6420	0	0	0
M00001507A:H05	39168	0	0	0
M00001511A:H06	39412	0	0	0
M00001512A:A09	39186	0	0	0
M00001512D:G09	3956	0	0	0
M00001513A:B06	4568	0	0	0
M00001513C:E08	14364	0	0	0
M00001514C:D11	40044	0	0	0
M00001517A:B07	4313	0	0	0
M00001518C:B11	8952	0	0	0
M00001528A:C04	7337	1	2	2
M00001528A:F09	18957	0	0	0
M00001528B:H04	8358	0	0	0
M00001531A:D01	38085	0	0	0
M00001532B:A06	3990	0	0	0
M00001533A:C11	2428	0	0	0
M00001534A:C04	16921	0	0	0
M00001534A:D09	5097	0	0	0
M00001534A:F09	5321	4	7	6
M00001534C:A01	4119	0	0	0

WO 99/33982

PCT/US98/27610

Table 7 All Differential Data for Libs 12-14

Clone Name	Cluster ID	Clones in Lib12	Clones in Lib13	Clones in Lib14
M00001535A:B01	7665	0	2	4
M00001535A:C06	20212	0	0	0
M00001535A:F10	39423	0	0	0
M00001536A:B07	2696	0	0	0
M00001536A:C08	39392	0	0	0
M00001537A:F12	39420	0	0	0
M00001537B:G07	3389	0	0	0
M00001540A:D06	8286	0	0	0
M00001541A:D02	3765	0	0	0
M00001541A:F07	22085	0	0	0
M00001541A:H03	39174	0	0	0
M00001542A:A09	22113	0	0	0
M00001542A:E06	39453	0	0	0
M00001544A:E03	12170	0	0	0
M00001544A:G02	19829	0	0	0
M00001544B:B07	6974	0	0	0
M00001545A:C03	19255	0	0	0
M00001545A:D08	13864	0	0	0
M00001546A:G11	1267	0	0	0
M00001548A:E10	5892	0	1	0
M00001548A:H09	1058	1	3	0
M00001549A:B02	4015	0	1	0
M00001549A:D08	10944	1	0	0
M00001549B:F06	4193	0	0	0
M00001549C:E06	16347	0	0	0
M00001550A:A03	7239	0	1	0
M00001550A:G01	5175	1	0	0
M00001551A:B10	6268	0	0	1
M00001551A:F05	39180	0	0	0
M00001551A:G06	22390	0	0	1
M00001551C:G09	3266	0	0	0
M00001552A:B12	307	6	11	4
M00001552A:D11	39458	0	0	0
M00001552B:D04	5708	0	0	0
M00001553A:H06	8298	0	0	0
M00001553B:F12	4573	0	0	0
M00001553D:D10	22814	0	0	0
M00001555A:B02	39539	0	0	0
M00001555A:C01	39195	0	0	0
M00001555D:G10	4561	0	0	0
M00001556A:C09	9244	0	1	0
M00001556A:F11	1577	0	0	2
M00001556A:H01	15855	1	1	0
M00001556B:C08	4386	3	0	1
M00001556B:G02	11294	0	0	0
M00001557A:D02	7065	0	0	0
M00001557A:D02	7065	0	0	0
M00001557A:F01	9635	0	0	0

WO 99/33982

PCT/US98/27610

Table 7 All Differential Data for Libs 12-14

Clone Name	Cluster ID	Clones in Lib12	Clones in Lib13	Clones in Lib14
M00001557A:F03	39490	0	0	0
M00001557B:H10	5192	0	0	0
M00001557D:D09	8761	0	0	0
M00001558B:H11	7514	0	0	0
M00001560D:F10	6558	0	0	0
M00001561A:C05	39486	0	0	0
M00001563B:F06	102	2	1	2
M00001564A:B12	5053	0	0	0
M00001571C:H06	5749	0	0	0
M00001578B:E04	23001	0	0	0
M00001579D:C03	6539	0	0	0
M00001583D:A10	6293	0	0	0
M00001586C:C05	4623	0	0	0
M00001587A:B11	39380	0	0	0
M00001594B:H04	260	1	0	0
M00001597C:H02	4837	1	0	0
M00001597D:C05	10470	0	0	0
M00001598A:G03	16999	4	2	6
M00001601A:D08	22794	0	0	0
M00001604A:B10	1399	6	3	3
M00001604A:F05	39391	0	0	0
M00001607A:E11	11465	0	0	0
M00001608A:B03	7802	0	0	0
M00001608B:E03	22155	0	0	0
M00001614C:F10	13157	0	0	0
M00001617C:E02	17004	0	0	0
M00001619C:F12	40314	0	0	0
M00001621C:C08	40044	0	0	0
M00001623D:F10	13913	0	0	0
M00001624A:B06	3277	0	0	0
M00001624C:F01	4309	0	0	0
M00001630B:H09	5214	0	1	2
M00001644C:B07	39171	0	0	0
M00001645A:C12	19267	0	0	0
M00001648C:A01	4665	0	0	0
M00001657D:C03	23201	0	0	0
M00001657D:F08	76760	0	0	0
M00001662C:A09	23218	0	0	0
M00001663A:E04	35702	0	0	0
M00001669B:F02	6468	0	0	0
M00001670C:H02	14367	0	0	0
M00001673C:H02	7015	0	0	0
M00001675A:C09	8773	0	0	0
M00001676B:F05	11460	2	0	0
M00001677C:E10	14627	0	0	0
M00001677D:A07	7570	0	0	0
M00001678D:F12	4416	1	2	0
M00001679A:A06	6660	0	0	0

WO 99/33982

PCT/US98/27610

Table 7 All Differential Data for Libs 12-14

Clone Name	Cluster ID	Clones in Lib12	Clones in Lib13	Clones in Lib14
M00001679A:F10	26875	0	0	0
M00001679B:F01	6298	0	0	0
M00001679C:F01	78091	0	0	0
M00001679D:D03	10751	0	0	0
M00001679D:D03	10751	0	0	0
M00001680D:F08	10539	0	1	0
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M00001686A:E06	4622	0	0	0
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M00003796C:D05	5619	0	1	0
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M00003871C:E02	4573	0	0	0
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M00003875C:G07	8479	1	0	0
M00003876D:E12	7798	0	0	0
M00003879B:C11	5345	4	8	3
M00003879B:D10	31587	0	0	0
M00003879D:A02	14507	0	0	0
M00003885C:A02	13576	0	0	0
M00003885C:A02	13576	0	0	0
M00003906C:E10	9285	0	0	0
M00003907D:A09	39809	0	0	0
M00003907D:H04	16317	0	0	0
M00003909D:C03	8672	0	0	0
M00003912B:D01	12532	0	0	0
M00003914C:F05	3900	0	1	0
M00003922A:E06	23255	0	0	0
M00003958A:H02	18957	0	0	0

WO 99/33982

PCT/US98/27610

Table 7 All Differential Data for Libs 12-14

Clone Name	Cluster ID	Clones in Lib12	Clones in Lib13	Clones in Lib14
M00003958A:H02	18957	0	0	0
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M00003968B:F06	24488	0	0	0
M00003970C:B09	40122	0	0	0
M00003974D:E07	23210	0	0	0
M00003974D:H02	23358	0	0	0
M00003975A:G11	12439	0	0	0
M00003978B:G05	5693	0	0	0
M00003981A:E10	3430	0	0	0
M00003982C:C02	2433	2	4	0
M00003983A:A05	9105	0	0	0
M00004028D:A06	6124	0	0	0
M00004028D:C05	40073	0	1	0
M00004031A:A12	9061	0	0	0
M00004031A:A12	9061	0	0	0
M00004035C:A07	37285	0	0	0
M00004035D:B06	17036	0	0	0
M00004059A:D06	5417	0	0	0
M00004068B:A01	3706	0	0	0
M00004072B:B05	17036	0	0	0
M00004081C:D10	15069	0	0	0
M00004081C:D12	14391	0	0	0
M00004086D:G06	9285	0	0	0
M00004087D:A01	6880	0	0	0
M00004093D:B12	5325	0	0	0
M00004093D:B12	5325	0	0	0
M00004105C:A04	7221	0	0	0
M00004108A:E06	4937	0	0	0
M00004111D:A08	6874	0	0	0
M00004114C:F11	13183	0	0	0
M00004138B:H02	13272	0	0	0
M00004146C:C11	5257	0	0	1
M00004151D:B08	16977	0	0	0
M00004157C:A09	6455	0	0	0
M00004169C:C12	5319	0	0	0
M00004171D:B03	4908	0	0	0
M00004172C:D08	11494	0	0	0
M00004183C:D07	16392	0	0	0
M00004185C:C03	11443	2	0	0
M00004197D:H01	8210	0	0	0
M00004203B:C12	14311	0	0	0
M00004212B:C07	2379	0	0	0
M00004214C:H05	11451	0	0	0
M00004223A:G10	16918	0	0	0
M00004223B:D09	7899	0	0	0
M00004223D:E04	12971	0	0	0
M00004229B:F08	6455	0	0	0

WO 99/33982

PCT/US98/27610

Table 7 All Differential Data for Libs 12-14

Clone Name	Cluster ID	Clones in Lib12	Clones in Lib13	Clones in Lib14
M00004230B:C07	7212	0	0	1
M00004269D:D06	4905	0	0	0
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M00004283B:A04	14286	0	0	0
M00004285B:E08	56020	0	0	0
M00004295D:F12	16921	0	0	0
M00004296C:H07	13046	0	0	0
M00004307C:A06	9457	1	0	0
M00004312A:G03	26295	0	0	0
M00004318C:D10	21847	0	0	0
M00004372A:A03	2030	0	0	0
M00004377C:F05	2102	0	0	0

We Claim:

1. A library of polynucleotides, the library comprising the sequence information of at least one of SEQ ID NOS:1-844.

5

2. The library of claim 1, wherein the library is provided on a nucleic acid array.

3. The library of claim 1, wherein the library is provided in a computer-readable format.

10

4. The library of claim 1, wherein the library comprises a differentially expressed polynucleotide comprising a sequence selected from the group consisting of SEQ ID NOS:9, 39, 42, 52, 62, 74, 119, 172, 317, and 379.

15

5. The library of claim 1, wherein the library comprises a polynucleotide differentially expressed in a human breast cancer cell, where the polynucleotide comprises a sequence selected from the group consisting of SEQ ID NOS: 4, 9, 39, 42, 52, 62, 65, 66, 68, 74, 81, 114, 123, 144, 130, 157, 162, 172, 178, 183, 202, 214, 219, 223, 258, 298, 317, 338, 379, 384, 386, and 388.

20

6. The library of claim 1, wherein the library comprises a polynucleotide differentially expressed in a human colon cancer cell, where the polynucleotide comprises a sequence selected from the group consisting of SEQ ID NOS: 1, 39, 52, 97, 119, 134, 172, 176, 241, 288, 317, 357, 362, and 374.

25

7. The library of claim 1, wherein the library comprises a polynucleotide differentially expressed in a human lung cancer cell, where the polynucleotide comprises a sequence selected from the group consisting of SEQ ID NOS: 9, 34, 42, 62, 74, 106, 119, 135, 154, 160, 260, 308, 323, 349, 361, 369, 371, 379, 395, 381, and 400.

30

8. An isolated polynucleotide comprising a nucleotide sequence having at least 90% sequence identity to an identifying sequence of SEQ ID NOS:1-844 or a degenerate variant thereof.

9. An isolated polynucleotide according to claim 8, wherein the polynucleotide comprises a sequence encoding a polypeptide of a protein family selected from the group consisting of: 4 transmembrane segments integral membrane proteins, 7 transmembrane
5 receptors, ATPases associated with various cellular activities (AAA), eukaryotic aspartyl proteases, GATA family of transcription factors, G-protein alpha subunit, phorbol esters/diacylglycerol binding proteins, protein kinase, protein phosphatase 2C, protein tyrosine phosphatase, trypsin, wnt family of developmental signaling proteins, and WW/rsp5/WWP domain containing proteins.
- 10
10. The polynucleotide of claim 9, wherein the polynucleotide comprises a sequence of one of SEQ ID NOS: 24, 41, 101, 157, 291, 305, 315, 341, 63, 116, 134, 136, 151, 384, 404, 308, 213, 367, 188, 251, 202, 315, 367, 397, 256, 382, 169, 23, 291, 324, 330, 341, 353, 188, 379, and 395.
- 15
11. The polynucleotide of claim 8, wherein the polynucleotide comprises a sequence encoding a polypeptide having a functional domain selected from the group consisting of: Ank repeat, basic region plus leucine zipper transcription factors, bromodomain, EF-hand, SH3 domain, WD domain/G-beta repeats, zinc finger (C2H2 type),
20 zinc finger (CCHC class), and zinc-binding metalloprotease domain.
12. The polynucleotide of claim 11, wherein the polynucleotide comprises a sequence of one of SEQ ID NOS: 116, 251, 374, 97, 136, 242, 379, 306, 386, 18, 335, 61, 306, 386, 322, 306, and 395.
- 25
13. A recombinant host cell containing the polynucleotide of claim 8.
14. An isolated polypeptide encoded by the polynucleotide of claim 8.
- 30
15. An antibody that specifically binds a polypeptide of claim 14.
16. A vector comprising the polynucleotide of claim 8.

17. A polynucleotide comprising the nucleotide sequence of an insert contained in a clone deposited as ATCC accession number xx, xx, xx, xx, xx, xx, xx, or xx.

18. A method of detecting differentially expressed genes correlated with a cancerous
5 state of a mammalian cell, the method comprising the step of:

detecting at least one differentially expressed gene product in a test sample derived from a cell suspected of being cancerous, where the gene product is encoded by a gene corresponding to a sequence of at least one of SEQ ID NOS: 4, 9, 39, 42, 52, 62, 65, 66, 68, 74, 81, 114, 123, 144, 130, 157, 162, 172, 178, 183, 202, 214, 219, 223, 258, 298, 317, 338,
10 379, 384, 386, 388, 1, 39, 52, 97, 119, 134, 172, 176, 241, 288, 317, 357, 362, 374, 9, 34, 42, 62, 74, 106, 119, 135, 154, 160, 260, 308, 323, 349, 361, 369, 371, 379, 395, 381, and 400;

wherein detection of the differentially expressed gene product is correlated with a cancerous state of the cell from which the test sample was derived.

19. The method of claim 18, wherein said detecting step is by hybridization of the test sample to a reference array, wherein the reference array comprises an identifying sequence of at least one of SEQ ID NOS: 1-844.

20. The method of claim 18, wherein the cell is a breast tissue derived cell, and the differentially expressed gene product is encoded by a gene corresponding to a sequence of at least one of SEQ ID NOS: 4, 9, 39, 42, 52, 62, 65, 66, 68, 74, 81, 114, 123, 144, 130, 157, 162, 172, 178, 183, 202, 214, 219, 223, 258, 298, 317, 338, 379, 384, 386, and 388.

21. The method of claim 18, wherein the cell is a colon tissue derived cell, and the differentially expressed gene product is encoded by a gene corresponding to a sequence of at least one of SEQ ID NOS: 1, 39, 52, 97, 119, 134, 172, 176, 241, 288, 317, 357, 362, and 374.

22. The method of claim 18, wherein the cell is a lung tissue derived cell, and the differentially expressed gene product is encoded by a gene corresponding to a sequence of at least one of SEQ ID NOS: 9, 34, 42, 62, 74, 106, 119, 135, 154, 160, 260, 308, 323, 349, 361, 369, 371, 379, 395, 381, and 400.

WO 99/33982

PCT/US98/27610

SEQUENCE LISTING

<110> Lewis T. Williams
Jaime Escobedo
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Julie Sudduth-Klinger
Christoph Reinhard
Klause Giese
Filippo Randazzo
Giulia C. Kennedy
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Radomir Crkvenjakov
Mark Dickson
Snezana Drmanac
Ivan Labat
Dena Leshkowitz
David Kita
Veronica Garcia
William Lee Jones
Birjit Stache-Crain

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WO 99/33982

PCT/US98/27610

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WO 99/33982

PCT/US98/27610

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WO 99/33982

PCT/US98/27610

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WO 99/33982

PCT/US98/27610

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WO 99/33982

PCT/US98/27610

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<213> Homo sapiens

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tcattcaata agcttttact gcataaaact tacatccagc actgtagtta agtaccctaa 180
attgaataga aataatggct ttgaaaatc gcacaaagca ggccaggcag ctgtgctcac 240
gcctgtaatc ccagcatctt gggaggccga ggcaggcgga tcacgaggtc aagagatcca 300

<210> 21
<211> 293
<212> DNA
<213> Homo sapiens

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ttcgtctcaa aaaaaaaaaa nnnnnnnnnn nnnnccttng gncgggttnt cccaaattnt 180
tttgagngn ccatggncaa ctgcttnanc ttgttttgg caaccccntg ccnaagtog 240
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<210> 22
<211> 300
<212> DNA
<213> Homo sapiens

<400> 22
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WO 99/33982

PCT/US98/27610

agggttttcatt	taagaagaaa	gagctagata	aatgtgctct	tctgggtacc	ccaccctgac	180
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<210> 23
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<212> DNA
<213> Homo sapiens

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agtagaaaagg	gtccccattc	ctgctcagca	cgcacctct	ctaccccccc	acagacacac	180
atgcagacac	acacatgcag	acaacacgca	gacacacaca	tgcaggcact	cacatgcagg	240
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<211> 300
<212> DNA
<213> Homo sapiens

<400> 24						
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tgcccgctcg	tcttaccacac	caggactctg	actctccaag	ctggggccac	tctcttctcc	180
aacactgcta	tggattgaat	gtttatgtta	tccccaaatt	tgcattgttc	aatcccaatc	240
tcacatgcca	tagtattagg	aggtgggggg	ctttggggagg	tgatttggtc	atgaaggctg	300

<210> 25
<211> 300
<212> DNA
<213> Homo sapiens

<400> 25						
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ctgtagctgt	gcctctacag	actcccgctg	cctggcctcc	acagatcctg	ctcagattca	240
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<210> 26
<211> 300
<212> DNA
<213> Homo sapiens

<400> 26						
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ggcagggcac	atgtttaaaa	cttgaacttt	ctgaggctaa	gactggaaaa	ggaatgggtt	180
cagctgatat	atttggalat	cagttgacta	tttttaggaa	aaaaacacaa	atggctttta	240

WO 99/33982

PCT/US98/27610

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<212> DNA
<213> Homo sapiens

<400> 27
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tttgagctct gcaacagtga cgcgcagccc ggtccggagc gtggtagact ttgtttgcct      180
tctgggtcag ctttcgctgt gtctcctgtg tgtgttagaa tccagagccc agaggaagtg      240
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<210> 28
<211> 298
<212> DNA
<213> Homo sapiens

<400> 28
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tggggnnnnn nnangnnaaa tnnngaaggg gngngannga ggggggggana naagggggga      180
ngagggcgaa ngncaggann nagaanaann ggggacgana ngngncaacag gnnnnaaacg      240
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<210> 29
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<212> DNA
<213> Homo sapiens

<400> 29
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caaaatacta ggtaagtac tgcagaccga cctccctgca gtttgggaaa gaagctgggt      180
tgtggagaa tcagagcatc ttgacatgac tctgcgacta aagatccctg gcatgggcca      240
gggactctgt ggaacctctt ctatgtcagg ggtgtgagca ttagactgcc agttgtctag      300

<210> 30
<211> 300
<212> DNA
<213> Homo sapiens

<400> 30
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gcatgttgtt taactgccct gcctactaca gtgtgtctgc tcccaaggct gagctactga      180
acaaaatcaa agagatgcca nnnnnnnnnn nntgaggaa aggaacaggc anatgtcaat      240
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<210> 31

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WO 99/33982

PCT/US98/27610

<211> 300
 <212> DNA
 <213> Homo sapiens

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 caccctacat galacgctcc cctctcatgg aacggagcct ccccatcgca gcccccactc 240
 aaatggagtt ttaaaggctg ggttcaggtt acggggggcgt ttctcacogt ctgaatgcgg 300

<210> 32
 <211> 300
 <212> DNA
 <213> Homo sapiens

<400> 32
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 ggccttcctg cctttctgaa aaatatgaca gtgatggtgt ctgggaccctc gagaagtggc 180
 atgcctctct ctaccagctc tcaggggcga gctcaccagt ggaagtcctg aagaaagagt 240
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<210> 33
 <211> 300
 <212> DNA
 <213> Homo sapiens

<400> 33
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<210> 34
 <211> 300
 <212> DNA
 <213> Homo sapiens

<400> 34
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 gaaagagccg tgctcgcca cagacctcgg agggctcgtc aactcgggct gctgcccaca 240
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<210> 35
 <211> 300
 <212> DNA
 <213> Homo sapiens

WO 99/33982

PCT/US98/27610

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<400> 35
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gcttctctcac ccagacaacca aggtatgaga tggccctgcc aagtgtcggc ctctcctgtt      180
aaacaaaaaac attctaagc cattgtttctt gcttcatgga caagaggcag cggagagagag      240
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<210> 36
<211> 300
<212> DNA
<213> Homo sapiens

<400> 36
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tcgagtcacat gtggggtctg gggacccatga ctattgtgtc cggagcagga cccccccaaa      180
aaagatgcct gccctagtca ttccagaggt gggctcccg tggaaatgtca agcgccatca      240
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<210> 37
<211> 300
<212> DNA
<213> Homo sapiens

<400> 37
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gggtccagccc tctgactctt tcctcatggt agagacaact gcatactttg aggcctacag      180
gcacgtcctg gaaggactcc aggaggtcca ggagggaagt gttcccttcc agaggaatat      240
cgtggagtgt aactctcatg tgaaggagcc aaggtacttg ctaatggggg gcagatatga      300

<210> 38
<211> 300
<212> DNA
<213> Homo sapiens

<400> 38
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cccaaacgct gcctcttggt gacagactca gcccaaaacc ccttctctct gtctctggag      180
accttgagc ttggggaaat atggagggtg gtgtgtctgc aatcaaggcc tctgcagctc      240
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<210> 39
<211> 300
<212> DNA
<213> Homo sapiens

<400> 39
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WO 99/33982

PCT/US98/27610

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ggaggacgcg	gtgggatagg	ctccctgggt	ccacagcttc	tgcccgtaga	tggggaacct	300

<210> 40
 <211> 300
 <212> DNA
 <213> Homo sapiens

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ttcacctttg	ctaattggagg	cgtggccacc	atgcgcacca	tggggacaga	gccccaaatc	180
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<210> 41
 <211> 300
 <212> DNA
 <213> Homo sapiens

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aaaagtcttc	ccagctccaa	ggagcagtcg	tgtctgacct	acattgggct	tttctcagaa	240
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<210> 42
 <211> 300
 <212> DNA
 <213> Homo sapiens

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cagctgggat	gaagtggaga	ttagtgtgag	ccttgccaaa	gatgagccctg	acacaaatct	120
cgtggcctta	atgaaggaa	aaggggtgaa	acttctaaga	gaagcaatgg	gaatttatat	180
cagcaccttc	aaaacagagt	tcaccagggt	catgatctta	cctacaatga	attggagagtc	240
agtagaccca	gtggggcagc	cagcactgaa	aactgaggag	cgcaaggcta	agcctgtctc	300

<210> 43
 <211> 300
 <212> DNA
 <213> Homo sapiens

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tgtgggccat	tatgttctct	atatcaagcg	ggaagcaaat	gggcaaggcc	acttccaaga	180
aagatccttc	tgtaaggctc	tgacctccaa	gaccaaccgc	cgatttgtga	agaagtttgt	240
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WO 99/33982

PCT/US98/27610

<210> 44
 <211> 300
 <212> DNA
 <213> Homo sapiens

<400> 44
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 aaagtggtgat cctacatgtg ccatagggtct tattgtttaca ggtatcgctg tgcgtgctgg 180
 agccagaaca caccgtgatg ctctgcttctg aatctgggat tccgctgtgc agccgaccgg 240
 ctgccacta tggactgaca accaaggaaa gtcttcccca gtccaaggag cagccgtgtc 300

<210> 45
 <211> 300
 <212> DNA
 <213> Homo sapiens

<400> 45
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 tctcacacct ggcgagctgt ggcctgcttt taaacagagt tcatttccag taccctccat 180
 cagtgacccc tgccttaaga aaatgaactt atgcaaatag acatccacag cgtcggtaaa 240
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<210> 46
 <211> 300
 <212> DNA
 <213> Homo sapiens

<400> 46
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 tctcacacct ggcgagctgt ggcctgcttt taaacagagt tcatttccag taccctccat 180
 cagtgacccc tgccttaaga aaatgaactt atgcaaatag acatccacag cgtcggtaaa 240
 ttaagggggtg atcaccaagt ttcataatat tttcccttta taaaaggatt tgttggccag 300

<210> 47
 <211> 300
 <212> DNA
 <213> Homo sapiens

<400> 47
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 gagtttctcg agagaatgat tctgagctcg gttttgacaa aagaggagct gctgaggcta 120
 aaagtggatg aaaaggccct tataattaaa agaaacaaga caggactcag aggtgtgaaa 180
 caaatattat gcatgggtgaa ttacaatgag ttgggggtat tctgtagccc taaagtacaa 240
 ggtataaaga gacagaaaat gatcctggaa tatagacaga ggataacttca tctctaatga 300

<210> 48
 <211> 300
 <212> DNA

WO 99/33982

PCT/US98/27610

<213> Homo sapiens

<400> 48

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agaccgcgcc	cccaacgcc	ctctaccccc	ctgctttgaa	ctatgctttg	agaaatgagc	180
ttatgagacc	actgagactt	gggggctgtt	gtttcagcag	ttcacctaca	cttattagga	240
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<210> 49

<211> 300

<212> DNA

<213> Homo sapiens

<400> 49

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atatctcgca	tggatagcat	tcactggaac	cactatgaga	agattatagg	aaaaacacca	180
agactagagg	actctgggtt	ccttttatgc	aaagtcaact	cttctgggtc	acagttaccc	240
agcaacaaaa	ataaagagag	gaccaggagc	atgcagcac	cccgtttacc	ctgagtgaac	300

<210> 50

<211> 300

<212> DNA

<213> Homo sapiens

<400> 50

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taacctcagg	tgatccacct	gccttgccct	cccaaatgct	tgagattaca	ggcgtgagcc	180
acccgccttg	gcctgattgg	ttttttaaca	tgatttttct	ctaaagcttaa	ataccacaag	240
gccaaagaga	aatggtcata	atttaaacca	ttattatatt	ggtgagggtat	ccctagctat	300

<210> 51

<211> 300

<212> DNA

<213> Homo sapiens

<400> 51

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gtaaccagga	agaccttagt	aaggactctc	taggtcctac	caaatcaagc	aaaattgaag	180
gagctggtac	cagtatctca	gagcctccgt	ctcctatcag	tccgtatgct	tcagaaagct	240
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<210> 52

<211> 300

<212> DNA

<213> Homo sapiens

WO 99/33982

PCT/US98/27610

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aatttgtttt cctttgtgga tgaagtggga gtaagacttg ttgctgtgag gattagatga      180
agtggctagg atatggacac accttacttg aattggaaaa caagccatgt atcccatac      240
tgcaaaatgt ggcattgtcac acgtgtaatc tctgagggtt agtttttgcg caagattgca      300

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<210> 53
<211> 300
<212> DNA
<213> Homo sapiens

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<400> 53
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cctattctga aatggggctt ctctttatgt tcttgagtea tccctgtgcc aaagagagtg      180
agtcgttgcg aagccctgtg ttccagctca ttgtgattaa cctaagacg actctcagcg      240
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<210> 54
<211> 300
<212> DNA
<213> Homo sapiens

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<400> 54
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agttgtaaaa gtatgtagat tcttgataac tctgcaccca ccttgccctt atgttaacat      180
cttaogtaac aatagaacat ttgtcaaaat taagaaatta accctgatat aatactaac      240
aaagtagaaa gtttaaaaaa tagagatttt agtcttttca ctaatgtcct ttactgttcc      300

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<210> 55
<211> 300
<212> DNA
<213> Homo sapiens

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<400> 55
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cctgtgtccc ccgtgtccg cggtgaggac agtgagggca gtgctacgtg gtggggagggt      180
gtgtgagaag ccacggaagg gcttcacagg gcagatgcga aggccagtgg gccccggaca      240
gagtcaaggct ccttgggcgg ccttgtgtct tggtggccct gatcatcctg ccaatgcaaa      300

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<210> 56
<211> 300
<212> DNA
<213> Homo sapiens

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<400> 56
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WO 99/33982

PT/US98/27610

attacattgt	tctggaagga	ctgaaaaata	cagaactcag	caccatgatc	ggaccgggac	180
aatcagatta	tttcattcct	cagcaaacgg	agatcgatcc	gaaaagtgga	aatatgagct	240
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<210> 57
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 <212> DNA
 <213> Homo sapiens

<400> 57						
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tgctctttga	nccttggtnt	ggngccttgc	ctanatgtat	ntnnntnnnn	tnntntnatt	180
tnnnnnntnn	ntnnntnct	ntnnntaaat	tgnttnnaan	tnntntann	tnnttnnatt	240
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<210> 58
 <211> 300
 <212> DNA
 <213> Homo sapiens

<400> 58						
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aaaaccattta	taccagatta	ctatccttgt	caaaaccccc	agtaactgcc	aatctcactt	180
agaataaaaat	cggactcct	gtgaagcaca	gcataaaactg	gccactgcct	atgcagcaac	240
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<210> 59
 <211> 300
 <212> DNA
 <213> Homo sapiens

<400> 59						
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ttcttggttt	gccccaatgt	ggtctattct	tgatgcagct	accaaagtaa	tgtttttaaaa	180
ccattatacc	aagttactat	ccttgtcaaa	accgccagta	actgccaatc	tcacttagaa	240
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<210> 60
 <211> 300
 <212> DNA
 <213> Homo sapiens

<400> 60						
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gaaataaggc	aggcacttgt	cccttcaggg	agggacttgt	ccctcactgg	gagggttggg	180
gttgaccttg	gctccagcag	agataccag	cctggcgtgg	aaggggcagg	tctgagctta	240
cgcttgactg	cagggaagc	tgaggccctc	ttctgccttc	cctgcattc	accaaggaca	300

WO 99/33982

PCT/US98/27610

<210> 61
 <211> 292
 <212> DNA
 <213> Homo sapiens

<400> 61
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 ctgtngnggt aaagnntca cctctcaca gcaccaccag cggcgagaca gaccccaacca 120
 ccatcttccc ctgcaaggag tngggcaaa gctcttctcaa gatcaaaagc cgaatgcac 180
 acatgaaaac tcacaggcag caggaggaac aacagaggcn aaaggctcag aaggcggtct 240
 tngcagctga gatggcagcc accgattgaga ggactacggg gcccggtgggg gc 292

<210> 62
 <211> 300
 <212> DNA
 <213> Homo sapiens

<400> 62
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 tagtaaaagg aactctttgt ttgcagaggt ggaagatcga agggcgagcaa tggaaactga 120
 gcttatcagt atgaaagtc agtatcagtc actaaagaag caaaatgtat ttaacagaga 180
 acagatgcac agaataagt taaaaattgc cacgttgcta cagatgaaag ggtctcaaac 240
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<210> 63
 <211> 300
 <212> DNA
 <213> Homo sapiens

<400> 63
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 aacagggact ccaatcaatc ggagttctcc ccttgccgga gctgcccttc acctttgggg 120
 ccogagacag tcataaggga tggacttagt tttcttgtag ggaaaaaggt ggacagcggt 180
 gtttcttaag gatgctgagg gcattggggcc aggcacaggg gagaggcaca gctccttctc 240
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<210> 64
 <211> 294
 <212> DNA
 <213> Homo sapiens

<400> 64
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 gtgcccgtct cttccgggtg gtgcaggtgg aatgttctgt gcgagagctc aagggtctgc 120
 tggatccctg acttgatccc ctttggtcca cagagagggc catgatgctc ttgagcttaa 180
 agagcaccag acatctgcct actctctccc acgtgcaggg caagagcact gaagacaccc 240
 tggctctccc ggaaggggcag tcccacaggc agcggcaccc atttctgggg cccg 294

<210> 65
 <211> 300

WO 99/33982

PCT/US98/27610

<212> DNA

<213> Homo sapiens

<400> 65

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atcttcagaa	gggtctcgcc	taagctggaa	catggataga	ttccattcta	acataaagat	180
ctttaagttc	aaatatagat	gagttgactg	gtagattttg	tggtagtgtc	ttctctggga	240
tataagaagc	aaaatcaact	gtcacaagta	aagaggggat	ggggaagggt	ttgcacattt	300

<210> 66

<211> 300

<212> DNA

<213> Homo sapiens

<400> 66

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gggcctatta	caaaggcttg	gaaaaagcac	tcaagccagc	taatattgta	gaacggctaa	180
aaatttatga	ggaagcctgg	actaaatata	ccagggggact	ggtgccaaga	aggctgccgt	240
taaacttttt	atctggtgag	aagtttaaag	aatgttttga	taagttccta	aggatgaatt	300

<210> 67

<211> 300

<212> DNA

<213> Homo sapiens

<400> 67

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anctaaacaa	cagacacatg	taagaaaaca	ccagttttgat	catggagagc	tggttttacc	120
tgcatgtcaa	ttgttagcat	atacagccct	tggtatttta	attatgagac	taaaactctt	180
cttgacacca	cacatgtgtg	ttatggcatc	actgatctgc	tcaagacagc	tatttggatg	240
gctcttttgc	aaagtacatc	ctggtgtcat	tgagtttgct	atattagcag	caatgtcaat	300

<210> 68

<211> 300

<212> DNA

<213> Homo sapiens

<400> 68

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ttgggtccag	tactacttgg	cacaacatta	tgacaaaatt	ggtcagccat	ctattgtctt	180
ggagtacata	aatactgcta	ttgaaagtac	acctacatta	atagaactct	ttctctgtgaa	240
agctaaaatc	tataagcatg	ctggaatat	taagaagact	gcaaggtgga	tggatgaggc	300

<210> 69

<211> 300

<212> DNA

<213> Homo sapiens

WO 99/33982

PCT/US98/27610

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<400> 69
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ccacaatgga ggcttcacca aggcgtgggt tgccatgaag acctttotta cggccagcat      180
cttcacatt atggtgtggt attggaggag gatcaccatg atgtcccgac ccccaagtgt      240
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<210> 70
<211> 300
<212> DNA
<213> Homo sapiens

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<400> 70
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ttgctatact caatagaaca agcattttta ataaatttct cgtaaagttgt tgctttcttt      120
atgtggtggg tgtggcttta aagagcacia aaccacaaca aatcaaagag tagctcgggc      180
ttgtcttttg ctttatggct gagggtttga aggatgattc atggacttgt gaatgccagc      240
cccagtcctg gcttaggtct atctgccaat accaccaggg ccaacaatt cacycaacaa      300

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<210> 71
<211> 300
<212> DNA
<213> Homo sapiens

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<400> 71
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gaaggaatag ttatatcaat acaccagtgg ctgaaattat catgaaacca aatgttggac      120
aaggcagcac aagtgtgcaa acagctatgg aaagtgaact cggagagtct agtgccacaa      180
tcaataaaag actctgcaaa agtacaatag aactttcaga aaattcttta ctccagctt      240
cttcctatgt gactggcaca caaagcttgc tgcaacctca tttagagagg gttgccatcg      300

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<210> 72
<211> 300
<212> DNA
<213> Homo sapiens

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<400> 72
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ggggttgatt ctgaccatag gaagtatgca atgtgaatca ctatttacag agaaacctac      120
aacagatgct tgatgttgta gaaactggga catatagata ccaagcaaaa ttataagaaa      180
cctataaggt gtccaatagc cttgtgtttc caaaattcac tgtacatgat cagtttggtg      240
ttctgtgacc acagttttta actgaaggaa ccagttgtaa cagtctcaat tttaactaaa      300

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<210> 73
<211> 300
<212> DNA
<213> Homo sapiens

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<400> 73
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gttgatcaat gaccattttt gctcagcatg gagaacacgt gccctgcagt aagggtagtg      120

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WO 99/33982

PCT/US98/27610

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agaataaaaa ggatcttacc acctttatca tgagggtggc tttgctctct ccattccaag    180
ttgtttctctg ttctagaaag cagatgtagt agacatctac tgtttttgcc taacacagaat    240
ccctttttcc tttttttgtt aaaagtactc atccctaata ttacattgtt ctggaaggac    300

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<210> 74
<211> 300
<212> DNA
<213> Homo sapiens

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<400> 74
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caaaactctc ttctcttagg gctactgaga cttgattcct gatcatcaga aatttcacca    180
gaacaacactt gcttccaata tacccaattc tatatgaaga attcatggag agtgtaactgg    240
cactgnnnnnn nnnnnnnngan ncntgctgct nogaanntnt nntattnact gannttgaat    300

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<210> 75
<211> 300
<212> DNA
<213> Homo sapiens

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<400> 75
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cacaatacgt gtacacttga ctgtgaagtg gctgtgagag tgggtggaga gttcttcttt    120
gacctctcgc ctgcggaatg ctctagaaac ctgctgttga ttgcaggagg agtcggaatt    180
aacctctcgc ttccatcctc gcggcacgca gcagatctcc tcagagagca ggcaaacaaa    240
agaatggat atgagatagg aacaataaaa ctattctaca gtgcaaaaaa taccagcgaa    300

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<210> 76
<211> 300
<212> DNA
<213> Homo sapiens

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<400> 76
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cacgtactcc ttctgaaac cactaagagg aaaaatgtct gtgacactgc atacagatgt    120
aggtgatatt aaaattgaag tcttctgtga gaggacaccc agaacatgtg agatggagtc    180
tcgctgtgtc cccagggctg gagtacaatg gcgcgatctc ggctcactgc aaactccgcc    240
tactgggttc aagcaagtct tctgcctcag cctcccgaga actgcaagag gaggcaactg    300

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<210> 77
<211> 300
<212> DNA
<213> Homo sapiens

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<400> 77
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gagacagaga gcaagtaagc tgtccctttt aactgttttt ctttggtctt tagtcacca    120
gttgcaactt ggcattttct tgctgcaagc tttttttaat ttctgaactc aaggcagtg    180
cagaagatgt cagtcacctc tgataactgg aaaaatgggt ctcttgggcc ctggcactgg    240

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WO 99/33982

PCT/US98/27610

ttctccatgg cctcagccac aggggtccct tggacccct ctcttccctc cagatcccag 300

<210> 78
 <211> 300
 <212> DNA
 <213> Homo sapiens

<400> 78
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 aacagcagca gggttcacag gtgtacatca gggcagacaa agggccagtg accagcatc 180
 tcccgctccta ggtaaacagt tctccagtta taaaccacct tcttttagga aagaagatga 240
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<210> 79
 <211> 278
 <212> DNA
 <213> Homo sapiens

<400> 79
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 gcagccgctg ctgggggaga ctctcttgcc ccattctctg ccggtttcct gccattattg 180
 gtgtgcaaga caaaacaggg ctgcacagtg gcagagagat cctttgcagt ggggaccttg 240
 gcagagacta ttcaggccct ggtgtgctgt cagccacg 278

<210> 80
 <211> 300
 <212> DNA
 <213> Homo sapiens

<400> 80
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 agtaaaaccc attgatctgc actactatgc ccagtcacgc ctggacctgt ttctggggagg 120
 ttgagagcag ccagaaaccc tggacaacat ctgtttgcca gcctttgagt ttgacatcca 180
 tcaagtaate aaagagtgca gcacgcctct gacgaactgg tgggttctgagg cccacctgac 240
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<210> 81
 <211> 300
 <212> DNA
 <213> Homo sapiens

<400> 81
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 agcacctcct cggcacacac gacttcagcg ccttccagtc cgctggcagc ccggtgcca 180
 gcccgctgag aacgctgcgc cgggtctccg ttccccagg ccaagccagc cccttggtca 240
 cccccaggga gacaggaag ctgcggttct ggaacctgga gtttgagagc cagtctttcc 300

<210> 82

WO 99/33982

PCT/US98/27610

<211> 300
 <212> DNA
 <213> Homo sapiens

<400> 82
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 gagtgtctgc cctcgggcc tccagggtggg gcacttagca ccagaaggg accaaaagca 180
 gggcatggcg gtgcagagga gtttgggagg tgtaaacagc cccatgcacg tggaggagga 240
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<210> 83
 <211> 272
 <212> DNA
 <213> Homo sapiens

<400> 83
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 gttaggaat ggcctctcat tgttttcac ttaatttgcg tcagcctgat tactcattga 180
 aacttgtgag gttgagaac tttttctaa gttattggcc attcaagttt cctcctttat 240
 gaaatgggtg ttcattgcat ttgctcattt tt 272

<210> 84
 <211> 300
 <212> DNA
 <213> Homo sapiens

<400> 84
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 aatagagctg cttggttggg ggaagtgaag ctggcttagt accagcagct gatctcttcc 180
 acgtgctgct gctttttttg ccactctgat actaaaccag agaaagctgc aggtgggataa 240
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<210> 85
 <211> 300
 <212> DNA
 <213> Homo sapiens

<400> 85
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 cagcactgat ttccattag cagttattat ttccctggcca tttcttctg aaggttttgt 180
 ggttaaacct cctgtctcca atattttatc agcagtaggg ctgtcattct tctggttatc 240
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<210> 86
 <211> 300
 <212> DNA
 <213> Homo sapiens

WO 99/33982

PCT/US98/27610

<400> 86
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 agaatagaaa catccagaat gctcctcccc atccccaat ccagacagc aattatgtca 120
 gcctgtgaag gcattgcctg ctcttgaccc tttggcccat ctttttattt ttaaaaaatt 180
 cccatgtcac agatgccctg tctatgcaga ggggtgctg ggaagggtga ccaactaagt 240
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<210> 87
 <211> 300
 <212> DNA
 <213> Homo sapiens

<400> 87
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 gccgtgcagc tgggtctcct tctcgtccgc ggccctacca ctctggtttt agtcaacagc 120
 gcattgtgctg tccccgggaa gaagagtgat ttcctgcccc ggaatgtatt tgacggggaag 180
 ctttttcac agaagtactt gcaatctgaa aagggttatg ctgtggagggt tcttttagaa 240
 caaataagat ctccgctcac caaattccac aacctgaagg cagtgtctg caaggcctgc 300

<210> 88
 <211> 300
 <212> DNA
 <213> Homo sapiens

<400> 88
 ctgaaacaaa agatgtattt caattaaaag acttggagaa gattgctccc aaagagaaa 60
 gcattactgc tatgtcagta aaagaagtcc tccaaagctt agttgatgat ggtatggttg 120
 actgtgagag gatcggaact tctaattatt attggtcttt tccaagtaaa gctcttcacg 180
 caaggaaaaa taagtgtgag gttctggaat ctacgttgct tgagggaagt caaaagcatg 240
 caagcctaca gaaaagcatt gagaaagcta aaattggcgc atgtgaaacg gaagagcgaa 300

<210> 89
 <211> 300
 <212> DNA
 <213> Homo sapiens

<400> 89
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 gaaccogagtg tcccacagcc agatatacac ccagctccat gccagccctt catgtttacc 180
 ttttgcttgg ttaattacat gtcagaactcc tagagggctt ccagactaat aggaagcatt 240
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<210> 90
 <211> 300
 <212> DNA
 <213> Homo sapiens

<400> 90
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WO 99/33982

PCT/US98/27610

tgatcccagg	cttagcacac	gattgcatgg	catccccttt	agccacttca	accactgcag	120
acatccaggga	aggtggatc	tctcctcagt	ccctccagac	ttctggccac	cacagaatga	180
aaaccccatt	ttcaactgag	ctatctttgc	tccagcctga	taactccagac	tgtgctggag	240
atagtcatac	cccactggct	ttttccttca	ccgaggagctt	ggaaagtctc	tgtttgcctag	300

<210> 91

<211> 300

<212> DNA

<213> Homo sapiens

<400> 91

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tgcaaaattg	caaagagaaa	atttatatcag	acaatggcat	tctgctgtgg	ttattcaggc	180
tgcatataaa	ggaatgaaag	caagacaaat	tttaagggaa	aaacacaaag	cttctattgt	240
aatacaaggc	acctacagaa	tgtatagcca	gtattgtttc	tacacaaaag	ttcagtgaggc	300

<210> 92

<211> 300

<212> DNA

<213> Homo sapiens

<400> 92

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cattgcactt	atcttaccaa	gctcttctga	aggttctatt	tctgaactgg	agcagctctc	180
caattctcta	ccaataaaag	aattgatgac	ctcaatctgt	gactgtctgt	tggtcacgct	240
agctaactct	gagagcagtt	acaactgttt	actgacatgt	gtcagaacaa	tgatgtttct	300

<210> 93

<211> 300

<212> DNA

<213> Homo sapiens

<400> 93

cgattcgcca	gttctccatt	ctgagagtca	atcacgttcc	tgatagggtg	tcattgattt	60
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ggtactaaaa	agaggtcccta	cccacacctg	ccctcacactt	ctcctttcca	aggctgcctg	180
agtttgagg	ggcttgggtg	tgtgtgaaca	agggccctgc	attgtctagg	cctgcagttc	240
ccaggcttgg	gttcactttc	accatgcatt	ggcaaaaacta	gaaaagtaag	cttgtgcaca	300

<210> 94

<211> 300

<212> DNA

<213> Homo sapiens

<400> 94

tttgtcctg	agcacccaca	atttcaggat	ttagactgtg	tgccacctca	gctttcctct	60
ggatgtaacc	actccttggt	gagagagggg	actcctcacc	aatccatttt	gacaaaggct	120
aggcaatctt	cattctgctt	ggcttttagtc	attcttgtca	ttgggtctga	gaagaaaaac	180
aacttttgtc	ggtgatccca	ctgccttgat	ttcaacctcg	agcgaggctg	ggccatgtcc	240

W0 99/33982

PCT/US98/27610

aagtcttatg aggtcaccct gactagaaaa aattgaactc acctacaaat agtctgaaag 300

<210> 95

<211> 300

<212> DNA

<213> Homo sapiens

<400> 95

gtgagtccga gcatcagtgg cttctggagc agaccagcca cgtggaagag aagccttaca 60
 gagatgggtc ggcagagccc tgctgatggc tgggccttgt gggcagccac tctgtgtgag 120
 cagggtgttg ggcccataca cttcaaagac cagagccctg cactgggaga gtgctcctgg 180
 ccaggctggg gaatcacctt tcgaggccct tcagactctg gcggggcttg ctgtggcctc 240
 cctccageta gtggtgtggc tgagcagact ccagggccag ggcaggttcc ctctccccct 300

<210> 96

<211> 300

<212> DNA

<213> Homo sapiens

<400> 96

acaactccag acataattaa agactggccc aggaggaaga gggcgggtgg ctgtggcgcc 60
 ggctcctctt cgggaggggg cgaggtcggg gcagaccttc ctgggagcct gtcactgtct 120
 gagacagagg gcaaggacca cggccttgaa ctcagcatcc acaggagccc catcttgag 180
 gatcttgagc tcgagggagtg gtgccagctc ccagaccagt cgctccccag gaacagcatg 240
 cctaaggccg aggaagcctc ttctctggga cagtttgggt tgagttccag gaagagagtc 300

<210> 97

<211> 286

<212> DNA

<213> Homo sapiens

<400> 97

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 tcacncnnnn nnnnnnnnnn nnnnnnnagg cctaggccgg tggatcacia ggtcagcagt 120
 tcaagaccag cctgaccagc atggtgagac cctgtctcta ctggaataac aaaaaaattg 180
 gctggcgagc gtggcaggca cctgtggtcc cagctacctg ggaggctgag gcgggagagt 240
 ctctgaaac tggaaaggcag aggttgccgt gagccagat tgcgcc 286

<210> 98

<211> 300

<212> DNA

<213> Homo sapiens

<400> 98

caccattttt attttgatgc ttacactcat ttattctgtt ttgtaaaaa agtttcggga 60
 atttaaaaa ctttcagttt aatagagctt ttgttattat attataattt tgtaaaacca 120
 ctttgttttt cccaacttaa agccaagggg tcgactcatg gatgatacct ctattgctgc 180
 tgcattgatg tcaagaccgg cccttgctgt ttgttacaga gatgttgggc agagctatgc 240
 aggtgtttca ttgtgaactc tagctttgat catgtgtaaaa agttaacctt ttctattttt 300

<210> 99

WO 99/33982

PCT/US98/27610

<211> 300

<212> DNA

<213> Homo sapiens

<400> 99

agcctcgcct	gggcgcgcct	gtggctccca	ttttcttttc	agcgggacaa	aggggacttg	60
ttaccaggcc	attttctgga	tggcctgtga	gatctctgcc	cctccaagac	cctccaagtc	120
tgagcctgac	ccacagctgg	gacactgaat	tcagccctgg	gaaccatggg	ggcttctatc	180
tggcaccagg	ctgcagcctc	cccaatccca	gccacttttg	ctgtgtctct	ggcgggctgt	240
ctctcttggt	gggagctgtc	ctgcacactg	taggatgctt	aaaggatatc	ctggcctcca	300

<210> 100

<211> 300

<212> DNA

<213> Homo sapiens

<400> 100

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atagagcact	ggtgccaggg	accaaactga	gacccccacca	cogtcaccaa	cacttacata	120
ccataaagggt	cttcagagtg	ccttggccct	agacctccct	tcattctttg	tagagatgga	180
atctaagaat	gaaacatctc	cactcagctg	tgcataatg	gaagtctctg	agataccttt	240
ttttggtaga	tacttgtgtc	ggtattctga	gagtcacttt	actctgatgg	tttgcaagat	300

<210> 101

<211> 300

<212> DNA

<213> Homo sapiens

<400> 101

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tagattctgt	tggttaogtgc	aacactgtat	atctctccat	agcacttaat	cagagtttgt	120
aattaggcat	ctttttgtgt	gattatttgg	taaatgtcca	tatccccctc	tagcctataa	180
gctccatgac	tcttaggtac	cctgtctgac	taogtgtatc	actgggtcta	ccgcctaaca	240
ttgcctagca	cattctatgc	ttcacaggca	tctgaatatg	ggtttataaa	atcacattgct	300

<210> 102

<211> 270

<212> DNA

<213> Homo sapiens

<400> 102

cctggccctg	ctgcccctcc	tgaatctcgt	atgatggtea	cagtcgggtg	gccgtggggg	60
tgetctgect	tcctctggcc	ccactgccca	tatctgtgga	ctgccccttc	caaagaccce	120
tggaggagggt	gtnnnnnnnn	nnntnntgn	nccactacc	ntgcactgaa	ctggcctnct	180
tacancaann	actgnncccn	nttgttatna	cacctntnac	aaacacctgc	tgtctgacat	240
gnctactact	taaggactnn	anacctgtgc				270

<210> 103

<211> 300

<212> DNA

<213> Homo sapiens

WO 99/33982

PCT/US98/27610

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<400> 103
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tgccccattc ttggccggtt tcttgccatt attgggtgtc aagacaaaac agggctgcac    120
agtggcagag aagtcctttg cagtggggac cttggcagag actattcagg gcctgggtgc    180
tgccctcagcc cagtttgtgt ctgggtgctt ccctgtgctg ttgagcaccc cccaagaggg    240
agaccccgag gtgcgaagca atgccatctt cgggatgggc gtgctggcag agcatggggg    300

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<210> 104
<211> 300
<212> DNA
<213> Homo sapiens

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<400> 104
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cagctggggt ggcgctgtct ccagagccgt gggteccaga ccttgcggtc cttttgttcc    120
tgtcgtttta tcaggacacg ggccccacct gtcaogtgcc cgagggccacc caagcccagc    180
ctgcggggcg ttcccactgc ctggatgcgg gcttgagtgc tgcgcacgca ggattcagtg    240
tggggacggc cctcgccgga taggcctagc cctggcccag gtggtgagcg gtttgacgtg    300

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<210> 105
<211> 300
<212> DNA
<213> Homo sapiens

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<400> 105
gggcactgtg gggctctccc cgcctctcct gccttgtttg cccctcagcg tgccaggcag    60
actgggggca ggacagccgg aagctgagac caaggctcct cacagaaggg cccaggaagt    120
ccccgccctt gggacagcct cctccgtagc cctgtcacgg caccagttcc ccaggggacg    180
cagcaggccg cctccgcgag cggccgtggg tctgcacagc ccagcccagc ccaagggccc    240
caggagctgg gactctgcta ccccagtga aatgtctgtt ccctctctcc cgttgccctt    300

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<210> 106
<211> 300
<212> DNA
<213> Homo sapiens

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<400> 106
gtcacaagcc tatgtgaccc atctccatgc cgaatacaat cgacagaagg acatctacct    60
agcacatcgt gtggcccaag cttgggaatt ggcccagttc atcccaccaca catccaagaa    120
ggcagacgtg gttctgtgtt gtggagacct caacatgcac ccagaagacc tgggctgctg    180
cgtctggaag gagtggacag ggcttcatga tgcttatctt gaaactcggg acttcaaggg    240
ctctgaggaa ggaacacaaa tggtaaccaa gaactgtcac gtacgccagc aggagctgaa    300

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<210> 107
<211> 300
<212> DNA
<213> Homo sapiens

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<400> 107
tgtgagtttc ctatctgttc cagactagta tcgccaatct ctcccagctc tcttctttcc    60
tccttgacct ttgtctgcga ggaggtagca tcacctcttg gcatattgta catgtcttta    120

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WQ 99/33982

PCT/US98/27610

aacaattgga	ggagctgccc	aggcagtttt	atggcctcct	ggttgtgtgc	cttcacaccc	180
gctcacagcc	ccacctcacc	atcaagcgct	gagccaatgc	gggtgtggct	ggcctcgagt	240
tctctgagta	gctccttgcc	agggccagag	ctggtaaacg	cggggcagca	gggtgggtag	300

<210> 108
 <211> 300
 <212> DNA
 <213> Homo sapiens

<400> 108	
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agcacaagct	gcccctcagc
tgcgcagctg	ggcgagcccc
ggggggcgct	cagcctcttg
tggagtaccc	tgactttctac
	cggaaagctct
	acggcctctt
	ggacccctct
	gtctttcacg
	60
	120
	180
	240
	300

<210> 109
 <211> 300
 <212> DNA
 <213> Homo sapiens

<400> 109	
cacaaggaga	agaaagttaa
attgggcctt	ggaagaagaa
gaggtaggaa	agtatagatc
ttaaggttaa	aaggatatac
gtggagagtt	atcagagtgt
	ttgaaaagga
	gggttattga
	gtaaataaat
	agactggtag
	60
	120
	180
	240
	300

<210> 110
 <211> 300
 <212> DNA
 <213> Homo sapiens

<400> 110	
gacacccag	atgcagccac
gtctggcccg	tggctccagg
gacaaggccg	cgctcctgca
agactactac	agagcttctt
tcactgtctc	cccgccctgg
	ccacaacttt
	gtgcggcacc
	atctgcggaa
	tcggccggat
	60
	120
	180
	240
	300

<210> 111
 <211> 271
 <212> DNA
 <213> Homo sapiens

<400> 111	
cctggccctg	ctgccctccc
tgtcttgcc	tccctgtgtc
tgggggggg	ggggnnitcc
ttantantat	ttncantn
ttantntang	ngatntacc
	ttntgtgaan
	g
	60
	120
	180
	240
	271

WO 99/33982

PCT/US98/27610

<210> 112
 <211> 300
 <212> DNA
 <213> Homo sapiens

<400> 112
 gttcctctcac cttattctctc caagttcccc cttgggaacc tctgagatta acttgataag 60
 ctctctggggc aagctcttcta tcttaagatt cctcagtgag ccttatagag ttgctgcgag 120
 aattacattt gttcatgatg tcaagtgtct ggtagtagc taatgcttat tgaacacata 180
 gtaatttatt gaataattgt catgatcact ggatgagata tagccactgt ggaggtaggc 240
 acaccagggt tttagaggct tgggatcttg caacaggatt tctctcttgc ctctcccaaac 300

<210> 113
 <211> 300
 <212> DNA
 <213> Homo sapiens

<400> 113
 cccacatgta ccaggttgag tttgaagatg gatcccagat agcaatgaag agagaggaca 60
 totacacttt agatgaagag ttacccaaga gagtgaaaagc tcgattttcc acagcctctg 120
 acatgcgatt tgaagacacg ttttatggag cagacattat ccaaggggag agaaagagac 180
 aaagagtgtc gagctccagg ttttaagaatg aatatgtggc cgacctgtga taccgcactt 240
 ttttgaagag ctctttccag aagaagtgcc agaagagaca gtagctcgca tacatcgctg 300

<210> 114
 <211> 300
 <212> DNA
 <213> Homo sapiens

<400> 114
 acagtttagtg taaaggatct gaatggcata gacttaactc ctgtgcaaga tactctctgtg 60
 gttcaagaaa aagaagatac atatgtacat tttaatgtgg acattgagct ccagaagcat 120
 gttgaaaaat taaccaaaag tgcatctatc ttctttgaat tcaaacacta caagcctaaa 180
 aaaaggttta ccagcaccaa gtgttttgct ttcatggaga tggatgaatg taaacctggg 240
 ccaattgtaa tagaactata cagaaaacc actgacttta aaagaaagaa attgcaatta 300

<210> 115
 <211> 288
 <212> DNA
 <213> Homo sapiens

<400> 115
 gtgatctgcc tgccttggtc tcccaaagtg ctgggaatac aggcattgagc caccgcactc 60
 ggccaggagc tagttttatc agcatcctgc tccactgcct tctctagtg cagcctggaa 120
 gacatggcag cgggtagctc ctggggctga gccagaagca tcactgcagt gaaagtctct 180
 gcttacctgt ctggctcagc ttgggcaagg gctgggcat atgtgctcag ggacgtgctt 240
 ctctgtgaag gcaggaggat anaanaggac cannaangn gggagctg 288

<210> 116
 <211> 300

WO 99/33982

PCT/US98/27610

<212> DNA

<213> Homo sapiens

<400> 116

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ctggaaaaga	gcagtgagag	gagtcggga	gatgtgtgat	gcattgtgaag	caacattggt	120
taacattcac	tgggtctgcc	aaaaatgtgg	atttgtggtc	tgcttagatt	gttacaaggc	180
aaaggaaag	aagagtctta	gagataaaga	actatatgct	tggatgaagt	gtgtgaagg	240
acagcctcat	gatacaaac	atttaattgcc	aacccaaatt	atacctgggt	ctgttttgac	300

<210> 117

<211> 300

<212> DNA

<213> Homo sapiens

<400> 117

gcactttcca	gaattctctc	atatttgtgg	gtcgggatca	agcctgcagc	ttgaggaaa	60
cacaaggaaa	ggaaagaaga	tctggtggaa	agctcaggtg	gcagcggact	ctgactccac	120
tgaggaaact	cctcagaagc	tgcgatcaca	actttggctg	aagccccctg	cctactctag	180
ggcacttgac	ctggcctctt	gcctaaacca	caaggctaag	ggctatagac	aatggtttcc	240
ttaggaacag	taaacacagt	tttctaggga	tggcccttgg	ctgggggatg	acagtgtggg	300

<210> 118

<211> 300

<212> DNA

<213> Homo sapiens

<400> 118

agaacgttct	caggttgacc	agctgctgaa	tatttcttta	agggaggaag	aacttagtaa	60
gtcattgcag	tgcatggata	acaatcttct	gcaagccctg	gcagcccttc	agacagctta	120
tgtggaagtt	cagaggtcac	ttatgctcaa	gcagcagata	actatggaga	tgagtgcaat	180
gaggaccat	agaatacaga	ttctacagg	attacaagaa	acatatgaac	cttctgagca	240
cccaggtttg	gcataagaa	ggtaccctct	gttcaaaatg	aacaagaagc	cttagatttg	300

<210> 119

<211> 300

<212> DNA

<213> Homo sapiens

<400> 119

gaacaaagaa	ggaatgtctt	cctcatgttt	gggtctatag	aagacgttaa	agaaaaactc	60
cagaagtgg	gtttgagcca	tgagccacca	cgctggcca	aaggatttaa	tgaattaatg	120
gatgtacagt	gctggggctg	gtattctagg	gcctgcatg	agactcacat	tttgccatca	180
aaagcctttt	aagagtgga	ggttgcggtg	agctgacatg	gtgccactgc	actccggcct	240
gagtgacaga	gtgagactct	gtctcacaaa	aaaaataatg	ccctttaaat	aatgaaat	300

<210> 120

<211> 273

<212> DNA

<213> Homo sapiens

WO 99/33982

PCT/US98/27610

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<400> 120
cctcagccctt ctaaaaagct ggggctacac ccagctgaag aaattgtaac taaagataga      60
ttgttttaag caaagcaaga aacttctgaa gaaatggaac aaagtggaga agcctcagga      120
aagcccaaca gagagtgtgc accccagatt ccttgtagta ctccatttgc tactgaaagg      180
acagttgcac atttgaacac tctgaaggac cgtcaccag gtgatttgtg ggcccgcatg      240
cacatctcat cccttggaat atgtctcgagg aga                                     273

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<210> 121
<211> 300
<212> DNA
<213> Homo sapiens

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<400> 121
agaacgttct caggttgacc agctgctgaa tatttcttta agggaggaag aacttagtaa      60
gtcattgcag tgcattgata acaatcttct gcaagccctt gcagcccttc agacagctta      120
tgtggaagtt cagaggctac ttatgtctcaa gcagcagata actatggaga tgagtgcact      180
gaggacccat agaatacaga ttctacaggg attacaagaa acatatgaac ctctcgagca      240
cccaggtttg gcatagaaat ggtacccctt gttcaaaatg aacaagaagc cttagatttg      300

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<210> 122
<211> 300
<212> DNA
<213> Homo sapiens

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<400> 122
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ccagaatgat acacggatca gtgcagaagt tcatcaggct ctccgacctt agggctgttg      120
gagaaggctt cagcagcaga actgatgggt aaggtctgtg ttctccatcc tcaactttct      180
ttgtcttcga catacacaa gatacatatt gaagggcaaa aaaatgaaca ctgtcgttca      240
ttgcagccgt gttttgtgac acagatgcac agtctgtctg gaagaccttc tctcaagtgg      300

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```

<210> 123
<211> 300
<212> DNA
<213> Homo sapiens

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<400> 123
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aagaactgac ggcctttggga tttgttttaa acttttataa taaggatcct aagactgttg      120
cctttaaata gcaaacgagc ctacctggag gctaagtcgt ggcagtgggc tggccctctg      180
tgtgagcatt agaccagcca cagtgcctga ttggtatagc cttatgtgct ttcctacaaa      240
atggaatttg aggcggggcg cagtggctca cgctgtaat ccacgacctt tgggaggcca      300

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<210> 124
<211> 300
<212> DNA
<213> Homo sapiens

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<400> 124
catgtggcc agcatccctg cctgtgcaag ctctggatga gctgtgagcc cctgccaccc      60
acacccccac tccctgccag cctggcctca gggcctctga tccatgtgca ctggagagga      120

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WO 99/33982

PCT/US98/27610

gatgactgac	agggccactg	gggcatttcc	acgttaacag	cagctgccac	tggcaaaaga	180
agtgaactcgc	caatgggagc	atctcagatg	tgggccccagg	agtcctgggga	gctactttga	240
acaggggctat	ccattcattg	tcccacaaaa	ggctatggag	cccaccacc	atgtgctgga	300

<210> 125

<211> 300

<212> DNA

<213> Homo sapiens

<400> 125

ggtaaatggg	ttgaattatt	gtattgaagc	ttgagctgta	gctaaaagta	atttaggttt	60
cccctaagat	gttattatgt	tagggacata	acacttttgg	gagggttggt	tgggagatgg	120
ttgattttag	ttttcaaaag	ctagaaaataa	aattttacatg	ccttagatgtt	cataaaattc	180
tgctctaatt	gggtgggaag	tgctgtatct	aacttggtgt	cctcctaagg	ttatgtccta	240
ataactatct	ttttaggagt	atacttctac	tttatagaag	gttgcttttc	tttttaattt	300

<210> 126

<211> 300

<212> DNA

<213> Homo sapiens

<400> 126

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aactccaat	caacagtatt	ttcaacaaga	aatgtgcaat	tgaaatcaag	tgctgtttta	120
gtgcagctag	gatttccaca	ggaagacact	tgcaagtgaac	agagttagtg	agcagcaaaa	180
acacagatct	atttggaaaa	agagaaaaaca	tatgcgttgt	attttgcttc	aattataaaa	240
taccatctct	tcaaaggttg	ttctaaatta	caaaggactt	tgatttctag	gtagattctg	300

<210> 127

<211> 300

<212> DNA

<213> Homo sapiens

<400> 127

ggtgattccc	atgctgaaca	gtttgatctc	ctgccagagt	gtcgggccac	aaactgggca	60
gcacatcagg	atcacctggg	ggccttcaaa	aatcaaaaat	ccacccccag	gccatgccct	120
ggacccactg	caccaggaca	agaaatccac	cccaggcctc	tccccagacc	cactgcacca	180
ggacaagaaa	tccaccccca	ggccaagccc	cagaccacct	gccctaggat	gtgggggtgg	240
gaaccagggt	gtgctttgta	aagacgtgca	ggtggtaacc	ccaggccccc	acgctcgga	300

<210> 128

<211> 300

<212> DNA

<213> Homo sapiens

<400> 128

tgagctggga	gaaggggaga	aagtttgtga	agaggagatc	ggtgacctgg	gtccttatg	60
tgccctgaaag	agtttgagtt	tctgtttaac	tcctaatcaa	cagtattttc	aacaagaaat	120
gtgcaattga	aatcaagtgc	tgtttaagtg	cagctaggat	ttccacagga	agacacttgc	180
agtgaaacaga	gttatggagc	agcaaaaaaca	cagatctatt	tggaaaaaga	gaaacatat	240
gcgtgtgatt	gtgtctcaat	tataaaaatac	catcctctca	aagggtgttc	taaaattacaa	300

WO 99/33982

PCT/US98/27610

<210> 129
 <211> 285
 <212> DNA
 <213> Homo sapiens

<400> 129
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 ctccactgag gaactgcctc agaagctgcg atcacaaactt tggctgaagc cctgacctca 120
 ctctaggcca cctgacctgg cctcttgctt aaaccacaag gctaagggct atagacactg 180
 gtttccttag gaacagtaaa ccagtttttc tagggatggc ccttggtctg gggatnnnnn 240
 nnnnnnnnnn nnnnnnnnnn nnaggaagat accatttctt gacgg 285

<210> 130
 <211> 300
 <212> DNA
 <213> Homo sapiens

<400> 130
 ccggacgcag gccctcgggc agggcatctt ggcagagtgg gggcgctggc aggcacccttc 60
 ctttgcaggg cgaggtgggg cctctgcagc catcctggac aggcgggggt ggcggcagct 120
 ttgccacagt ggaagcgggg tgggtctcac ttgcgtgggt gcccttggcc ccactctgcc 180
 tgcctcggcc tggggcggc gcgctgggtg gtgggtctgc ctgcttgctg ctcggtccccc 240
 gggcatgcgt gggcagcggg gggcatgcgt gggcagcagg gggcgctggg cagcggggggc 300

<210> 131
 <211> 300
 <212> DNA
 <213> Homo sapiens

<400> 131
 gatctctata ctagtgaaca gtgccagttc cacacttttg acttagaact gttctctagt 60
 tattgttaaca cagaatactg tcaatcccta atttacttaa tgttacttat tggaaagtggg 120
 gctgatgaaa tacgcacagg agggaaatct actgtgttta ggcacaggca gccccagtgt 180
 ataaggagat catattccaa aagggtgtca gttggttggt tgcaacctgg aatgtatttt 240
 cctttataga ccaggttatc catggttggt agggccctag agcagctgga aaagatgata 300

<210> 132
 <211> 300
 <212> DNA
 <213> Homo sapiens

<400> 132
 ctcccatgga ggtggtggga atggcacoga gaagtttgat gacagttatc taatggacta 60
 gaggttgcca aactttctgt aaatggccag gtagtaaata gttctgcttt tgaaggcata 120
 tggttctctg cacctactcg aggctgaaag cagctataga caatacataa atgaatgagc 180
 gtgagtggtg tccaataaga aaaaaacatg cgtgtttgct tcggccccag ggttgtagct 240
 taccagtctc gtaacagatc acagtttgct cttttggtca caaataactg aacccctccc 300

<210> 133
 <211> 269
 <212> DNA

WO 99/33982

PCT/US98/27610

<213> Homo sapiens

<400> 133

atgctatgcc	aaagcctgct	gccagctcca	tagcctggac	ctacagcact	gcattggtgga	60
gtccacagct	gtggtgagct	tcttgaggga	ggcagggtcc	cgaatgcgca	agttgtggct	120
gacctacagc	tcccagacga	cagccatcct	ggcgcgactg	ctgggcagct	gctgccccca	180
gctccaggtc	ctggaggtga	gcaccggcat	caaccgtaat	agcattcccc	ttcagctgccc	240
tgtccaggct	ntgcaaaaag	gtgccctc				269

<210> 134

<211> 300

<212> DNA

<213> Homo sapiens

<400> 134

gatggatgag	actgttgctg	agttcatcaa	gaggaccatc	ttgaaaaatcc	ccatgaatga	60
actgacaaca	atcctgaagg	cctgggattt	ttgtcttgaa	aatcaactgc	agactgtaaa	120
tttccgacag	agaaaggaat	ctgtagtcca	gcacttgatc	catctgtgtg	agggaaaagcg	180
tgcaagatc	agtgatgctg	cctgtttaga	catcatttat	atgcaatttc	atcagcacca	240
gaaagtgttg	gatgtttttc	agatgagtaa	aggaccaggt	gaagatgttg	acotttttga	300

<210> 135

<211> 300

<212> DNA

<213> Homo sapiens

<400> 135

ggcgagcggg	aacagctctt	gaggagtggg	actgcaggag	atgtggggcg	tgccaaagag	60
atggatgaga	ctgttgctga	gttcatcaag	aggaccatct	tgaaaaatccc	catgaatgaa	120
ctgacaacaa	tctctgaagg	ctgggatttt	ttgtctgaaa	atcaactgca	gactgtaaa	180
ttccgacaga	gaaaggaatc	tgtagtccag	cacttgatcc	atctgtgtga	ggaaaagcgt	240
gcaagtatca	gtgatgctgc	cctgttagac	atcatttata	tgcaatttca	tcagaccacg	300

<210> 136

<211> 300

<212> DNA

<213> Homo sapiens

<400> 136

gacttctaaa	tatatcttgg	atataatagg	tgataagttc	tgtaaatag	taacatctga	60
aaaaacagct	ttgtcctggg	tgaaaaagga	tgccaaaatt	gcctggaaaa	gagcagtggg	120
aggagtcggg	gagatgtgtg	atgcatgtga	agcaacattg	tttaacattc	actgggtctg	180
ccaaaaatgt	ggatttgtgg	tctgcttaga	ttgttacaag	gcaaaaggaaa	ggaagagttc	240
tagagataaa	gaactatatg	cttgatgtaa	gtgtgtgaag	ggacagcctc	atgatcacia	300

<210> 137

<211> 300

<212> DNA

<213> Homo sapiens

<400> 137

WO 99/33982

PCT/US98/27610

ttgacaaaatt	gcttgaacac	acttattgtg	gtttaccogg	ttttaattat	gtcagagatt	60
gcatcatcct	tatgtctggt	tacatctata	atcttctatg	aaatgggtgt	accaaggggc	120
gccccaaagc	ttttatcccc	attcttagag	catattcttt	attataatga	ttatcccaaca	180
tatttcttta	attttaatac	aaaaaataca	tcatttaatt	ttgttacat	atgaacattc	240
atttttaaat	gtcagcctc	aagtgcaggc	atttttgagt	ggcctgatta	catattcctc	300

<210> 138

<211> 300

<212> DNA

<213> Homo sapiens

<400> 138

ggaaggggag	ggttgggtgag	tcccagacct	taaaaataca	aggttaagag	ggaccccaaa	60
gcaaaaaatt	ccaacccttt	tctccccagt	cattgaaaca	ccaaaaactat	tataccggag	120
ggtgtaatag	ttttgctgcc	cagttgtggt	aggccagtag	tggcctccca	agatgcccat	180
gtcctaatec	caggaacctg	tcaaaattac	cttgatggc	caaaggggct	ttgcagatgt	240
aatgaagtta	aggattcttc	gccaggaaga	ttatcccaga	ttgttcaggga	gggcttgatg	300

<210> 139

<211> 300

<212> DNA

<213> Homo sapiens

<400> 139

gacatcattt	tcttattcta	gtaagagaaa	gtacacagat	tcaactttag	agaggacttt	60
tttttttctg	gagctaaatc	aaggaaggat	tatcacgtgg	cctcccttga	atataatttt	120
gaagctttag	acagtaccat	cagtaacatt	ttatggacag	ctctgatggt	ttttatacca	180
cggcactctt	cttacctttg	ggggaagcta	tctggagtta	tgactgatgt	gtaaagtgggt	240
ttactgttag	aatcctgggt	tgctaggatt	ctgggagagt	cacttccagg	aagttacctg	300

<210> 140

<211> 300

<212> DNA

<213> Homo sapiens

<400> 140

gctgccccag	cagttttatg	gcctcctggt	tgtgtgcctt	cacaccgcc	tacagcccca	60
cctcaccatc	aagcgtgag	ccaatgcggg	tgtggctggc	cctgagttcc	tgagtcagct	120
ccttgccagg	gccagagctg	gtaacacggc	ggcagcaggg	tgggtagcct	ctagaccacca	180
gggcagtcct	tgagggggcca	gcagggggggc	tgactgccta	gtggctcaac	ctcctgaacc	240
caccacatcc	cagcgatgct	accagaaacc	ccaacggcat	gaatcctgca	cagtgccggg	300

<210> 141

<211> 300

<212> DNA

<213> Homo sapiens

<400> 141

cccaaaacta	tcggggggtgc	cagaggcaga	gtagacaagc	cttagtgccc	gccatttggt	60
gaatatctac	tgtagcgcaa	gcagtcgctc	acaactttat	gaagtaggta	ttattatcat	120
ccccatttta	caggtaaga	aactgagctc	ctagagagacc	aacttttcca	aggtcacaca	180

WO 99/33982

PCT/US98/27610

gagggtgggat ccagcccact tccgtctgac cccaagcccc tgcgtgtaac cectgcccga 240
ttgtggggag gtctcggccc actctggagt tctctggtct gcgtcagtc ccaggagaag 300

<210> 142
<211> 300
<212> DNA
<213> Homo sapiens

<400> 142
gaaagggtggc gcgcttctca cggtcagatt gctgcgcctg cagacggaag ctccccacag 60
gcagagctgc ttggatgtgt gagtcatgaa gccagagaag ccccgctcca tgagcagtga 120
ctccccaggg cctgtgacct cctcctctgc ttgcagctcc tctcggcacc agtccccagg 180
gctcctctgt tggtagttcc tgcctttctt cttggaatt cctcgtggac ctgcagatct 240
ttaccctaaa atagtctctg tgaattcac cctggcaatg taaattgata gcttatcttc 300

<210> 143
<211> 300
<212> DNA
<213> Homo sapiens

<400> 143
cttggccttg cttctctgag aaaacttttg tcacacctcc agagccaggg tgggtgcctc 60
cctggaggag ggggctttcc tgggtggttg cacagcagga gtccaggctt tgtaccgttg 120
acaccatggg ctatggcaac acctcctca ccatcctcc atgaggacct cgggagagag 180
tggacatgaa accctttgtg ctctgaagca tccaacagaa gctttctggt tctgtgccta 240
ttctcttggc acttgagcgt gtttgacgtt tcattacaca catgatgaaa gctctggccc 300

<210> 144
<211> 300
<212> DNA
<213> Homo sapiens

<400> 144
cctgactgag tgccctgacgg tggacccctt cagtgcacgc gtctgaaggc agctgtacct 60
taagcacctg tcacagtcca gcctctctgt ggagcacttg ctacagctcct gggagcagat 120
tcccaagaag gtacagaagt ctttgcaaga aaccattcag tccctcaagc ttaccaacca 180
ggagctgctg aggaagggtg gcagtaacaa ccaggatgtc gtcacctgtg acatggcctg 240
caagggcctg ttgcagcagg ttcagggtcc tcggctgccc tggacgcggc tcctcctggt 300

<210> 145
<211> 300
<212> DNA
<213> Homo sapiens

<400> 145
gccagagcct agaggagaga tcaaagacct tggccgaagt gaagccatt ctgcaagcaa 60
ctgggttccc atggcatgtg gtggccttag aggaggtgtt cagcctgcca ccgtcggtgc 120
tttggtgctc tgcccaggag ctgggtggat ccgagggggc ctacaaggcg gccgtggaca 180
gctcctcca gcagcagcat gtgctggggg ccgggggtgg tcttggnccg actcaagggg 240
annnnnnnnn nnnncaacc ccgctggac cccngaancc tggcaagacc ngctgcccct 300

WO 99/33982

PCT/US98/27610

<210> 146
<211> 300
<212> DNA
<213> Homo sapiens

<400> 146
tgactttgta cctgtggtccaa gctgttgagg aattgctgct gttgacccag gcaggagtct 60
gactagagaa caaactaagg ttgctgcaac aaacaaggac ctcttccaag aagggtctcc 120
aggcctggcg cagtgaacta tgctgtgat ccagcactt gggaggccga ggcgggtgga 180
tcatttgagg ccaggagttc gagaccagct tggccaacat gatgagaccc cgtctctatt 240
aaaaatacaa aaattagcca ggcgtggttg cgctgttagt ccagctact caggaggttg 300

<210> 147
<211> 295
<212> DNA
<213> Homo sapiens

<400> 147
ggnaangcna nngnaggaga nagagaagna ncagtnnagn cccangaaac cmntgaaac 60
ccttagaagn cagaggagng aaaggangaa aananngnn ggangagaa nnannnnngn 120
caaannaagg anganngnta gngngnaaaa anaanaacaa anggggaaaa ngggaaaaaa 180
ggcganaaag gnaaanannag nanaaggngg aananannnn annagaaagg ncaanaaaag 240
aagnacaag aaaaangana anaagnaann annanannga cagagacaag aagga 295

<210> 148
<211> 300
<212> DNA
<213> Homo sapiens

<400> 148
cgctgtgctt gagaccaacc tgacgggtac cttctacatg tgcaaaagcag ttacagctc 60
ctggatgaaa gagcatggag gatctatcgt caatatcatt gtccctacta aagctggatt 120
tccattagat gtgcattctg gagtgcaag agcaggtgtt tacaacctca ccaaatcttt 180
agctttggaa tgggacctga gtggaatacg gatcaattgt gttgccccgt gagttattta 240
ttcccagact gctgtggaga actatggttc ctggggacaa agctctcttg aagggtcttt 300

<210> 149
<211> 300
<212> DNA
<213> Homo sapiens

<400> 149
agtgctcagtt ttctaatct cagtcacaggt aggaattaag aaatatctca agtgttgatg 60
ctatccaagc atgttggggg ggaagggagt tggtgccag aaatgggac tggagtggag 120
aatatctttt cttttgagag tacccccagt ttatttctac tgtgctttat tgctactgtt 180
ctttattgtg aatgtgttaa cattttaaaa atgttttgcc atagcttttt aggaacttgg 240
gttaaaaggag ccagtggtct ctctgggtgg gtactataat gagtatttgt gaccacacag 300

<210> 150
<211> 300
<212> DNA

WO 99/33982

PCT/US98/27610

<213> Homo sapiens

<400> 150

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ctattctgac	aacttttttaa	ttcctttgat	cttataagtt	aaagctgtaa	caactgaaat	120
tgcatggatc	aaataagcat	agttttatcc	agggagaaaa	ataaaaaggaa	gccatagaaat	180
tgctctggtc	aaaaccaagc	acaccatagc	cttaactgaa	tatttaggaa	atctgcctaa	240
tctgcttata	tttggtgttt	gttttttgac	tgttgggctt	tgggaagatg	ttatttatga	300

<210> 151

<211> 300

<212> DNA

<213> Homo sapiens

<400> 151

gogggcccg	ccagcggaag	ccoctgogcc	ogcgccatgt	caaaagaaaa	aggactgagt	60
gcagaagaaa	agagaactcg	catgatggaa	atattttctg	aaacaaaaga	tgtattttcaa	120
ttaaaagcat	tggagaagat	tgctcccaaa	gagaaaaggca	ttactgctat	gtcagtaaaa	180
gaagtccttc	aaagcttagt	tgatgatggt	atggttgact	gtgagagatg	cggaaacttct	240
aattattatt	gggcttttcc	aagtaaagct	cttcatgcaa	gaaaacataa	gttggaggtt	300

<210> 152

<211> 300

<212> DNA

<213> Homo sapiens

<400> 152

gatatttcaca	cagtatgtat	tatattaacc	atatacacact	taagttatta	aattcagact	60
atttgttaact	tattgtttata	gggcctgccg	tatggcttag	gatatttgag	taatcatata	120
tttaaaagtaa	aaactttggg	ctgggacagc	tggctcacac	ctgtaatccc	agcaacttggg	180
gaagctgagg	tgggcagatc	agttgaggtc	aggagtctta	gaccagcctg	gtcaacatg	240
cgaaacccca	tctctactaa	aaatacaaaa	attagctggg	cggtgtggca	cacacctgta	300

<210> 153

<211> 300

<212> DNA

<213> Homo sapiens

<400> 153

cagagaccag	ccttctccag	aggctgtcac	tgcaggagcc	gtgggccttg	gaagacttgg	60
aagcggcctc	tctcaactgg	tttctgtctc	cgtggagctg	gaactgcctg	cacttgcctt	120
cagaggggagg	cacagttccac	ccagatccac	ctttccagca	agacccccag	tggctgcccc	180
gcctggggagc	acctctttgc	ttttcacacc	aaacaaaac	tggcgagagc	ccctctagc	240
caccagtgat	ccccagcat	ccagtacaga	accaggcacc	gagctagctc	cctgcacggc	300

<210> 154

<211> 300

<212> DNA

<213> Homo sapiens

WO 99/33982

PCT/US98/27610

<400> 154
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 gtttagctag aaatctatgt atttatccct ttcttatttt gcattcttct cccactattt 120
 ttaaaaaact atttacagta gaaaccattc ttctttctcc caacagtatc ctttgccaag 180
 accatgagaa cagtatggga gcatgtgtgt ggtcagggtt tcagaatacg cgtgatgtca 240
 ctgagaatgt ttgtctcacg tcaataattg tctttgtgga tgtgataatt ttggagatac 300

<210> 155
 <211> 81
 <212> DNA
 <213> Homo sapiens

<400> 155
 gatcattgtt aatttagtgac atagtaacat ctgtagcagc tggttagtaa acctcatgtg 60
 ggggaggtgt ggggaggttt a 81

<210> 156
 <211> 300
 <212> DNA
 <213> Homo sapiens

<400> 156
 ggcagcacaa gtgtgcaaac agctatggaa agtgaaactc gagagtctag tgccacaatc 60
 aataaaagac tctgcaaaag tacaatagaa ctttcagaaa attctttact tccagcttct 120
 tctatgttga ctggcacaca aagcttgcgt caacctcatt tagagagggg tgccatcgat 180
 gctctacagt tatgtgtgtt gttacttccc ccaccaaact gtagaaagct tcaactttta 240
 atgcgtatga tttcccgat gagtcaaaat gttgatatgc ccaaaactta tgatgcaatg 300

<210> 157
 <211> 300
 <212> DNA
 <213> Homo sapiens

<400> 157
 ctggtgagga gtctttgcga gagcgaggag cagcgggttac tggaaacagt gcatggcgaa 60
 gaggagcggy ccacacagag catcctgaca cagcgggtgac actgggcccga ggcgctgcag 120
 aaacttgaca ccattccgac tggcctggtg ggcattgctta ctacactgga tgacctccag 180
 ctgtaccaga aggagcaaga gattttcgag aggaccgaag aagcagaggg cattttggat 240
 cccacaggagt cggaaatgtt aaactttaat gagaagtgca ctccggagccc actactgacc 300

<210> 158
 <211> 300
 <212> DNA
 <213> Homo sapiens

<400> 158
 cgacagctct ccaatactca ggttaatgct gaaaaatcat ccaagacagt tattgcaaga 60
 gtttaatttt tgaaaaactgg ctactgctct gtgtttacag acgtgtgcag ttgtaggcat 120
 gttagctacag gacattttta agggcccagg atcgtttttt cccaggggcaa gcagaagaga 180
 aaatgttgtt tatgtctttt acccggcaca ttcccttgca ctaaatacaa gggctggagt 240
 ctgcacggga cctattagag tattttccac aatgatgatg atttcagcag gtagcagctc 300

WO 99/33982

PCT/US98/27610

<210> 159
 <211> 300
 <212> DNA
 <213> Homo sapiens

<400> 159
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 tggatgaaga aaggccctt agaatggcaa gattacattt acaaagaggt ccgagtgaca 120
 gccagtgaaga agaatgagta taaaggatgg gttttaacta cagacccagt ctctgccaat 180
 attgtccttg tgaacttct tgaagatggc agcatgtctg tgaccggaat tatgggacat 240
 gctgtgcaga ctgttgaac tatgaatgaa ggggaccata gagtgagggg gaagctgatg 300

<210> 160
 <211> 294
 <212> DNA
 <213> Homo sapiens

<400> 160
 ctttgagcta ggataaaaaa tgggtaaagg acatttgctt acctgcaaat gaatcactgt 60
 ggaatgtga tcttcccata tcatcaagaa acttgcttct tggatgaata ctggagagaat 120
 aaaaatgagaa ctctggagtg agctaaattg atcccaatta agtttttctg ctatgcagac 180
 agaaagtata attttttgac accctttccc acctgggtgcc tatgctaggc ttgttctgat 240
 aacatccctc actnaetnga tnnccacatn gnncttnenc tgangtccca tttt 294

<210> 161
 <211> 300
 <212> DNA
 <213> Homo sapiens

<400> 161
 ctctctcaaa gcatgggtgc tgagtaccga gagttgcgag gagtttttta actgatttag 60
 ccaggtggca atcatgagtg aatggatgaa gaaagggccc ttagaatggc aagattacat 120
 ttacaaagag gtcgcgagtga cagccagtga gaagaatgag tataaaggat gggttttaac 180
 tacagaccca gtctctgcca atattgtcct tgtgaaactc cttgaagatg gcagcatgtc 240
 tgtgaccgga attatgggac atgctgtgca gactgttgaa actatgaatg aagggggacca 300

<210> 162
 <211> 300
 <212> DNA
 <213> Homo sapiens

<400> 162
 gccctgtgtg gggagacgga cagcacccct ctcactctgc aggtgccctt gatgetatag 60
 cgctctccct ctccctcag agggcacagc tcagggcctg accaaggcca cgcccgctc 120
 tcgtgctcta ggacctgcac gggacttgtg gatgggctg gactctccag aaactacttg 180
 ggccagagca aaggaaaacc tcttgtttta aaaaaattt tttcagagtg ttttggggag 240
 gagtttttag gcttggggag agggaggaca catctggagg aaatggcctt ctttttaaaa 300

<210> 163
 <211> 300
 <212> DNA

WO 99/33982

PCT/US98/27610

<213> Homo sapiens

<400> 163

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ggagggcaaa	aaggctoggg	tgatggccac	cattgggggtg	acccgaggct	tgggagacca	120
cagccttaag	gtctgcagtt	ccaccctgcc	catcaagccc	tttctctcct	gcttccctga	180
ggtagcagtg	tatgacctga	cacaatatga	gcactgccca	gatgatgtgc	tagtcctggg	240
aacagatggc	ctgtggggtg	tcactactga	ctgtgaggtg	tctgccactg	tggacagggg	300

<210> 164

<211> 300

<212> DNA

<213> Homo sapiens

<400> 164

aaaatttata	ngtaatgaca	aatgacttat	cagtggttcat	catctgaaag	ctaagtgggt	60
cgttcaatca	ctttttcaaa	gttgatagta	gattgcattgg	tttcatgttt	cctcatattg	120
gtttattaat	tctatttaat	caaggaaaat	aacttcagat	tccataaagt	ttcagtttat	180
ttttagttta	ctactagggtg	agatggacaca	ttacatactt	ttactatcaa	atattctttt	240
agcagcttcc	catagtacca	aatgatttga	ttccctactc	tcatttttta	aagcatataa	300

<210> 165

<211> 300

<212> DNA

<213> Homo sapiens

<400> 165

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gtggacacca	gatcctggga	gctcctgggt	agcaagtggag	atctctggga	tgtcagtgag	120
gctggttgaa	gaccagaggt	aaactgcaga	ggtcaccacc	cccaccatgt	cccaggtgat	180
gtccagccca	ctgctggcag	gaggccatgc	tgtoagcttg	gogccttggt	atgagccag	240
gaggaccctg	caccacgcac	ccagccccag	cctgcccacc	cagtggttctt	actacaccac	300

<210> 166

<211> 300

<212> DNA

<213> Homo sapiens

<400> 166

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ttcttttgtt	ttttaacaaa	cttttatttg	tgacttactt	tcttgagaag	tgttcttaat	120
gaattgcata	aaatagtggt	agcagcttat	ttcttaagta	ctttattatt	tgtgctttac	180
catttcaggt	tcttatcttt	aacccttatt	tactcagttt	tccatctgaa	tgatcctatc	240
tctaaattaa	ggattttaata	aatgctgcaa	attgtccact	ttgcaaatgt	tccaaaaagt	300

<210> 167

<211> 300

<212> DNA

<213> Homo sapiens

<400> 167

WO 99/33982

PCT/US98/27610

gcgagatgaa	gctacactgt	gaggtggagg	tgatcagccg	gcacttgccc	gccttggggc	60
ttaggaacgc	gggcaagggc	gtccgagccg	tgttgagcct	ctgtcagcag	acttccagga	120
gtcagcgcgc	gggtccgagcc	ttcctgctca	tctccaccct	gaaggacaa	cgccgggaccc	180
gctatgagct	aagggagAAC	attgagcaat	tcttcaccaa	attttagat	gaggggaaag	240
cctactgtcg	gttaaaggag	cctcctgtgg	atatctgtct	aagtaaggat	tccatatggc	300

<210> 168

<211> 300

<212> DNA

<213> Homo sapiens

<400> 168

gtctgggagc	cctacgcttt	cggataaaaa	atggcagaat	gaaagaatta	tgagtggAAC	60
tagagaatag	gaaagacatg	aaccaacgcc	caaaatgaga	aagaaggaca	tataaagaaa	120
aagacaaata	caagtgaAAA	aaatatacta	atggattaac	gtccctgtcg	agtgcacattt	180
tctgactatg	gaaatgatat	tagacaaaaa	gcaacttcaa	gtgggtttct	tatttgagtt	240
caaaatgggt	cataacgcag	catagataac	ttgaacatg	aacagcgcat	ttggcccagg	300

<210> 169

<211> 296

<212> DNA

<213> Homo sapiens

<400> 169

gagatctctg	ggatgtcagt	gaggtctggt	gaagaccaga	ggtaaaactgc	ggaggtcacc	60
accctcacca	tgtcccagggt	gatgtccagc	ccactgctgg	caggaggcca	tgctgtcagc	120
ttggcgccct	gtgatgagcc	caggaggacc	ctgcaccacc	caccagcccc	cagcctgcc	180
ccccagtgtt	cttactacac	cacggaaggc	tggggagccc	aagccctgat	ggccccgtgc	240
ccctnacttg	gnccccctgg	tanttcancn	agncccnacg	gtngagncca	aagcca	296

<210> 170

<211> 300

<212> DNA

<213> Homo sapiens

<400> 170

gggtgttgga	gcagattgta	gttgatccac	agcaaagagc	atcaccaaag	ccattccagg	60
aggaactaga	tccaccactt	cctctgctgg	gcatgtctcc	aaaatggttg	tggtctccag	120
agaggactcc	aaaagaaagc	acaaaaacta	gacagtggga	gggcataccc	aaaagccctg	180
agtttctgaa	aaaatatgga	aagtttctat	ggtgaaatag	gaagttaagt	tgcttaggaa	240
gaaaaaagtg	gtaatgattc	aaggaaacat	aatcacacac	ggttttagtt	ttaatggaca	300

<210> 171

<211> 300

<212> DNA

<213> Homo sapiens

<400> 171

atggaggcac	cagcaggtag	tggccccctgt	aagcaggggc	agagtcgggg	caaagagcag	60
gagtgaagca	gccaaagagc	agaggaccag	gctggagcca	gtgggcacgc	aggagcctgc	120
ctgggaaaaag	ccgggggggca	aggctggcat	gggaatgaac	acctgctggt	gacacctctc	180

WO 99/33982

PCT/US98/27610

tgagcttcag	tcccttaac	tagaaaaata	gaacaggccc	ggtgcggtgg	ctcatacctg	240
taatcccagc	actttgggag	gctgaggcgg	gtggatcatg	aggtcaggag	atcaagacca	300

<210> 172
 <211> 300
 <212> DNA
 <213> Homo sapiens

<400> 172						
ggcggaggag	cagaagctca	agctggagcg	gctcatgaag	aacccggaca	aagcagttcc	60
aattccagag	aaaatgagtg	aatgggcacc	tgcacctccc	ccagaatttg	tcogagatgt	120
catgggttca	agtgtggggg	ccggcagtg	agagtccac	gtgtacagac	atctgcgccc	180
gagagaatat	cagcgacagg	actacatgga	tgccatggct	gagaagcaaa	aattgcatgc	240
agagtttcag	aaaagactgg	aaaagaataa	aattgtctga	gaggagcaga	ccgcaaagcg	300

<210> 173
 <211> 300
 <212> DNA
 <213> Homo sapiens

<400> 173						
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agttctgtca	agcacacttc	tgttctctta	gaacttagaa	gtgtttctaa	gagaacagaa	120
gtaataagag	aaacagttac	gtgtggaatt	caacatcttt	ggttggaacg	catggccttt	180
ttttttcttg	ttttgataga	aatggaatta	agcaaaagta	gtttttgtct	tttctgttgt	240
cttcaaattt	caggccatct	atttttaatt	taatcccggt	caagtaactg	atgtgtatac	300

<210> 174
 <211> 300
 <212> DNA
 <213> Homo sapiens

<400> 174						
attatttcca	aagcagccta	cagtagaaaa	tagtcattat	ggcagcagct	tctgatgttt	60
ttgtttggta	ggttttctga	tttcaatata	tagaatcata	ttcatagagt	atcttctttt	120
aacgaattgc	acaaagtacc	cattttaaatt	ttacatgcac	agtttcattg	cacettttct	180
aggcctatgc	atagttaata	aggttataat	ctactcaaca	tggaaaaatg	agcctatttg	240
caaacacaca	agtaattaaa	gtaccaattc	tctcttagtt	tcttttttta	tagttggttt	300

<210> 175
 <211> 300
 <212> DNA
 <213> Homo sapiens

<400> 175						
tgganactct	ttantatgga	agggtgaattt	cctgtcaaca	tagtccagga	caaagcagtt	60
ccaattccag	agaaaatgag	tgaatgggca	cctcgacctc	cccagaattt	tgctcgagat	120
gtcatgggtt	caagtgtctg	ggccggcagt	ggagagttcc	acgtgtacag	acatctgcgc	180
cggagagaat	atcagcgaca	ggactacatg	gatgccatgg	ctgagaagca	aaaattggat	240
gcagagtttc	agaaaagact	ggaaaagaat	aaaattgctg	cgaggagaca	gaccgcgaag	300

WO 99/33982

PCT/US98/27610

<210> 176
 <211> 300
 <212> DNA
 <213> Homo sapiens

<400> 176
 tataaaccttt attttattctt cttctggggt agagttacat gacaagaaat tgaattaatt 60
 caataaaaatt ttagtctggg ttgcttaggt ttttactgct cccattcttg cttttactaa 120
 tttatccaag attagatgtg attactattt aataataatt tagtcctcac acttacaacac 180
 cacttacaat accagcatgc ttctatcact gtaattctat tcaattctca ggcccatgag 240
 gcatgccagc cagacgacca gacagcattt atagagaggg cactcaatc cagccacaaa 300

<210> 177
 <211> 300
 <212> DNA
 <213> Homo sapiens

<400> 177
 gactggagaa gtcagaagta gaaaagcaga ttgctaggag agacaggatg acagattttg 60
 gtcagaaaaat gggatattgg agtttaaagt atcaaataca gaatagttcc agatgttcag 120
 agatccagca tgggattagg tactgaaatg gattagaact aaaagtcact agaatttaga 180
 aatggagaac catggagatg gatgcaatga cttgttgctt gattgaaaaa taaatttaata 240
 ataataaagg accatgagac tagcctgtta taggggggtat ctccatgann nttgtttttc 300

<210> 178
 <211> 300
 <212> DNA
 <213> Homo sapiens

<400> 178
 tcctgggtgc aaacactata aacctttgac cagctgagct gtgactgctg tcacatatct 60
 gagtctctgtg tgcacagtaa tatcctgggt caggtaaaat ccagggtcttc aagttttaag 120
 gattttttga agaatttcggg cttctttaag acgatccatg cccaaatcca caagcttggt 180
 gacagtggat tacagtttgt gtggcaaaat ccaagttggt acactgtgct ttaaaaaaaa 240
 tcctatctgc atgtattggt aacttagaga ccatgagatc tatttatcag gaccaggaag 300

<210> 179
 <211> 300
 <212> DNA
 <213> Homo sapiens

<400> 179
 ctcatgcctg taatcccagc actttgggaa gcagaggtgg caggatcatt ccagcccagg 60
 agttcaagac cagcctgggc aacacagtga gtgagaccct gtctctattt aagaaaaaat 120
 aattaaagaa ttttattaaa aaagaagaat caggaaacca agtccaacc aactaaacct 180
 caaatgaacc agccctaac acagatgagg ggaattggga ctgataagct ctgtgctgtg 240
 tccatggccc gtcattttac aaggctgcag ctttggtaaat gtggctattt ttatgtttgt 300

<210> 180
 <211> 300
 <212> DNA

WO 99/33982

PCT/US98/27610

<213> Homo sapiens

<400> 180

gtgatctgcc	tgccttggtc	tcccaaagtg	ctgggaatac	agggcatgagc	caccgcactc	60
ggccaggagc	tagttttatc	agcatcctgc	tccactgcct	tcctctagtg	cagcctggaa	120
gacatggcag	cgggttagctc	ctggggctga	gccagaagca	tcactgcagt	gaaagtctct	180
gcttacctgt	ctggctcagc	ttggggcaagg	gctggggccat	atgtgctcag	ggacgtgctt	240
ctcttctaag	gcaggaggat	agaagaggac	caagaaggga	gggagctgcc	ctgtggtgca	300

<210> 181

<211> 300

<212> DNA

<213> Homo sapiens

<400> 181

cccatccggg	gatcttcccc	caccgcctct	cacagatcca	gccccagccc	cttgcttccc	60
agggcatctc	tcagcagcac	ctgcaggatg	cgggcacccg	ggagtggagc	cctcagaacg	120
catccatgta	ggagtctctc	tcacatcccag	cttccctgaa	cgacgcggct	ttggctcaga	180
tgaacagtga	ggtgcagctc	ctgactgaaa	aggccctgat	ggagcttggg	tgtgggaagc	240
cgcttcogca	ccccggggcg	tggttcgtct	ccttggatgg	caggtccaac	gctcacgtta	300

<210> 182

<211> 300

<212> DNA

<213> Homo sapiens

<400> 182

tttgcagtgt	tgtcagaaac	aaataataaa	gccccaaaag	attaactagt	tgaaaaaact	60
ggcaaaatct	gtatacgtgg	aaatttacca	ggacagagac	tgaagaataa	agaaaaatgag	120
tttcattgcc	agatcatgaa	atccaaagaa	actttaaaga	agatgagtgt	tgtaaatgga	180
actgaaggga	gggaagagct	gccttcgcct	gggacaaaaga	aaacatgtgt	atacacatgg	240
gtcaagcagt	gctggtctgt	ggctgcctgt	ccagaggaat	ggaaatatcc	ctgtctctta	300

<210> 183

<211> 300

<212> DNA

<213> Homo sapiens

<400> 183

cggaccctac	ggagcgtaac	ctggatctcc	gcaggcctgg	cggaggccgg	ccacctggag	60
gggcattgct	tggttcgctg	ggtagcagag	gagcttgaga	atgttcgcat	cttaccacat	120
acagtctctt	acatggctga	ttcagaaact	ttcattagtc	tggaaagatg	tctgtggccat	180
aagagagcaa	ggaaaagaac	tagtatggaa	acagcacttg	cccttgagaa	gctattcccc	240
aaacaatgcc	aagtccctgg	gattgtgacc	ccaggaattg	tagtgactcc	aatgggatca	300

<210> 184

<211> 300

<212> DNA

<213> Homo sapiens

<400> 184

WO 99/33982

PCT/US98/27610

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ctgttttgca gatgaggaaa ctgagggtaca gaattcttag ggaacttacc caaaatggct      60
tttctgcact ctgccctttg gtattgtccc atgtgaattg tttaaaactt atgtgtatag      120
tgccatgagt aggtgatctc agaaacagaa ctcaactttg ttgtttggct ttaaaattag      180
gaacttttct tcactctggc ttcatctccc tgcacctccc cagctttcta gtcatgcaag      240
ccacatgtct ccaagtgagg gggttcattgg aaagcagcca cagagccacc ccctggctgg      300

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<210> 185
 <211> 260
 <212> DNA
 <213> Homo sapiens

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<400> 185
attatagaga ttaatctcct ttgctcgaag tctattttaa tattagtcac atctaaaaca      60
tactttttaca gcaacatcta gactgggtgt tgaccaaaaa actggggcac atagctgaca      120
cataaaatta accatcacaa ccatgttcta ggcaactgtc ctcaactgctc gagaagacac      180
cgttatgttt attagggttt ttgagtttta tccacagctt ttggtttatct gcaaccatgt      240
ctcccacctt taacatagtt                                     260

```

<210> 186
 <211> 300
 <212> DNA
 <213> Homo sapiens

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<400> 186
gataaaactct tcagtgcaga atattagaaa aagtttagtta tacatttgag gaaaaactata      60
aaagtaccaa taatgagtag gaaatcactt ctgcagtatt ttggagcat ttcccttaag      120
catgacataa aagccaaagg tcacaaggga aaaaactgat agatttgtct gtgatattga      180
gagatgtatg cacataaca tacaacagtc atagtaagac accgttagac aaaaggtgat      240
gtatgaaaaa gaggcaaaac aacaagaaga aaagattgaa aaaatgagag ctgaagacgg      300

```

<210> 187
 <211> 300
 <212> DNA
 <213> Homo sapiens

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<400> 187
aaaaagtaaa gcttttctat agcacaaatc ccttgcatgt tttgatgtta ctgatattcg      60
taaaatgaat attttttgtt ttgttttgtt ttattttttt gagacaagtc ttgcttttgt      120
gccagggtg gagtgcaatg gcatgatctt ggctcactgc aacccctgcc ttgcgagttc      180
aagtgtattc tctgctcag cctcctgagt agctgggatt acaggcgctc accaccacac      240
ccagtaattt tctgtatttt tagtagacac aggggtttac catgttggcc angctggtct      300

```

<210> 188
 <211> 300
 <212> DNA
 <213> Homo sapiens

```

<400> 188
gagcattcct cctttgttaa cgaagcaaca ttacacaag atggacatta cattattagt      60
gcatgctctg atggcactgt aaagatctgg aatatgaaga ccacagaatg ttcaaatacc      120
tttaaatccc tgggcagcac cgcagggaca gatattaccg tcaacagtgt gattctactt      180

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WO 99/33982

PCT/US98/27610

cctaaaaacc	ctgagcactt	tgtggtgtgc	aacagatcaa	acacgggtgt	catcatgaac	240
atgcaggggg	agattgtcag	aagcttcagt	tctggtaaaa	gagaagggtg	ggactttgtt	300

<210> 189
<211> 300
<212> DNA
<213> Homo sapiens

<400> 189						
ctaataatcca	gaatctacaa	agaactcaac	aagaaaaaaa	ccaacccccc	aagcggggcaa	60
aggacatgaa	cagacatttc	ccaaaagaag	acatacaagc	aacctaaaaa	aatctaaaaa	120
aattttttaa	aagaaaaaat	gcttgacaga	gttttgatag	tacttagtaa	aaagtataat	180
ctagtggctt	tttgtttgtt	tgtttttgtt	ttgtttttaa	gaaatagtct	ctgttcccca	240
agctggagta	cagtggcgca	atcttggctc	actgcaacct	cgaaactctg	ggctcaagcg	300

<210> 190
<211> 300
<212> DNA
<213> Homo sapiens

<400> 190						
aaccactatg	gaggcatgat	tgggtggccc	tacactgcct	gtgcacgcct	gcccaatgat	60
cgtagcagtc	agcgacgtga	cgtgggctgg	cgcttgtttg	atgacagcac	agtgacaacg	120
gtagacgaga	gccagggtgt	gacgcgttat	gcctatgtac	tcttctacgc	ccggcggaac	180
tctcctgtgg	agaggccccc	caggggcaggt	cactctgagc	accacccaga	cctaggccct	240
gcagctgagg	ctgctgccag	ccagggaacta	ggcctctggc	agggcccccga	ggtggcccca	300

<210> 191
<211> 300
<212> DNA
<213> Homo sapiens

<400> 191						
goggogctga	ccggcgccgc	cccacacccg	ctcttctctt	tcttttgcgc	ggactccctt	60
tcctgcctcc	aagacctggt	gtctcccact	gtgagcccag	ctgtcccaca	ggcagtcctc	120
atggacctag	actcaacttc	cccttgcttc	tatgaacctc	tgctggggcc	agcccctgtc	180
ccagctccgc	acctgcactt	cctgctggac	tcaggcctcc	agctccctgc	ccagcgagcg	240
gcctcagcca	ccgcctcccc	tttcttcocg	gcctctgctg	caggcagctt	tgcaagaagc	300

<210> 192
<211> 300
<212> DNA
<213> Homo sapiens

<400> 192						
gacagaccgt	tgagaggacg	tggaggcccg	agagggggta	tgcgcggcag	aggcagaggt	60
ggccctggga	acagagtttt	tgacgctttt	gaccagagag	gaaagcgaga	atttgaaaaga	120
tatggtggga	atgacaaaat	agcagtcaga	actgaagaca	acatgggtgg	atgtggagtt	180
cgaacctggg	gatcgggtaa	agataccagt	gatgtggagc	caactgcacc	gatggaggaa	240
cccacagtgg	tggaggagtc	ccagggccacc	ccggaagagg	agtcctccagc	caaagttcct	300

WO 99/33982

PCT/US98/27610

<210> 193
 <211> 300
 <212> DNA
 <213> Homo sapiens

<400> 193
 ctcaagaaag gagaagtttt ttgtatgaa attggaggaa atattgggga acgctgcctt 60
 gatgatgaca cttacatgaa ggatttatat cagcttaacc caaatgctga gtgggttata 120
 aagtcaaagc cattgtagaa gacttaacaa gctgcagata accatgtgga cttctgtcat 180
 aattctgtct gagtcaagag tgtaataaaa agaaatggca ggactcatat tattcagttg 240
 taccacaagta tttaaaaatg actctcttaa gacctaaaaa gtcatagatt tgtgtgctgt 300

<210> 194
 <211> 300
 <212> DNA
 <213> Homo sapiens

<400> 194
 cagaagctta gtcatatctt aaaaatgatca aatatcaaga aaaaattctga gctgcataac 60
 ttgtataaag taattttcag tgattttttt catggttatg ataaaaaga tggattagca 120
 gaaactttta ccttgaatca agatttaatt tttcttttag ctcatcttaa ggatattcga 180
 acatagggag caaacgatgg tgtggctgcc tcagtgcctg atttttaacg gttttgaaga 240
 gaatagttac attctctctc ctagtaagaa ctaataataa cattaacaga aatgaattcc 300

<210> 195
 <211> 300
 <212> DNA
 <213> Homo sapiens

<400> 195
 ctctactaaa aatacaaaaa ttagctgggc gtggtggcac acacctgtaa tccagttac 60
 ttgggaggct gaggcacaag aatcgcttga acccgggagg cggaggttgc agttagccaa 120
 gatcgccctg ctgcaactca gcttgggcaa cagagggaga ctctgtctcc aaaaaacaaa 180
 acaaaaaact ttagtgaagg ttccctggga cttttgatat tttaaaaatt gatcttatga 240
 ctaagtagat aaattcattg ccataatgag gctagctccc agataaacag cgtattttct 300

<210> 196
 <211> 300
 <212> DNA
 <213> Homo sapiens

<400> 196
 tggatactga caatggtggc aggcatttca agccttttaa attagtactt ttgtgctgtc 60
 tgcttattaa aattttgtta attttagcaa agaccaattg ttgtgataaa ctggtgtttt 120
 ttggatgctt caagcacacg ttaaccaatt ttttaattcc ccttttgggt cctcccatgt 180
 ttctaaaaa ggaactttcat attattaaaa cctcaaaaga tgatccaccc aggatgaaca 240
 aagatcacca aggggaaaga aaacattttt tatctttaca gaaacatgt taagattata 300

<210> 197
 <211> 300
 <212> DNA

PCT/US98/27610

<400> 201

WO 99/33982

PCT/US98/27610

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tctctactttg ggtccgcgcg aagcccactc acgtgtgac tgtgttgccc ctctcggttg 60
tcccaggcga tccagccatg cccctgccc ctctgcccag atgcttcagg ggcccggctt 120
ttcagcgttg ccttcaccag cggccgtcag cgcacactca gggatgtagc taacaccact 180
ccgcccagtgc ttctagttag aagagctgag cgtgcctggg aggcccgggg gcaccggaaa 240
agggctctct caagtctga aaagagaatc tgccaccaga tcgaatttcg acccctgagc 300
```

<210> 202
<211> 281
<212> DNA
<213> Homo sapiens

```
<400> 202
ggccatggga cagttgcaac agcagttaaa tggactgtca gtcagtgaag gtcattatcc 60
tgaagatat ttgagcaaaa gtaacctgaa cccagatgcc aaggagttaa ttccaggaga 120
gaagtactga gccagaaaa ctttgaggaa gacttgtctg tcccacatc tggggatagt 180
aatgcccata atggtggagc tgaagagggg gatggggcgg gcgaggggtg cacagcgga 240
aggggagtgg tgggtccacg atactgtgac tctgagtaac t 281
```

<210> 203
<211> 300
<212> DNA
<213> Homo sapiens

```
<400> 203
gccctcagcc acccccatcc ctgccccttc tgagactcac agcaccctt tcttctctct 60
cctcccacct cctccctcag cccctcatte tcttgggaa tctgcagagg gctctgggac 120
tcaactgccg atgtgaaatc caggcgtcag ctgtttccta ggcaagggca ggaaagtgtg 180
ctccagccct tgctccactc atgcctgggg gcctggggct gagtggatc cctacctggc 240
ctcccctcgg cctctggggc tccagcgctg ggttgttga tctgagagaga gagaggagct 300
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<210> 204
<211> 269
<212> DNA
<213> Homo sapiens

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<400> 204
gcggactctc aggcagaaaa gagccaaacc tttttgggaa aatcagagga agtaactgga 60
aagcaagaag atcatgttat aaaggagaaa ggggtcccag tcagcgggca ggaggcgaaa 120
gagccagaga gttgggatgg gggcaggctg ggggcattgg gaagagcgag gagcagggaa 180
gaggagaatg agcatcatgg gccttcaatg cccgctctga tagcccctga ggaactctct 240
cactgtgacc tgtttcagga gcctcatat 269
```

<210> 205
<211> 300
<212> DNA
<213> Homo sapiens

```
<400> 205
ttctactttg ggtccgcgcg aagcccactc acgtgtgac tgtgttgccc ctctcggttg 60
tcccaggcga tccagccatg cccctgccc ctctgcccag atgcttcagg ggcccggctt 120
ttcagcgttg ccttcaccag cggccgtcag cgcacactca gggatgtagc taacaccact 180
```

WO 99/33982

PCT/US98/27610

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ccgccagtgc tttagtagg aagagctgag gctgcctggg aggccccggg cgaccgaaa 240
aggctctctc caagtctcga aaagagaatc tgccaccaga tcgaatttcg acccttgagc 300
```

<210> 206
 <211> 300
 <212> DNA
 <213> Homo sapiens

```
<400> 206
gggattacag gcatgaccca cgcgcgccag cctgtaattt cttatacttg gtatttttga 60
cttgatttat gcttctgata cgctataaatt atttatgtac atgttatttt tcttcaatag 120
actgtgaact cttcgaatgt aggactccta gagctagata ctcaattatt ttattattaaa 180
ttgaatgact tgaaactaca gatcctttat ttaaaactcc caaattttctg ctttatctag 240
gcaactcttt aaattctttg atctcatgta gattccaag gctgaaataa ttgagatttt 300
```

<210> 207
 <211> 300
 <212> DNA
 <213> Homo sapiens

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<400> 207
tcctgaagct cggggggcctg caggtcctga ggaccctggt gcaggagaag ggcacggagg 60
tgctcgcgtg gcgcgtgtgc acactgctct acgacctggt caccgagaag atgttcgccg 120
aggagagcgt tgagctgacc caggagatgt ccccagagaa gctgcagcag tatcggccag 180
tacacctcct gccaggcctg tgggaacagg gctggtgcga gatcacgccc cactcctcgt 240
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<210> 208
 <211> 300
 <212> DNA
 <213> Homo sapiens

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<400> 208
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attaaaaacg tttagtagcc ttcagttttg tgaaaatagt ttccagcaca gaaactgact 120
tctttagaca aagtttttaca caatgatggt gtttgcctct aggatataca cttttaaaga 180
actcactgtc ccagtgttgg tcaatgatgg cctttagtaa attggagctg cttaatcata 240
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<210> 209
 <211> 300
 <212> DNA
 <213> Homo sapiens

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<400> 209
gagacagcag cccccaggga atgaagctga tgccagagtc agaccggagg aggaagagga 60
gccactgatg gagatgcggc tccgggatgc gctcagcac ttctatgcag cactgctgca 120
gctgggcctc aagtaacctc ttatccttgg tattcagatt ctggcctgtg ccttggcagc 180
ctccatcctt cgcaggcatc tcattgtctg gaaagtgtt gccctaagt tcatatttga 240
ggctgtgggc ttcatgtga gcagcgtggg acttctcctg ggcatagctt tgggtgatgag 300
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WO 99/33982

PCT/US98/27610

<210> 210
 <211> 300
 <212> DNA
 <213> Homo sapiens

<400> 210
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 acgtcatggc cctgctataa ggtagtagtt ctagaagact gtttatctaa taattcagac 120
 taaagctatt tatattgctg tgacaccacg tggaaaactt ttataattcc attcttatttc 180
 tgaatgtatat gttttatttt ctctgcttcc ttaagaacta aaaaccaaag ttatttaagt 240
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<210> 211
 <211> 300
 <212> DNA
 <213> Homo sapiens

<400> 211
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 cttgtgggaag aacagaatgc agagaagcgc aggaagccgc aagagatgag gcggcagcag 120
 aagctaaagc agggcaaacct ggtggagcag tacagagaac aagctggat gactattggcc 180
 aatttggaga aagagctcca ggagatggag gcacggtaag agaaggagtt tggagatgga 240
 tcgatgaaaa atgaaatgga agaactgaa ctcaaagatg aggaggatgg taaagacagt 300

<210> 212
 <211> 300
 <212> DNA
 <213> Homo sapiens

<400> 212
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 tgtcggccct gctgcgagcc cacaagcccc tccacatggc tgccctcctc ctgcttccct 120
 ggctcatggt gctcacaggc agagtgtctc tggcacagtt tgccttggcc ttcgtgaagg 180
 aacgtgtgct ggcggtgtgc ctgctgtgcg ggcgtgggct gctcttccat gggatgctgc 240
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<210> 213
 <211> 300
 <212> DNA
 <213> Homo sapiens

<400> 213
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 taattcatac aatgaatgta tttggaatac ttacatatta taaaataaac tatacctctt 120
 caagaggat cctgttctgt aagatcagat gttttatttg cagggtcaata taatactgcc 180
 agagacagaa aataccccct tatcagtcct ttagtgcctc ttctgttttg tggcatgggt 240
 agaaaaccca tgctgaaaag attgtacttt gtgatcccaa tcagagggag gagctaatct 300

<210> 214
 <211> 300
 <212> DNA

WO 99/33982

PCT/US98/27610

<213> Homo sapiens

<400> 214

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atgcagagagc	aaacccccag	aagaggagaa	acgaaagaaa	cgaggaaagaa	agaggggaaga	180
caaagaggac	aagtcagaga	aagcagtgaa	agattatgaa	caggaaaagt	cttgggcaaga	240
ctcagagaga	ttaaaaaggaa	tcttagaacg	tggaaaagaa	gaattggctg	aagctgagat	300

<210> 215

<211> 300

<212> DNA

<213> Homo sapiens

<400> 215

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ttagtatttg	tgccagaaaa	caagtcctaa	agtattttgt	tttattttga	ccatccactt	180
gtgccttaac	gtatcctgtg	tcatgtccaa	tcagtgtgtg	acaatggcat	ctttgaacag	240
tgtgatgaga	ataggaatgt	ggtgttttaa	agcagtgttg	catttttaac	agtaactcac	300

<210> 216

<211> 300

<212> DNA

<213> Homo sapiens

<400> 216

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ctgcgtgctg	ccacgcatac	gagcgattgc	tctgtgaaga	gttgtacact	gaacattttc	180
aggggaggct	gtttaccacg	gcaatgtcct	caaaccaagc	tgtgcggggg	agtcctggaa	240
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<210> 217

<211> 300

<212> DNA

<213> Homo sapiens

<400> 217

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ttttgcagtg	ataaaaaatgt	cctaaaaattg	actgtagcga	tgggtcacaca	actctgaata	180
tgcttaagac	cattgaatta	cacactttac	gttggtggaat	tgtatggtat	gtaaaattata	240
gttcaataac	atagttacaa	aagataatca	aaagcatgaa	agcactgttg	atgtggtttg	300

<210> 218

<211> 300

<212> DNA

<213> Homo sapiens

<400> 218

WO 99/33982

PCT/US98/27610

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agtccaaggt	ggccaactac	tgccggcagg	tgacgagct	gcttggaag	gttcaggaga	180
actcggcata	catctgcagc	cgccgccaga	gggtttcctt	cggcgtctct	gagcagcagg	240
cagtgggaagc	ctgggagaag	ctgacccggg	aagaggggac	acccttgacc	ttgtactaca	300

<210> 219

<211> 300

<212> DNA

<213> Homo sapiens

<400> 219

caactagaga	agattggaca	gcaggtcgac	agagaacctg	gagatgtagc	tactccacca	60
cgggaagagaa	agaagatagt	ggttgaagcc	ccagcaaaag	aaatggagaa	ggtagaggag	120
atgccacata	aaccacagaa	agatgaagat	ctgacacagg	attatgaaga	atggaaaaga	180
aaaattttgg	aaaatgctgc	cagtgtctca	aaggctacag	cagagtgtat	tcagcttcca	240
aactgggtata	cattccaac	tgatagtaca	ttgccatctc	caggaagact	tgacgggttt	300

<210> 220

<211> 260

<212> DNA

<213> Homo sapiens

<400> 220

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tactgtcttt	gtgatttggt	ttcaacatat	atagtctttt	ctccggagtt	accttaggtc	180
agtgccagct	glttcagccc	ctggaaaagg	catgggctgc	cactgaggtt	ggtcacaggg	240
ctctcagctc	atggtgggag					260

<210> 221

<211> 300

<212> DNA

<213> Homo sapiens

<400> 221

gggttccatc	ccttccaccc	aggaaatgga	ggcacgactt	gcagcgttgc	aggcgagagt	60
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gcagacacag	gatctgttaa	cgcagctggc	agctgaggtg	gctatcgatg	aaagctggaa	180
aggaggaggc	ccagtgaccc	tccaggacta	tcgcctccca	gacagtgatg	acgacagga	240
tgaggagaca	gccatccaaa	gagtcctgca	gcagctcact	gaagaagctg	ccctgatgat	300

<210> 222

<211> 300

<212> DNA

<213> Homo sapiens

<400> 222

gcggtgaccc	acgtgtcctg	catgattgcc	ctactgctgt	ggagacctcg	tgctgaccat	60
ctggcagttg	tcttcgtatt	ctctggcctg	tgggcgctgg	cagatgcctg	ctggcagaca	120
caaaacaatg	ctctctaocg	cgttctgttt	gagaagagca	aggaagctgc	cttcgccaat	180

WO 99/33982

PCT/US98/27610

taccgcctgt	gggaggccct	gggcttcgtc	attgccttcg	ggtacagcac	gtttttgtgc	240
gtgcacgtca	agctctacat	tctgctgggg	gtcctgagcc	tgaccatggt	ggccgtatgg	300

<210> 223

<211> 300

<212> DNA

<213> Homo sapiens

<400> 223

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agatgggtcga	ggtgatgaga	aacggaaaaa	taaaggcact	tcggacagct	cctctggcaa	120
tgtatctgaa	gggggaaagc	cctcctgaca	gccaggagga	ctctttccag	ggaagacaga	180
aatcaaaagc	caaagctgcc	actccaagaa	aagatgggtcc	caaacgttct	gtactgtcca	240
agtcagtacc	tggtgtacaag	ccaaaaggcca	ttccaaatgc	tatatgtgga	atttgtctga	300

<210> 224

<211> 300

<212> DNA

<213> Homo sapiens

<400> 224

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ccatggagct	tacgccccgg	gagtcctcca	gtatccttgg	agtggctgag	tccgggtgggc	120
ataccactga	gatcctgagg	ctgcttgagg	gcttgacca	tgccctactca	cctagacatt	180
atgctcattg	tgacactgat	gaaatgagtg	ccaataaaat	aaattctttt	gaactatgat	240
cgagctgata	gagaccctag	taacatgtat	accaaatact	acattcaccg	aattccaaga	300

<210> 225

<211> 300

<212> DNA

<213> Homo sapiens

<400> 225

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tggttgtagt	tctctgtttt	cttctctggaa	attcctcgtg	gacctcgaga	tctttaccct	120
aaaatagttc	tgttgaattc	caccctggca	atgtaaaattg	atagctttatc	ttcacagatg	180
ccagacaagt	gacaaactac	catacgtcct	ctgctcacct	gagacaaatg	catgtctgat	240
tgttctctct	gccctatttg	ttatgtgaaa	atgcagattc	actgagccag	actaaggcat	300

<210> 226

<211> 300

<212> DNA

<213> Homo sapiens

<400> 226

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gtcaggagac	ctggattctt	gtgcccgcct	tggtttttac	agtcctgccta	actctatgca	120
gtcacttcct	gccagctcgt	ttccttacct	acaagaggga	gagacactcc	ctggccagcc	180
tagttctcag	ggtgaacgaa	aggctcattat	cactgcaccc	tctagtcatc	tgctctctcg	240
ctaattaaaca	catcttgagc	acctgcgatg	ttccaggaaac	aggagatggc	agcgtgcaag	300

WO 99/33982

PCT/US98/27610

<210> 227

<211> 300

<212> DNA

<213> Homo sapiens

<400> 227

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atgtctcata	ctaaccaaga	agcaagaaaa	gccccatgca	ttcatttttc	acttggagtg	120
acaatgggag	aggtcaggaa	tcaagttcac	tttcaagatc	taagggagtc	cactatctgt	180
gcaattgtat	ttggcttttt	tttgcaactgt	ttcaatgctg	gtaattgaaa	ccatttttaat	240
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<210> 228

<211> 300

<212> DNA

<213> Homo sapiens

<400> 228

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atttccttga	cacacctagg	atgttcttgc	ctcttagcct	gcctaccttt	ctctcatcat	120
ttgggctctc	gcgaggatct	catctcctca	gagaagcctt	ctgtgaccat	gctatctaaa	180
atactccagc	acttccagta	ccctttatcc	cattactctg	ctttttcaga	aacatttggtg	240
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<210> 229

<211> 300

<212> DNA

<213> Homo sapiens

<400> 229

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agaaaaaagc	atatcttcat	tgacataaca	gaagtgcgat	ggcccagctc	tgatacagat	120
ggatccatga	tatatatgga	gagtgccatt	gtgaagataa	catctttaga	tggtcatgca	180
tacctctgcc	tgcccagatc	tcagcatgaa	tttacagtac	attttttggt	taaatgttagc	240
cagaagtcag	atcatctcgc	agtgttgtca	gaaacaaata	ataaagcccc	aaaagataaa	300

<210> 230

<211> 300

<212> DNA

<213> Homo sapiens

<400> 230

acttcttggt	tgcttttttt	ataaggaat	gttgagaggt	tacatcattg	ctaattgtaga	60
aatgttaagt	gaaaaaatat	acagtttggt	aaaataaact	agattctaca	tttattttgtg	120
ggtttttttt	ccctctcttc	tttccacagc	acttttgata	tcaagcaagt	ggcttctctt	180
ttgagatatt	aaaaaaaaaa	agaaaaggaa	aaaagtaaat	gannnnnnnn	nnnnnaacct	240
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<210> 231

<211> 300

<212> DNA

WO 99/33982

PCT/US98/27610

<213> Homo sapiens

<400> 231

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ccactaatta	gactttttan	ntaaaaaang	taggggggtt	taaaactact	ttcctactac	120
caaaaatca	naaagtatct	agctttctaa	atnggggaaag	caagcaatgt	tataaaaaacn	180
ctgaaggaa	ctctttcttc	gggacctttt	gttaaactcg	gttnaagctg	taaaccttat	240
ttaaaataaa	atttaccaca	naacaggaaa	tanaacctgg	ggaanaactcn	aaatacnctt	300

<210> 232

<211> 300

<212> DNA

<213> Homo sapiens

<400> 232

ggaagccaag	gctcggagct	gcaggtcccc	cgcatctct	ctctgtcccg	gcagcccagg	60
atggcctggg	gcccccacct	gctgcagcag	gagccccaag	gagtgtctagc	tgagggtgggt	120
tgatgggggtg	gtctctcatgg	acagtgaggt	gtgcaagggt	gcactgaggg	tggtggggagg	180
ggatcacctg	ggttccaggc	catccttgct	gagcatcttt	gcagcctgctt	tccggtggga	240
gcagaaaaag	ccagaccctg	ctgagttaga	ggctgctggg	atccactgtt	tccacacagc	300

<210> 233

<211> 300

<212> DNA

<213> Homo sapiens

<400> 233

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gcctggagct	gcaggtcccc	cgcatctct	ctctgtcccg	gcagcccagg	atggcctgggt	120
gccccacact	gctgcagcag	gagccccaag	gagtgtctagc	tgagggtgggt	tgctgggggtg	180
gtcctcatgg	acagtgaggt	gtgcaagggt	gcactgaggg	tggtggggagg	ggatcacctg	240
ggttccaggc	catccttgct	gagcatcttt	gagcctgcct	tccggtggga	gcagaaaaag	300

<210> 234

<211> 300

<212> DNA

<213> Homo sapiens

<400> 234

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gtttgccttt	ctttaactct	ggctccttct	ctctctctctg	tttgtgtatc	tgtttaattc	120
attgagttag	gaggacaggc	agaactgtgt	ctgccaaagg	ccggatgtac	tcttttccct	180
gctcttgggt	ttttgtcac	ttttatatgt	aaggtattag	tacaaacct	aaggagagaa	240
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<210> 235

<211> 300

<212> DNA

<213> Homo sapiens

<400> 235

WO 99/33982

PCT/US98/27610

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ggagtgcctt	ccttttgctc	ctctctagct	gggagtgaag	ggtgggagtg	tgtgtgccca	180
ggtgggggtg	tctcctggct	gggaaggagg	gaaagggagg	gagagttttg	cgggggttgg	240
cagtggagag	cagctggag	aggagatggc	taatagctgt	ttaatggaaa	cctgctgggc	300

<210> 236

<211> 300

<212> DNA

<213> Homo sapiens

<400> 236

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gatgccttct	aaatgtctat	ctccagtatg	gtcttttccct	ttaagctcta	gatccattga	120
cacctcacc	atctctaaaa	ggcatttcaa	actgaacaca	tctgatacag	aaattttcat	180
ttccttccca	acttttgcca	cgccagcctg	ctctcctctc	acgttttcca	cttagtatat	240
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<210> 237

<211> 300

<212> DNA

<213> Homo sapiens

<400> 237

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ataggcagca	tgctcatccat	ggaagtgaac	gtggacatgc	tgagcagatg	ggacctgatg	120
gacatatcgg	accaggaggc	cctggacgtc	ttctctgaact	ctggaggaga	agagaacact	180
gtgtctgtcc	ccgccttagg	gocctgaatcc	agtacctgtc	agaatgagat	tacctccag	240
gttccaaatc	cctcagaatt	aagagccaag	accactttct	cttctccacc	ctgcaccgac	300

<210> 238

<211> 300

<212> DNA

<213> Homo sapiens

<400> 238

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agtgaaactg	gacatgctgg	agcagatgga	cctgatggac	atatcggacc	aggaggccct	120
ggacgtcttc	ctgaactctg	gaggagaaga	gaacactgtg	ctgtcccccg	ccttagggcc	180
tgaatccagt	acctgtcaga	atgagattac	cctccagggt	ccaaatcccc	cagaattaag	240
agccaaagcca	ccttcttctt	cctccactcg	caccgactcg	gccaccgggg	acatcagtaga	300

<210> 239

<211> 300

<212> DNA

<213> Homo sapiens

<400> 239

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aagaactggg	ggaaacacagg	aacctagggg	aggaggggag	cgctgggcat	cctcaggctg	120
gcggccaagg	cctgccctcg	gaggcactag	aggagggcat	ctgtctgtgg	gagccacagag	180

WO 99/33982

PCT/US98/27610

gctgcagggg ggaggaggag ggaggtatct ggtgtgagcg ttgcccctgc gacatttggg 240
accacacagg tgggcttctt tattccctga caaagcctct gtttccagct cttccgcctt 300

<210> 240
<211> 274
<212> DNA
<213> Homo sapiens

<400> 240
catgagtgat attttggctt gggtttcttc ttaagatttt agtttgtctg aattaaggaa 60
aaatgttttt aatatacatt cttattttgt cccacccctc cagaaataag ctggaaatct 120
taactttttt ggggggtcttt ttgggtgttt taatgggccc agaactgtgg tttaaatttt 180
tatgtatgta ttttcttttt tgtggagtat aaatttaaaa actggatttg ggaactaaaa 240
tactctcag gttgatgtat tcatgaaagt tttta 274

<210> 241
<211> 300
<212> DNA
<213> Homo sapiens

<400> 241
ctgttgctcg ccaagctcag ggcccattta tcatgcattt tcccatcctt gtctccccc 60
actgtccctt acctgagtc caatttctgc aaagccaaag ggattgtcct aagccaatgt 120
tgatttatca ctcttctgc tcaaaagccc ccaagatcac ctatcaatca cctacttgag 180
tgcaagcttt gactctgtca cctgacattc aagtccctct ctgcccccat gccagtctta 240
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<210> 242
<211> 300
<212> DNA
<213> Homo sapiens

<400> 242
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tccagcagga taccaaaggt ttggtggact tcagagatgt ggcccttgca ctgacagctc 180
tggaatggggg caggagcctg gaagagctaa ctgctctggc ctttgagga atgggggggtg 240
gcggtgggtg ggggtgctta gtggctatgc tcacccgcct ccaggaggcc tattttggtta 300

<210> 243
<211> 300
<212> DNA
<213> Homo sapiens

<400> 243
caagatctgg aggaatgcag agaggaaact gatacagatg aatatgaaga aacaaaaaag 60
gaaactctgg agcaactaag tgaatttaat gattcactaa agaaaattat gtctggaaat 120
atgactttgg tagatgaact aagtggaaat cagctggcta ttccaggcagc tatcagccag 180
gcctttaaaa cccagaggt catcagattg ttgcaaaaga aacaaccagg tcagcttcgg 240
acaaggttag cagagatgga tagagatctg atggtaggaa agctggaaag agacctgtac 300

WQ 99/33982

PCT/US98/27610

<210> 244
 <211> 300
 <212> DNA
 <213> Homo sapiens

<400> 244
 agtaaaatttt ttatgcatat ttatttgc aaataaatga aaacagtttc aatctaggag 60
 gatcttggat gcatctatgc cttgagaaat gaatggtttg atgtaaatgc atggtagcaa 120
 gaataaataa ttatgttaat tcatataata tgttatatat agttttaaag aaaattctat 180
 cactgtcttc ctatgggtag ggcataaatg tccagttctt tcagggatta agagggtagg 240
 gctctgaagt aatccttgtt tgtctgaatg ttattaattt attcaaccaa gacttaattg 300

<210> 245
 <211> 300
 <212> DNA
 <213> Homo sapiens

<400> 245
 tagacattaga aaacatacac taagaatatg gtattataat cttacgggac cactgtcaaa 60
 tacgcggtct gtctttgaaa agttgtaatg cgcgcgatga ctataaatac cttagctggtt 120
 agcatttaca ttcttgcga gggagtttga aatttact atagaaataa cttttaggttt 180
 taggttagagt taaagaggta aagcacatgt tgccacaacc caggaaagta tttttaagaa 240
 agattggatt ttctacctt tagagatcta aaaaaattt aatataaaaa atcatattgt 300

<210> 246
 <211> 300
 <212> DNA
 <213> Homo sapiens

<400> 246
 tggaatatgt gctgtgaagg gagaaaggga gagaaaactc ttctgaggat catttgtctt 60
 ggtagtatat taaaaccaac cagctgaacc ttacaggcta caagagaacc cgggtcggta 120
 atgtcttttt aagaataatt tttaattgct tataacaagc atattttgtg gcatttgaac 180
 tatatttact gctccaatat cgttatattt ccaaaggatt ttgtatcttt ttgaaaatgt 240
 ttacatcctc agatgatcca cagaattcac ttatgtgtg atctcccag agtttccatc 300

<210> 247
 <211> 300
 <212> DNA
 <213> Homo sapiens

<400> 247
 gtgttgctca gtgagcagac cagactccag aaggacatca gtgaatgggc aaataggttt 60
 gaagactgtc agaagaaga ggagacaaaa caacaacaac ttcaagtgtc tcagaatgag 120
 attgaagaaa acaagctcaa actagtccaa caagaaatga tgtttcagag actccagaaa 180
 gagagagaaa gtgaagaag caaattagaa accagttaag tgacactgaa ggagcaacag 240
 caccagctgg aaaaggaatt aacagaccag aaaagcaaac tggaccaagt gctctcaaa 300

<210> 248
 <211> 300
 <212> DNA

WO 99/33982

PCT/US98/27610

<213> Homo sapiens

<400> 248

gagaggatca	cttgagctta	ggagttcaaa	tccagcctga	gccaacataa	caagactttg	60
tctctaaaca	aaacagttat	tgtttaaaga	atctgaaatc	tctcatctta	atccaggtag	120
caatgaatcg	agcccaagtt	tgtttgatat	ccagttccaa	gtctggagag	aggcatcttt	180
atcttattaa	agtatcgaga	gacaaaatat	cagacagcaa	tgaccaagag	tcagcaaat	240
gtgatgcata	agggctatca	aagggaggct	ttttacagag	aactaaggaa	gagaaggagg	300

<210> 249

<211> 300

<212> DNA

<213> Homo sapiens

<400> 249

ctagcctggg	caatatagta	cgaccctgtc	tttactaaaa	atgcaaaaa	taaccacgta	60
tggtggctca	cacctgtagt	cctggctact	gaggaggctg	atgcaggaga	atcatttgaa	120
cccaggaggt	caaggctgca	gtgagctatg	attgcaccac	tgcaatccag	cctggacaac	180
acagtggagc	cctgcctcac	aaaaattata	ttctgatttt	ctgagttcat	cacacattg	240
tcacaaatgga	ttttctatgc	tctccaagt	tacagatagt	tccacgcaca	cacagaactc	300

<210> 250

<211> 300

<212> DNA

<213> Homo sapiens

<400> 250

aggaaggtgg	aggggcagga	acaggacgga	caggccccgg	gctctggcac	atcctgggga	60
acaagggacc	acaaggacgg	gggcagtcct	cagacttccc	ctgggcgctt	gaccccaggc	120
cttgacgggg	agagagccag	ggcctccctc	aggctcttgt	tcatgtctgt	ttccctgccg	180
tggacacctt	ttcccgtctc	cagattctct	aaatcctgcc	ccatctccca	gatcttgttc	240
atgtccaagc	ttttccagga	agtcttagca	gctcccacac	cgcagagctc	gagatgtctc	300

<210> 251

<211> 300

<212> DNA

<213> Homo sapiens

<400> 251

gaaggcagaa	gtgtaaatga	acatacagaa	gaaggagaaa	gcctgctgtg	tttggcttgt	60
tcaggcaggt	attatgaatt	agcacagta	ttgcttgcta	tgcatgctaa	tgttgaagat	120
cgagggaata	aaggagacat	aactcccctg	atggcagctt	ccagtggagg	ttacttagat	180
attgtgaaat	tattacttct	tcatgatgct	gatgtcaact	ccagttctgc	aacaggaaac	240
actgcgctaa	cttatgcatg	tgctggagga	tttgttgaca	ttgttaaagt	gtcctctaat	300

<210> 252

<211> 300

<212> DNA

<213> Homo sapiens

<400> 252

WO 99/33982

PCT/US98/27610

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gcactctctct ctccactggaa agagaactgt tctcctttct ctttctctctg cctattaagc      60
ctctgtctctt aaactcctca tgtgtgtctg tgtcctaaat ttctctggca tggcaggaca      120
aaccccggtt atttaccaca gacaacaaaa ccgcttctact atgatgtatg catgtctgcaa      180
aggaagagac agaattcttg tctatcacc agctggagtg cagtggcacc attgcagctt      240
actgcagcct caaactcctg gctcaaggga tccttcagct tcagctcctt ggttaactag      300

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<210> 253
 <211> 300
 <212> DNA
 <213> Homo sapiens

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<400> 253
gtctgatgca ggagaattgc taaaacccag gaggggagagg ttacattgag ccgagattgc      60
gccactgcac tctagcctgg gogacagagc aagaactcgt ctcgaaagaa agaaagagaa      120
aggaatttcc ccagggaagt acctcggtt atttcataaa caggtactga aggaagcaga      180
ggcatgtgga ggacttcccc acctcgtgca gctatttggg ccgtggcctc tgaattttct      240
tatttcagag tcaccccttt gatgaccttg gcagtgaaact gcagtcctct gtttaggcct      300

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<210> 254
 <211> 300
 <212> DNA
 <213> Homo sapiens

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<400> 254
atgttacaga catgaaatat gaacagaatg ctaaaagaac ataaaaaat aagagctcct      60
taagatttat aaataaattg tgatgttaaa gtaatagcac cattggacga agctagggaa      120
tcaacacttg acagaaagat acatatTTTT ttatacaaaa ctacatatat ttgagcaatc      180
aagttagtag catagagaat tttcttttta tggaaagtact ctaataagta aagggctgat      240
agaatttatc cagcattttc tagctcctgg ggaattatgc attgggcctc catggctgct      300

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<210> 255
 <211> 300
 <212> DNA
 <213> Homo sapiens

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<400> 255
gctgcctgtg gcatagccac tgcgtgactg ttttggttgt tnttaagaaa ctctatgaag      60
aggggtgtca ttctgggtct ggggtggttg ccaatttttc accagaaagg gagccacccc      120
ttgcaaccac ttctgtctcc gttagccccc cctctgcctt cctccaagcc aaagcgtggc      180
ctgggttttg tcttcccat tagttttcct cttttacctt tccttttctg ctaattttat      240
taaatagtt gctgtataat ttattttcat aaactataaa aaaatactaa atgggttaaaa      300

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<210> 256
 <211> 300
 <212> DNA
 <213> Homo sapiens

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<400> 256
acagtctcgg gtttcattat ttgctgtttt tgatggacat ggaggaattc gagcctcaaa      60
atttgcctga cagaatttgc atcaaaaactt aatcagaaaa ttctctaaag gagatgtaat      120
cagtgtagag aaaaccggtg agagatgcct ttggacactt ttcaagcata ctgatgaaga      180

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WO 99/33982

PCT/US98/27610

gttccttaaa	caagcttcca	gccagaagcc	tgcttgga	gatgggtcca	ctgccacgtg	240
tgttctggct	gtagacaaca	ttctttatat	tgccaacctc	ggagatagtc	gggcaatctt	300

<210> 257

<211> 300

<212> DNA

<213> Homo sapiens

<400> 257

atagaactag	gcactgattt	gtttatat	atctctgctc	agacacatga	tgtttcattg	60
atctgtggct	ttttatagtt	taaaataa	tcctggaaa	tcctagtc	tatctcttta	120
acgcgtccct	ctcttccatt	ctctttgttc	tcctctcctc	gaactcctgt	tagtcatttg	180
atcctccata	tcctctgaata	ttttttgatt	tcctttatta	tttattctct	gtctctgcta	240
cattttcat	tgagtataaa	tgggatgtga	cagtgggaaa	tcatttagtg	cttagaaatt	300

<210> 258

<211> 285

<212> DNA

<213> Homo sapiens

<400> 258

tactctatta	tattgtgcat	gctcctgatt	tagctgctct	tgggcatcatt	ggtcgcagtg	60
gaaccttgaa	atgcctctgg	ctagatttat	gctcaaatca	ttctcagtta	gccttttagt	120
gcctcttcaa	aggttttttt	ttgtatgttt	tcattctcta	ataaaagctt	aggatttaatt	180
agaaaagatc	tgatatggtt	atgtttcccc	ttgtgtacgc	tgacctcatt	catacgtttt	240
tcctagtcga	gtgggtctaaa	cgctttcaag	agcccagctc	cttgg		285

<210> 259

<211> 300

<212> DNA

<213> Homo sapiens

<400> 259

gccttctctg	gcctcaccaa	ttaggtcaaa	tgttcccttag	aatgtgttgt	ggggcatggt	60
ctctccctgt	gaggacctgt	ccagctggac	ctccgccttc	ctgcgactgt	attggtgtct	120
ttccctctca	agcctatag	ctctgcaagg	gcaggagacc	tgtagtattt	tgccatctgt	180
atgtctctca	gccccagca	cagcgctctg	tgtccagtga	gagctcagca	aatactttgt	240
gagtttaagg	caggcggtctg	ggtagatgga	tcgtctgcct	agacagggca	gttattcgtc	300

<210> 260

<211> 300

<212> DNA

<213> Homo sapiens

<400> 260

gaaaaggagg	ccgcgcagcg	cctaogggag	tcogcgogga	gcagccggta	ccggcaacca	60
cgggcagctc	tcaggggaatc	tcogtcgtga	ggccagaggc	tcagtcctcc	gcgagtcag	120
atgcctgtcc	agcctccaag	caaagacaca	gaagagatgg	aagcagaggg	tgattctgct	180
gctgagatga	atggggaggga	ggaagagagt	gaggaggagc	ggagcggcag	ccagacagag	240
tcagaagagg	agagctccga	gatggatgat	gaggactatg	agcgagccg	cagcgagtgt	300

WO 99/33982

PCT/US98/27610

<210> 261
 <211> 300
 <212> DNA
 <213> Homo sapiens

<400> 261
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 ttctactatg tccaagacta ggactgggtt ataaagattt tcttttgtga aggaaaaataa 120
 aagaaaattt gccactactg catttacttt actattgtaa acttaagatt cattccttag 180
 tctttggaat ttgtatgtct caaaaccaga tgagtgtgaag tgctgaattt gcaaaaataaa 240
 gctaagaatg cttaactctg cactttaagt tctactctga ccaaattgaa gatgagcaga 300

<210> 262
 <211> 300
 <212> DNA
 <213> Homo sapiens

<400> 262
 ttttttaaga gataaggtct tgctatgtta tctaggtctgg cctaaacttc tgggctgaag 60
 tgatcctcct gtgtagctgg gactacaagc atgtgccacc aatgcctggc ttctcacact 120
 gttttgtaac atagatatgt gaagatgtgt attatagaat tgtttgtaat actgtagtgt 180
 tgtaggcaat gtgactgtct ataggggaagt ggacagggtta ttgttggtaa atactcatgg 240
 aaaaagggtca agcagttaaa agcaatcaat tatggtcacc cagcaatgca gataaatctt 300

<210> 263
 <211> 300
 <212> DNA
 <213> Homo sapiens

<400> 263
 agaacagggg gaagagagga agagggagct gcaggtgccca gaagagaaca gggcggactc 60
 tcaggagcga aagagtcaaa cctttttggg aaaatcagag gaagtaactg gaaagcaaga 120
 agatcatggt ataaaggaga aaggggtccc agtcagcggg caggaggcga aagagccaga 180
 gagttgggat gggggcaggc tgggggcagt ggggaagagc aggagcaggg aagaggagaa 240
 tgagcatcat gggccttcaa tgcccgctct gatagccctt gaggactctc ctcactgtga 300

<210> 264
 <211> 300
 <212> DNA
 <213> Homo sapiens

<400> 264
 ttaaaaggtag ttttagaagg aagtacaaat tggctttcat ctgcaaaaca atcgtttttt 60
 attcattat cttaatttgc ttgtcactc ataaaaagga aaccatacct gagttgtaga 120
 caatgaggaa acacttgagg cttctgctgt gtgttctttt gttattgttg ttattgttgt 180
 tactcaagtaa ctggaatatt gttaaattgt ttgtaagacg tagagtttat ctcaagctgt 240
 taaaaatggt aatgtacaaa tgtgaataga cacttatcta tataatatg gtaagttttg 300

<210> 265
 <211> 300
 <212> DNA

WO 99/33982

PCT/US98/27610

<213> Homo sapiens

<400> 265

caggaaagtc	ttcctagaggt	taatttttaa	gctgattgtt	ttagaattag	tagaagcttg	60
ccagatggaa	aagtcaggc	aaagtgtaac	atgaatggga	aaggccacag	tctagaaatg	120
gcagatgtgt	ttcctagttt	gtttgtttgt	ttgtttgtac	ctgccttgtt	ccaggaaagga	180
ttcaatgtgt	tttatattcc	agtcctttaa	tgctggaaag	gctgagatga	gactgaaaga	240
tgggcaggaa	gtatatcatc	acaagctttg	tgtttgatgt	taatgtgtat	gatttttata	300

<210> 266

<211> 300

<212> DNA

<213> Homo sapiens

<400> 266

tgtgccacca	caccagctc	attattatta	ttattattat	tattattttg	agacgaagtt	60
tcactcttat	ccccaggtc	ggagtgaat	ggtgcgatac	tggctcactg	caacctctgc	120
ctctggggtt	caagcggttc	tcttccttg	gcaggacact	gtagtgtcag	ctactcgaag	180
gctgaggtg	gagaatcgct	tgaacctggg	ggcgggagat	tgcaatgggt	tggtctcggc	240
tcactgcact	cgagctctgc	gacagagcaa	gactctgtct	caaaaaaaaa	aaaaaaaaan	300

<210> 267

<211> 300

<212> DNA

<213> Homo sapiens

<400> 267

atataactct	ggaggtcagg	acataggaga	tattgattca	ggacttgcca	gagtatggtc	60
ttgggggtgt	ccctgatatt	acaacacagg	atcttagtgg	ctaggtgatg	aggccatggc	120
aaatgtagat	ggaccaagat	caatttgcct	ttctagatga	ggttttctag	gtgaaatggt	180
tttgaacta	ttttgtagcc	tagtataatt	tataaaagta	gagagaaact	ataaatataa	240
atttggaag	ggttagctaa	aaggagaaaa	cagcagaatc	ttcatatata	tagaaatgga	300

<210> 268

<211> 300

<212> DNA

<213> Homo sapiens

<400> 268

cctaacttatt	ggatgttggc	tctttggtgt	catggagatg	gctttactgt	aggtttgtgt	60
gtgtgtgcatt	acttttcatt	gggattgaac	tgagaaataa	caaacaagct	ttaaagtggga	120
aattaaaaaa	aagaagttaac	ctatgttagat	ccaaacttaa	aatgtgagaa	attattgaaa	180
tttcaatttc	tacaaacttg	aaattagcct	gctaattgtg	aagtgttttt	aataatgctg	240
acaaatgtca	gttaactgtt	caaaggagtg	tatggttcta	ggtatttgcc	tactgttacc	300

<210> 269

<211> 300

<212> DNA

<213> Homo sapiens

<400> 269

WO 99/33982

PCT/US98/27610

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tgttgcatta	cttttcattg	ggattgaact	gagaaataac	aaacaagctt	taagtgggaa	120
attaaaaaaa	agaagtaacc	tatgtagatc	caaaactaaa	atgtgagaaa	ttattgaaat	180
ttcattttct	acaaacttga	aattagcctg	ctaattgtaa	agttgtttta	ataatgctga	240
caaatgtcag	ttacgttttg	aaaggagtgt	atgggtctag	gtatttgccct	actgttaacc	300

<210> 270

<211> 300

<212> DNA

<213> Homo sapiens

<400> 270

cctacttatt	ggatgttggc	tctttggtgt	catggagatg	gctttactgt	aggtttgttg	60
tgttgcatta	cttttcattg	ggattgaact	gagaaataac	aaacaagctt	taagtgggaa	120
attaaaaaaa	agaagtaacc	tatgtagatc	caaaactaaa	atgtgagaaa	ttattgaaat	180
ttcattttct	acaaacttga	aattagcctg	ctaattgtaa	agttgtttta	ataatgctga	240
caaatgtcag	ttacgttttg	aaaggagtgt	atgggtctag	gtatttgccct	actgttaacc	300

<210> 271

<211> 300

<212> DNA

<213> Homo sapiens

<400> 271

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ttacttaggy	tcaaattaa	ttgtaaaatc	cccccgga	ttttgtatgt	aagtcacagt	120
gaattgtatt	tgaagaaga	actggggagc	ccacctctgg	tatttttttt	atgtccctca	180
tatggacaaa	taaacctctg	gtattaaatg	aattttcttt	tgggggattc	tatatattcg	240
ggatttcaac	caccaacctc	tctgtttttt	cccgctgaaa	tgttgggtga	tggaaatcagg	300

<210> 272

<211> 300

<212> DNA

<213> Homo sapiens

<400> 272

gaacgcttcc	attttatacc	tgtgtctagt	tagtttctgc	ctatctatcc	aagaagcttt	60
tatcaagggt	ccaccatgtg	ccagccactg	aagtagatat	aaatacaagg	atgtgtaagg	120
tatggatgat	ggtatacgaa	ctgtcatctt	actggatttg	tccgctctgt	taaagatacg	180
gttccgaaaa	cttttttaag	ccctagagag	ggctttaagg	caatgtatga	tcatatatag	240
aggctacaac	ctgttcatat	ctttctattt	aacagaactg	tgcacctggg	cacaagggtg	300

<210> 273

<211> 300

<212> DNA

<213> Homo sapiens

<400> 273

gaatggcgtg	aaccggggag	gcagatgggc	ttaaagtggg	gagaccgggg	ttacagggcct	60
gactgcatac	ctaactcgct	gtgtgtccct	gggcaagtca	gtgcagtgcg	gtagcctctc	120
cgtctccgac	tgaggagcaa	agccctccgc	tcaagatcct	ccactacttc	acagggattt	180

WO 99/33982

PCT/US98/27610

gaaatagtgc agtcaacagc aaaagaaaag cgctatagaa atgctcgacg ctatcacttg 240
 gggccacgt ggaagtatca acgtataaat tggccacaggc agacagaagg atgcaggggga 300

<210> 274
 <211> 300
 <212> DNA
 <213> Homo sapiens

<400> 274
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 ccattggagaa caccaggagc cacagaccgc agaccacagg agcacacagg ggaggggcagc 120
 gggcggcggg ggcagggtgt ctgctgcctc gtttatggga ttgtctccgc gtctagcaca 180
 ctgctgcctg cagtgtctct gtcacctgca gtggctactc tgggcctacg ggcctaattc 240
 tggttggtcat gaaaatgtcc tgaggctact gtgacaattc tccacaagct gagtggctta 300

<210> 275
 <211> 300
 <212> DNA
 <213> Homo sapiens

<400> 275
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 aagaagaatc aggaacaacaa tctcaaccga actaaacctc aaatgaacca gcccttaaca 180
 cagatgaggg gatttgggac tgataagctc tgtgctgtgt ccatggcccg tcatattatc 240
 aggctgcagc tttgtaaatg tggctatatt tatgttgtgt atagtttcta tcatattatt 300

<210> 276
 <211> 300
 <212> DNA
 <213> Homo sapiens

<400> 276
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 acctogtgat ccgcctgcct cgaacctcca aagtgtctgg attacaggca tgagccacca 120
 tgcccagcca aagatcaatt ttttatatag acttcagccc tttgtaaaata ttgtaactgg 180
 ggagtagata gtagaaaaaa agtatagtta aaacatttgt tctacaaatt aaacttttaa 240
 aataaatta ctgtcaaaaa tagagtgtgt ttacacttaa ggaaaattag tgccattttg 300

<210> 277
 <211> 300
 <212> DNA
 <213> Homo sapiens

<400> 277
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 gattgtcga tcccacccct agactctctg attcagttag tttggggtaa ggccgaagac 120
 tgaatttttc acaagttttc cagtgtgtgt gatacttctg gtccaggaac ttagtgggag 180
 agaacgacta atctagacca ttctacttca cattctgagc ttcttgta cactgcacact 240
 gcatcctttt aacaatgcat tccctatcct attgcaatac tgacatctca tcaatatttt 300

WO 99/33982

PCT/US98/27610

<210> 278
 <211> 300
 <212> DNA
 <213> Homo sapiens

<400> 278
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 actggtatca agaatacagtc agcaaggagg ccctcaccag acgccagtgc catgtttctg 180
 gactttctcag cctccatatt catgaactaa gtttttggaa tccttaggct tccacgtgtg 240
 gaaagcctga gctaacctac tggaggatga gccatcacct ggagcagatt caggccatcc 300

<210> 279
 <211> 300
 <212> DNA
 <213> Homo sapiens

<400> 279
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 gatattatata attaaatggg cagataatag aaatctgtcc aagcaaaact ctggataaatt 120
 tttatgttgc ctattttttt gttttctgtg aactccaaga aaaatgagat accagttttg 180
 aacagatgta atattgtctga ttttaacagtt tagggatact ccccaagttc aataattttg 240
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<210> 280
 <211> 300
 <212> DNA
 <213> Homo sapiens

<400> 280
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 tcaggcactg gaactatctg taatactgga acctctgcga agtgccagggt ataaagtttt 120
 tcccaactgc aagcatccag agcttttggga aatttggaaa tcagagagat cagggcattg 180
 ttttgttctc ctgatgatga aagtgaanaag caagtactac tgaagtctgg aaatataaaa 240
 gctgtgcttg gcttgacaaa gaggaggcta gttagtagca gtgggacctc tctgatcaa 300

<210> 281
 <211> 300
 <212> DNA
 <213> Homo sapiens

<400> 281
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 actgttggtg aatcttaagt gattctccca cctcagcctc ccaaagtgtc gggattacag 120
 gcatgagcca ctacccttgg ctgtgatcaa gtatttagtc tgttgttaaa tgtttactaa 180
 atagctctga gttagagaaa tagcacccaa tctaaaataa ggtgaggtct agtcacttat 240
 ttaaatctac attttaagct atagtgtact attagtttaa actttaagac aggtaagtgt 300

<210> 282
 <211> 300
 <212> DNA

WO 99/33982

PCT/US98/27610

<213> Homo sapiens

<400> 282

gcaacctctcg	cctcctgggt	tcaagtgtatt	ctcctccctc	agcatcccaa	gtagctggga	60
ctacaggcac	gtgccaccac	acccagctaa	tttttgcatt	tttagtagag	gcagggtttc	120
atcatgttgg	ccagggtgggt	ctcaaaactcc	tgatctcaag	taatctgccc	actttggcct	180
cccaagtgct	tggcattaca	ggaatggagc	caaccgcgcc	agcctgattt	ctttttttag	240
gtcttgtcag	gaaagatatt	gattcttttg	attcgtgaac	atgggttttg	gtcgtcttta	300

<210> 283

<211> 300

<212> DNA

<213> Homo sapiens

<400> 283

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aatcactttg	ccagggaatt	caaggccgca	gtgagctatg	attgcaccac	tgcactccag	120
gcaacagagt	gagacccctg	cttaaaaaaa	gaaggggagaa	agtgtcagat	gggtgacagg	180
tctggggggg	aaatagagaa	tggggatcag	gagtggtgat	gggtgtattc	cctcaccaag	240
aggtgacatg	tgagcaggga	gctgggaggt	gagggtgtga	cccgtgtgga	aatcagggaa	300

<210> 284

<211> 300

<212> DNA

<213> Homo sapiens

<400> 284

ggtgtcctcc	ccagtcgcgc	gcgatttttg	tgtccaagcc	ccagagtccc	tctgagacca	60
acccccagcc	agcacagact	tctgccttc	ccagctcgga	agcgccctcg	agaagtgtct	120
aaaggagaca	gttgatagcc	aaacaacagt	tttggattca	ctgactgatt	atgaaagaag	180
cagtagactg	gtatcaagaa	tcagtcagggt	tttttggaatc	cttaggcctc	cacgtgtgga	240
aagcctgagc	taacctactg	gaggatgagc	catcacctgg	agcagattca	ggccatccta	300

<210> 285

<211> 300

<212> DNA

<213> Homo sapiens

<400> 285

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gtgatgggta	aagcgcagtc	gcctgctata	tattgtctat	ttttggtttt	tcacttacct	120
tttatattta	tgtcttttat	gtacaacagg	attataagta	gcttgagtcc	agtgaatata	180
ccatttcatt	ttgctatcct	tcactgcact	tagcttagag	gaaataatca	cagcttatta	240
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<210> 286

<211> 300

<212> DNA

<213> Homo sapiens

<400> 286

WQ 99/33982

PCT/US98/27610

agccaatgag	gcttttgctt	gccagcagtg	gacccaagcc	attcagcttt	acagcaaggc	60
tgtgcagagg	gcccctcaca	atgccatgct	ttatggaaac	cgagcagcag	cctacatgaa	120
gcgcaagtgg	gatgggtgacc	actatgatgc	cctgagggagc	tgccctcaagg	ccatctccct	180
aaacccatgc	cacttgaagg	cacactttcg	cctggcccgc	tgccctcttg	agctcaagta	240
tgtggctgaa	gcctggaggt	gcctggacga	cttcaaaagg	aaatttccgg	agcaggccca	300

<210> 287

<211> 300

<212> DNA

<213> Homo sapiens

<400> 287

gggtgcagaga	gtgaaactcg	tatctccaaa	caaacaaca	aaaagtcctt	aaacatatgt	60
gaacaaaaat	tttgtgatgg	aaggattcta	gttaatgagt	attgcatcaa	gatttacatc	120
tttcttacta	aggaagagag	ttaataaaaa	ttgttcttta	ttttacaggc	agttactgag	180
gctcttccca	gatctcagta	aacagccact	cagccttgaa	aatggagtgt	tgttgtttct	240
aaacataata	ttatgtcatt	tattaagtac	agtttcactta	aataacataa	gtagattttc	300

<210> 288

<211> 300

<212> DNA

<213> Homo sapiens

<400> 288

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tgatagaaat	ttgaagagca	attatatatt	tcaaaaagag	ttttgaataa	tgtaaagata	120
gattgcaaat	tgactatcaa	ttcttccctt	cccatcaaa	gagagagtcc	gtttatccag	180
catttgaatc	ttgattattc	aagtgacttg	cttaccacca	tgtaacataa	ataagaccaa	240
tacaagcaga	ggcttgccaa	gaacttgggt	tgtttctcaat	gcttagaaga	agaatgggtg	300

<210> 289

<211> 300

<212> DNA

<213> Homo sapiens

<400> 289

tgtccttctc	tgaaaattcag	cgatcttcat	gaataagcat	ttctctgatt	gtggnatatg	60
cccttaattt	tattttctaga	gtgacaaatt	tttggttttg	acagtttttt	tctagcttta	120
tagtttcttc	ttggggagag	aatatgtcaa	cctcactcca	tcatgctgaa	gtaaatcttc	180
attctctta	tttatctctc	aaaaatatcc	taaggattcc	cctggagccc	tgataagtaa	240
ttgcagtatc	tggtttctat	ggttggatga	ttcaggattc	cagggaataa	agttactttt	300

<210> 290

<211> 300

<212> DNA

<213> Homo sapiens

<400> 290

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tgggtagaga	tacatcatta	ctggcctcag	gggtttaccc	aaagaaagg	tattttttgag	120
caaataatgt	gatttctcgg	ctattttgtt	gggggcttaa	gatttttttt	tttcaaatgc	180

WO 99/33982

PCT/US98/27610

atTTTTagtc actaaaaatt aactgtcgta ccatctagaa ctatactgtc cagtaccata 240
gcctctagcc gtatgtagct atttgtatta agattaatgg aaatttttaa tccagttcct 300

<210> 291

<211> 300

<212> DNA

<213> Homo sapiens

<400> 291

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gaaatttata cttgaaatta aaagtctaca agggggagga ccttaaagct aagctaccag 120
taagacaatg aataattcag aagagaaacac tattctttta ctgactgagt gcccaagatg 180
ccaatttcca tgaagtcttg atttatatat atgtacacat gttatgcaca tacatgtttg 240
ttttctaaca gttattcttt aagcctttga gataatttta gacttacaga agagtgggaa 300

<210> 292

<211> 278

<212> DNA

<213> Homo sapiens

<400> 292

cccagaccta tggagtcaga cagtaggttt gaggccagc aatctatggt ttaacaagcc 60
atccaggtgt ttcgtatgca cagtgaattt ggggtaccac tggattagg tttggtatgg 120
caacttttct atcacttggt ttatgtagtt gtctgatcaa ttgtgaaaac ataagtaagt 180
ttggaaatgg aacagtaaaa taacgaaagc caactttttt tttttttttn nnnnnnnnnn 240
nntgntttnn ccccaggnr gnanngcagg gncccaat 278

<210> 293

<211> 297

<212> DNA

<213> Homo sapiens

<400> 293

ggaaggcagt gggaggagag gaccaagtct caaactccag aagccccacc tccctgagct 60
cagctctctt gccaaagccc ctacagcgca agtctctgtc cagagaaggc aacggcgaga 120
aacaaaacca acatcctggg ctgcttttct ctccccccac ttttttaaaag tttgggtgcc 180
aagtcacttg acaaaaccag accctaacaa tgatatcttg ttagaatttc tgggatcaaa 240
atataatttc aaaaataata tattttctga catcccccaa aaaaaaaaaa aaaaaaa 297

<210> 294

<211> 300

<212> DNA

<213> Homo sapiens

<400> 294

ggaacagtgt gagcaaaagg tctcaagtaa taggggtgtct gacttgttca tttttgaaag 60
tagaactaat aggatttctt attggaacgt aggggtgaag agaaaagagg agtcaaaaaag 120
agccacaaga tttttgtgtc cagcaattag aaggatagaa ttgacattta ctgagatttt 180
tgtttttgtt tttgagacgg agtttgccta ttgttgccca agctggcgctg caatggcgctg 240
atctcggttc agtgcacct ccaactccca gattcaacgg attctctctc ctcagcctcc 300

WO 99/33982

PCT/US98/27610

<210> 295

<211> 299

<212> DNA

<213> Homo sapiens

<400> 295

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actgtcacag	aatggctggg	ctgagaacgc	tgcccagggc	cctgcagctg	gcgggagnnn	120
nnnnnnnnnn	nnnnngtcn	tgctgcaaca	tntggttana	tngtatcctt	ccctanagnt	180
gctacnncct	nnatccccct	gtnaatatgt	tgagntnnct	tnsgnttcnn	gntnntccng	240
ntnnttgaca	cntatgnaa	ttntntngtc	tngtctctgt	ngatnncttn	nanctgoc	299

<210> 296

<211> 300

<212> DNA

<213> Homo sapiens

<400> 296

gcagaacctt	ttccccctta	ctcttgtcta	aaagttctgt	gtggcacaca	gagatgcgac	60
ctactcaat	tgacttagta	aaacatgcct	gaaaaatttt	ggtctaaaaa	ggaccacatac	120
ccagcaccca	tgaaataaaa	gattcatctg	taattgggat	tcaaaagggat	taaattcctt	180
tggtcactac	cataaatagc	actaaagtgt	tataacattt	tcatttacct	atttttagtt	240
ccttcatttt	aacttaataa	aaatcttgga	ttgatattct	tttttttttt	ttttgggaag	300

<210> 297

<211> 300

<212> DNA

<213> Homo sapiens

<400> 297

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tgtttctcac	tatgggaaac	catcccacc	caaaccttgat	gaccgcatta	tgtgctttta	120
tagaacatgg	cacttctcca	ggatagcatt	tattctgttt	tgtaaagtgtg	aatgtaatta	180
ccctacacac	agcatacaca	taactctcat	attctttgcc	ttgtcttgtg	aaggcaaggg	240
ccatgtctat	cttattctgc	attagattcc	caatcccaac	atagtcctgg	ggacagcacc	300

<210> 298

<211> 300

<212> DNA

<213> Homo sapiens

<400> 298

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ggtccagctct	ccagcctgca	ggcgtgcaca	ctgggggtgga	cgatgggtgg	ccccgcaggt	120
gtacacattt	gggtggcccc	ggccccctata	ccccagtggt	ctctttgatc	cagtccecgaa	180
acagaggggag	ccctgtgtac	acgcctccaa	agtggaagctg	ggaggtagaa	ggggaggagaca	240
ctggtggttc	tactgaccca	actggggggca	aaggtttgaa	gacacagcct	ccccgcgcag	300

<210> 299

<211> 300

<212> DNA

WO 99/33982

PCT/US98/27610

<213> Homo sapiens

<400> 299

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attagtgcac	gcaccccacc	ctcctctcag	tgtggtacgc	agatttgccc	atctcttgaa	120
tcaaagccag	caagacttct	ctgctgctgt	gatctgcaca	ccctccaacc	tgggcaggga	180
ctggggggat	cgagtgtgtg	ttagtgccca	tgtggcattg	tggcactgtt	gcccccatg	240
gcggcatggg	caagatgacc	ttcatttagc	ttcaagtctt	gttctcttgt	ctgtggtctg	300

<210> 300

<211> 300

<212> DNA

<213> Homo sapiens

<400> 300

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gtgcacccaa	gttcacgctc	gcctccttcg	ccatagtggc	agcatccgtc	gtcacagcgg	120
catcatcctt	catcatagcg	gcagcatccg	tcgtcacagc	ggcagcatcc	ttcgccacag	180
cggcagcatc	tgtcgtcaca	gcggcagcat	ccttcgccaa	agcggcagca	ctcttcgtca	240
tagcggcagc	atcctttgcc	atagcggcaa	ggtggaaacc	ctgtccatcc	actgaggcgt	300

<210> 301

<211> 300

<212> DNA

<213> Homo sapiens

<400> 301

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attttttaga	tcagtgcagc	ggtgtgtatt	tgggaagcatt	tcaaatgtgt	tacctcgtg	120
ttacttcctg	gggcacctgg	tggtatttgt	tggactagtc	aggattctcc	agagcagcag	180
aagcaatggg	atgtgtgtgc	atgtgtttgt	gcagagacag	aaagagagat	tttaaggaac	240
tggcttatgc	agttgtgggg	gctagcaagt	ctgaaatttg	caggggcggc	cagcaagctg	300

<210> 302

<211> 300

<212> DNA

<213> Homo sapiens

<400> 302

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ttcaacttga	actgtatcta	tctcccagaa	ttcccacatg	ttgtgggagg	gacccagggg	120
gaggtaactg	aatcatgggg	gctggctctt	cccgctcat	tctcgtgatg	gtgaagtctc	180
acagatctcg	atgggtttat	caggggtttc	cacttttgtt	tcttcatttt	ctcttgccac	240
cagcatgtaa	gaagtgcctt	tggtctccta	ccatgattct	gaggctctcc	tagccatggg	300

<210> 303

<211> 300

<212> DNA

<213> Homo sapiens

<400> 303

WQ 99/33982

PCT/US98/27610

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ggatagacat caggatgaag agaataaggca gttgaaaagt ccagaaaagg ggagtgtgct    120
tagagtgttt gaggaaacgc aaggaagcaa gcccttgttg aaacagattg agcaaggtag    180
aaagtggtta aagatgaagt taaagaggtta gctgagagcc agatcatgta aagccttggt    240
aaggactgac ttttatttta agagggttag gaagacattg gtagggtttg actctgctgt    300

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<210> 304
<211> 300
<212> DNA
<213> Homo sapiens

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<400> 304
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aggctcggct ggcaagagga gaaaagggaag aggaggaggga agaggaggaa gagatcaaca    120
tctatgcagt caccgaggag gagtccggacg aggaaggcag ccaggagaaa gggaggggacg    180
acagccagca gaagttcatt gctcacgtcc ctgttccttc gcagcaagag attgaggagg    240
cactggtgcg aaggaagaaa atggaactcc tccagaagta tgcaagccag accctgcagg    300

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<210> 305
<211> 300
<212> DNA
<213> Homo sapiens

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<400> 305
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aggcccatgc acacacacgt gcacacacat gcagagacat gcagacacgc aggcacacat    180
gcacacatgc aaagacacgc atgcaggcac acgcagacgc acacagagac acacatgcag    240
atacacatgc acacacacat acacacactg gccctgtttt ttctgtgttg tcactgggtg    300

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<210> 306
<211> 300
<212> DNA
<213> Homo sapiens

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<400> 306
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ggagtactac tacacgtgga aaaagatcat gcggtctgggg cggaaacacc ggacacgcct    120
ggcagaatcc atcagcagat gtgtgacaag tgaagaagaa gaagagttag aggaggaggga    180
ggagggagac ccggaagaa ataggaatcc cacaagaaga gaagggagtg aggtgcacga    240
gtccccggag ccaccacccg tccccgtcct ggctcccaag gagggggccgc cctgcaggcg    300

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<210> 307
<211> 300
<212> DNA
<213> Homo sapiens

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<400> 307
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tcagggtgtg ggaaatgggg accccgtctt ctggacacca gtatgccctg gtcccatgga    180

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WO 99/33982

PCT/US98/27610

accagatggc aaggatgag aggaggagga ggaggannnn nnnnnnnna ntggccctnt 240
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<210> 308
<211> 300
<212> DNA
<213> Homo sapiens

<400> 308
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ttaacctctc tgtgctctca atttctccct ctgggggatg ttaggagatg acaaatatac 120
acatgtaaag tgcttagaat agattggtac gtgtaaatat gagctaacgt cacatttgat 180
atttttttaa aaagaaaaaa tcattatgga gtctcagtcg tagagattct gattcattaa 240
ttctgcttct cggcaaggag cgatttgctg gtgtagacat tccgggtccg tgtaagggtt 300

<210> 309
<211> 300
<212> DNA
<213> Homo sapiens

<400> 309
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ctgcagcctt gacctccagg acaagtgtac tccacacctc gcctccggaa tagctgggac 120
tacagctcaa caacgcccct ctgaaagttag gactccttga aatgaacctt gttgggagta 180
aagtgtaacc ttcacctctc ctttccaggga ttctactcca ttcatacggc ctccactga 240
attaatggtt ctagcagcca catcactttg ttaccacatt gatctagtag taaagctctc 300

<210> 310
<211> 300
<212> DNA
<213> Homo sapiens

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tgtcaaacaa acaaacacac aaacaaaaaa acccatcac atctcatgag acttatattac 120
tatcatgaga gcagctcagg aaacacccac tcccggtgatt cagttacatc ccaactgggtc 180
tgtccccaaa attgtgggag ctacaattca agatgagggt tgggtgggga cacagccaaa 240
ccctatccc atgtaaaata atatctaatt tgtagagatt aaagaacaa gataactaaa 300

<210> 311
<211> 300
<212> DNA
<213> Homo sapiens

<400> 311
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attaaaggtt atgtttgggt cacacactgg ttcccatgta attgatgttg attcaggaaa 120
ctcttatgat atctacatac catctcatat tcagggaacat atcactctc atgctattgt 180
catcttgctt aaaacagatg gaatggaaat gcntgtttgc tatgaggatg anggggtgna 240
tgtaaacacc tatggcggga taacnaagga tgtggtgctc caatggggag aaatgccac 300

WO 99/33982

PCT/US98/27610

<210> 312
 <211> 275
 <212> DNA
 <213> Homo sapiens

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 tntnntattn ttctnttttt ttttnnttn aaatatnttg nnnntttttt ntantantta 180
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 natntttttt ttgttcttct ntnttattnn atctt 275

<210> 313
 <211> 300
 <212> DNA
 <213> Homo sapiens

<400> 313
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 aagaggaaaca cactggcaga agaacaatc gaaagacgct ggcaggccat tgatgggtga 180
 acgattcgga cgccaaggga aattcggcca aggacagtag gagatccogg ctgctgagca 240
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<210> 314
 <211> 300
 <212> DNA
 <213> Homo sapiens

<400> 314
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 agcccttacc aggaacagac ttggctagca ccttcactgt ggcactccag cctccagaat 180
 tgcaagaaaa tacatttcg tcgttgaaac caccacgtct gtggtatttt gttatggcag 240
 cccaggcaga ctaatactg aagcctgctc taatatagata aaataagaaa ttactacaga 300

<210> 315
 <211> 300
 <212> DNA
 <213> Homo sapiens

<400> 315
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 gacggccggg tagtgggctt ccacacagca tgggagccca gcaggccctt cctctgtgat 120
 atggctggat ttgcctgggc cctgcccttg ctgttagata agcccaatgc ccaatttgat 180
 tccacgcgtc cccggggcca cctggagagc agtcttctga gccacctgt ggatcccaag 240
 gacctggagc cagggtctgc caactgcact cgggtactgg tgtggcatac tcggacagag 300

<210> 316
 <211> 300
 <212> DNA

WO 99/33982

PCT/US98/27610

<213> Homo sapiens

<400> 316

gaaatgcctc	tatgtaggtg	aagtgttctc	tctgcatgca	acaggaaaaa	ttaatataat	60
attttcccca	caaaaagaaa	acttaacaga	ggcaagtgc	atttataaat	ttatatctaa	120
aggggaaatca	tgattataag	tccttcagcc	cttggaactc	aaattgaggg	gattaaaaag	180
aatttaaaat	aattttgaac	gaatttat	tccttcagc	ttttgagggc	attaaaaagg	240
cattaaatca	agacaaatca	tgtgcttgag	aaaaataaaa	ttaatgaaa	cacagcactt	300

<210> 317

<211> 295

<212> DNA

<213> Homo sapiens

<400> 317

acactgtccc	actccatcac	ccaggctgga	gtccagtggt	gtgatcatag	ctcgtctgcat	60
ctctccagttc	ctgggtttcaa	gccatccctc	ctgcctcagc	ctccccagta	gctggaacta	120
caggtgtgtg	ccatcacacc	tggttttaca	tttttctgtg	gggacttact	atgtttccca	180
ggcggcctc	aaactcctga	gctcaagtga	tcctctgctc	cagcctccag	agtatctggg	240
attacatatg	tcggctacgg	tgtctggccg	ttcacatctt	tggccactat	ttgct	295

<210> 318

<211> 261

<212> DNA

<213> Homo sapiens

<400> 318

cctgaatata	aagaggagga	ggaagaccaa	gacatacagg	gagaatcag	tcattcctgat	60
ggaaaggttg	aaaaggttta	taagaatggg	tgccgtgtta	tactgtttcc	caatggaact	120
cgaaagggaag	tgagtgcaac	tgggaagacc	atcacgtgca	ctttctttaa	tggtgaactg	180
aagcaggtca	tgccgaccca	agaannnnnn	nnnnnnnnnn	nnntngccnn	aacnnttcac	240
caaatncccc	gggggggctt	g				261

<210> 319

<211> 300

<212> DNA

<213> Homo sapiens

<400> 319

gggacacctg	cccaagaaag	cctgggtatt	gaccaaggtt	ccccccccc	tgagacagcc	60
tgagatatgg	cctcatggga	agggaaagac	ctgactgtcc	cccagcccca	cacctgtaaa	120
gggtcggtgc	tgaggaggaa	tagtgaagga	gggagggctc	tttgagttg	agataagagg	180
aaggctctctg	tctcctgctt	gtccctggta	atggaatgtc	tcggtgttaa	gctgaccatt	240
cccattcgtt	ctattctgag	ataggagaaa	accgacctgt	ggctggaggt	gagatatgct	300

<210> 320

<211> 289

<212> DNA

<213> Homo sapiens

<400> 320

WO 99/33982

PCT/US98/27610

caccttgccct	ggccaagggg	ctagacctcc	caggctaagc	ctcagattca	gtgcaggaca	60
caagctcatg	cccccgctctt	gccagtgaca	cttgaagcct	cccgacttcc	acagagtgtct	120
tcaggacaca	ttttgagtg	tattttcttt	tcttttttct	ttctttttct	ttttnnnnnn	180
nnnnnnntgt	tntgtnnccc	aggctgnann	gcaggggcct	gatntnggt	aantgnaacc	240
ttngcctccn	aggctaaagc	nattttttng	cctaancctc	naaagtacc		289

<210> 321

<211> 300

<212> DNA

<213> Homo sapiens

<400> 321

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aagagaacgc	accagagaga	gagagaggga	gcgtgatcac	agtctctacac	caagtgtttt	120
caacagcgat	gaagaacgat	acagatacag	ggaatatgca	gaaagaggtt	atgagcgtca	180
cagagcaagt	cgagaaaaag	aagaaacgaca	tagagaaaga	cgacacaggg	agaaagagga	240
aaccagacat	aagtccttctc	gaagtaatatg	tagacgtgcg	catgaaagtg	aagaaggaga	300

<210> 322

<211> 300

<212> DNA

<213> Homo sapiens

<400> 322

cgcccttttaa	ctgcagttct	gctctatttt	cttttctctc	tctggagctg	agagtcagag	60
ggcccttctc	ctcctctctt	cagcccccac	cactaagctg	atggattgat	aaatacctca	120
gcccctcgcc	ttctctcaac	cacctggcaa	gtcttcttag	gatctgatcc	cagttttctg	180
gaagcaatcc	taccccagcc	caagcttccc	aagagtcgag	ccttaactct	tctcacttct	240
cagtgctcaga	cgagaaatga	atcctggggt	tgactgtgtc	cattcggtt	attagcagct	300

<210> 323

<211> 300

<212> DNA

<213> Homo sapiens

<400> 323

agattatgag	catgtagaag	atgaaacttt	tctctcttct	ccacctccag	cctctccaga	60
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tgtaacctca	aagagacag	ttaaaagaaa	tatacccaag	ctggatgtct	agagattaat	180
ttcagagaga	ggacttccag	ccttaaggca	tgtatttgat	aaggcaaaat	tcaaaagtaa	240
aggctactgag	gctgaagact	tgaagatgct	aatcacagac	atggagcact	gggcacatag	300

<210> 324

<211> 300

<212> DNA

<213> Homo sapiens

<400> 324

gtctgagaag	tcaaggatcg	gggtgctggc	ctattcagtt	cctggtaagg	gctgtcttcc	60
tggcttgca	ttgaactact	tcttgctgtg	tcttcacaag	catgcoccca	tcttgctgcc	120
ataagaactc	cagaccccaa	actcagctca	tacacacacg	gaagagagaa	gcattctgaac	180

WO 99/33982

PCT/US98/27610

atcaagaaga gaagaagctg ctggacatca gaaactgtga aaggagagga gtttggtga 240
gctccagggg aagactgcct gcacattcta tccccttttc agttcccat cctgctgtca 300

<210> 325
<211> 283
<212> DNA
<213> Homo sapiens

<400> 325
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aacaagtgtg ccttctccta tgttttccag aaatgacttc agtatctgga gcatcctcag 120
aaaatgtatt ggaatggaac tatccaagat cacgatgcca gttatattta atgagcctct 180
gagcttcta cagcgcctaa ctgaatacat ggagcatact tacctcgctc acaaggccag 240
ttcactctct gatcctgtgg aaagatgcn ngtgtgtagc tgc 283

<210> 326
<211> 300
<212> DNA
<213> Homo sapiens

<400> 326
atgacatcct cattatccac actgcaaaag caaccatccc tatgatgggt tcattgtgga 60
tcattgacta gtgggtcaa agtttggag ttggtcagct gggcggttct tctgctccat 120
gtggctgcca gatggtaccc tgctggtggg cagctctggtc tagagggtcc atgatgctgt 180
tactcacatg cctggcatct tgacaggagc agctggaagg caaggttcag ctgggactgt 240
ccacagagct cctccctgtg gcttttccag catggtgtgc tcagggtagc tggacttctc 300

<210> 327
<211> 300
<212> DNA
<213> Homo sapiens

<400> 327
ggtagactgg ctagggatcc tggaccagg gtccacgta gcaacacctg ctgagttctc 60
tgggttttct tcttgcctca tgtagccag acttggaact gaagaagctg gaaacatgga 120
aacaccaca gctacagacc aaaaaaagtc ccaacaaagg cctgtcagtc tggcagcctg 180
ttctgtggat ttccaactca agattgcagc atcaactcac acctgaagtt ctggtctccc 240
tacaaacttt gaacttgcca gtccccaca tggcataagc caattcctta aaatgaatgt 300

<210> 328
<211> 300
<212> DNA
<213> Homo sapiens

<400> 328
gtcacaggca ggtttaatgt ccagtttaaa acttatgcta tctgcggggc cattcgtagg 60
atggttgagt ttccctggg ctttgcctat cacttcggga catcgtggac ttaccgtgc 120
gcattggagt gtgtgatggg gcttgatgag atctgctggc agagttagtt gagccagctg 180
gactgggctg gccgcctgcc gcttcttgag ggtggaagag ggggtgctctg agaagacact 240
caggcagcag actctgcctc tcaactaagg tgcccccccg accccgctcc accatagtca 300

WO 99/33982

PT/US98/27610

<210> 329
<211> 300
<212> DNA
<213> Homo sapiens

<400> 329
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ggatattttaa aaatttcaat ttctaattgt tcattataga aacacaattg ggttttatat 120
attggcattg tattttgcaa ctttctaaa ctcactagta attctagtag ctttttttgg 180
tagattctta aggattttct gtgtaaatag tcatgtcatt tgtgaataaa gccatttttt 240
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<210> 330
<211> 300
<212> DNA
<213> Homo sapiens

<400> 330
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ttgaactact tcttgctgtg tcttcacaag catgccccca tctgtgtccg ataagaactc 120
cagaccccaa actcagctca tacacacacg gaagagagaa gcactctgaac atcaagaaga 180
gaagaagctg ctggacatca gaaactgtga aaggagagga gtttggtctga gctccagggg 240
aagactgcct gcacattcta tccccttttc agttccccca cctgtgtctga gccacattta 300

<210> 331
<211> 300
<212> DNA
<213> Homo sapiens

<400> 331
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acactgagat gtttgggtaa agagaacaat aaatctagcc tacgtgcaca tctgggcaca 120
gtacctttcc ttgaacttat tctgtataca gattcctttg ctcacatgtt tccctgctga 180
ccttcttccc acctgttgcc ctgctacact cccctcgtca agacagtaaa aataatgac 240
aataaatact gagggaaact agaggccagc gccggtgcgg gctcccccca tctgtgagcg 300

<210> 332
<211> 300
<212> DNA
<213> Homo sapiens

<400> 332
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acaagcttgt cctatgtcct atttgagtgg cagcagcgcc agcccagcaa gaagcctggg 120
ggttgtcaag gttgtcccca gacctgtt gtcagtggtt gagaaaccag ggggctgcct 180
tgggcccctc ggcacagagg aagcgggcag ctctagccct ggagattgtg gtcacatgg 240
ggcttgttta ggattggagg gccaggctac ctccccagcc accctccctt ctctcctctg 300

<210> 333
<211> 300
<212> DNA

WO 99/33982

PCT/US98/27610

<213> Homo sapiens

<400> 333

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tgacggcgct	aagctctggg	gctccgtgca	ctgacgtggg	gccagccaca	gggagggcgg	120
gatcaagtag	cggaggccag	gattttggcc	acctcccg	caagttgcag	ggcagtgggc	180
ccgggagcaa	aagcagcatg	atgcagctca	tgacactgga	gtccttttat	gaaaaaacct	240
cctcctgggc	ttatcaagga	agatgacact	aagccagaag	actgcatacc	agatgtacca	300

<210> 334

<211> 262

<212> DNA

<213> Homo sapiens

<400> 334

gccatgccca	tttgtttact	cattgtctat	ggttgctttc	atgccctcac	agcaaggcgg	60
agtagttgtg	atggatcaaa	tgcccacaa	agcctgaaat	atttactctt	tgacctttta	120
cagaaaaaaa	ccttgttgac	cctgtcttta	gagaatgaga	agccatgcag	ggatcagtga	180
tgccagagga	agggaaaggaa	ctgcttccag	ctattgtgac	aataataata	ataataatat	240
tggtgtcttg	actagaacgt	gt				262

<210> 335

<211> 300

<212> DNA

<213> Homo sapiens

<400> 335

tctntctctn	ntattnttgn	gtagtnccct	ntttccttgt	ncnntnntcn	ncntntgnet	60
tttgcggaac	ctcgattcta	tctcatatga	gtgagaaacg	ttaccagtgc	agcgaatgtg	120
ggaaagcctt	cggaggccac	tgggaacttt	ctaggcatca	gagtcaccac	agcagtgaga	180
ggccttatat	gtgtaatgaa	tgtggaaaaa	ccttcagcca	gaactcgagc	cttaaaaaagc	240
acccaaaagtc	tcacatgagt	gagaagccct	atgaatgcaa	tgaatgtggg	aaggctttta	300

<210> 336

<211> 300

<212> DNA

<213> Homo sapiens

<400> 336

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gcgcceccgt	cacctccacc	tcacctgtgc	tgccacttcc	tagtgcacac	ctcaccggctc	120
atcctcaagc	tggaaagatac	ctctctggcc	coggcacatg	tcacccctgc	actcctgcct	180
tcccgtaggc	acttccacat	cctctgggcc	tctggcagctt	cccagggact	gttttcacct	240
ctgctgtctc	tggggtcagc	tgtctgctcat	cagctgcccg	ctagcatgtg	gccaggggtg	300

<210> 337

<211> 300

<212> DNA

<213> Homo sapiens

<400> 337

WQ 99/33982

PCT/US98/27610

agacaaccca	gaaacaaatt	catacatcta	tggtagccac	ttttgacaaa	ggaatgaaga	60
acatacactg	gggaaaagat	aatgtcttta	ataaatgggtg	ctgggaaaac	tggatatcca	120
tatgcagaag	aatgaaacta	gacccccatc	tcttagcata	tacaaaaatc	aaaattaatt	180
aaaaagttaa	atctaagacc	tcaaaactatg	aaacagctaa	aagaaaacat	cggggaatct	240
ctccaggtaa	ttggagtggg	caaagatttc	ttgtgtaata	cctgacaaac	aggcaacca	300

<210> 338

<211> 292

<212> DNA

<213> Homo sapiens

<400> 338

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actcgcatct	tcattggttat	tgaggggcaag	aaggctgccc	aaagacacga	gactttaaca	120
agcttgaact	tagaaaagaa	agctcgtctg	aaagagggaag	cagctatgaa	ggccaaaaca	180
gagtagcaga	ggtatccgtg	ttggctggat	tttgaataac	cagggaattat	gttataacgt	240
gcttgattta	aaaaggatgt	ggtacgagga	tccatttcat	aaagtatgat	tt	292

<210> 339

<211> 300

<212> DNA

<213> Homo sapiens

<400> 339

gaaatttgca	ctgatggctc	agaaggctta	cgtcatggag	agtatgacct	acctcagagc	60
agggggggct	ggaccaacct	ggctttcccg	actgtcccat	cgaggcagcc	atgggtgaagg	120
tgttcagctc	cgaggcccgcc	tggcagtgtg	tgagtgaggc	gctgcagatc	ctcgggggct	180
tgggctacac	aagggactat	cagtaagcag	gcatactgcg	tgacaccgcg	atcctcctca	240
tcttcagagg	aaccaatgag	attctccgga	tgtacatcgc	cctgaagggt	ctgcagcatg	300

<210> 340

<211> 300

<212> DNA

<213> Homo sapiens

<400> 340

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acctcaacct	ctcgagtgc	taggactata	ggcacacagc	acctgcccc	ggctattttt	120
ttatttttga	gagatggggg	ctcactatgt	tgcccagggt	agtcttgaac	tcttgccctc	180
aagcaatcct	cccacctcgg	cctcccaag	tgctgggatt	aaaggcgtga	gccaccgtac	240
ctggcccttg	gtggaaattct	tagggttttc	tattcataca	tataaaatca	tatcattggc	300

<210> 341

<211> 296

<212> DNA

<213> Homo sapiens

<400> 341

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caactttttc	atcacttggt	ttatgtagtt	gtctgatcaa	ttgtgaaaac	ataatgaatg	120
ttggaaatgg	aacagtaaaa	taacgaaagc	caactttttt	tttttttttt	ttnnnnnnnn	180

WO 99/33982

PCT/US98/27610

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nnnnnnnnnt tnncccceng ncngnanngc agggggcccaa nntnggntnn ntgnancnc 240
cnccnccggg nttnncccc ttntcmngcc taaccnccc nagnacnngg aactac 296

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<210> 342
<211> 300
<212> DNA
<213> Homo sapiens

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<400> 342
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gcctaccaag tagctgtgac cacagctgcc cctcaccatg ctaagctaatt ttttttaatt 120
agatagtaca taaacgtccc aaaattagaa gataaaaaga catgagggat ccattctaatt 180
ttgtgtttgg agtgtaatgg tccagctcca ttcttctgca catggatatc cagttttaca 240
caacactgtg aatgtaatag atgccactga atcatacact caaaaatagc taaatgggca 300

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<210> 343
<211> 300
<212> DNA
<213> Homo sapiens

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<400> 343
gttttcataca ctacatatcc tacacacact gggaagctct gacaacttat tccctgctat 60
tatcaactaa agatcacctc ttctactgct gtctctggag caggagctgg caaactatgg 120
cctgctgtct gtttttgtac agttttactg aaacacagcc atgccattt gtttactcat 180
tgtctatggt tgctttcatg ccttcacagc aaaggcgagt agttgtgatg gatcaaatgg 240
cccacaagc ctgaaatatt tactctttga ccctttacag aaaaaaacct tgttgacccc 300

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<210> 344
<211> 300
<212> DNA
<213> Homo sapiens

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<400> 344
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agcgggccga gagactgggt cgccttggat tcctctgcc tccgaggacc ccaaaagaca 120
cccccaacc caggccagcc ggccctgctc tggcgcgctc aaaatactac ctagcacagg 180
cctctgtcgt aggcaccccc aaactaccta tgtatccagc cccagagggc ctccattccc 240
aggaagtccc tatgtatccc aacctggcca gacaccagc accaccctcc cagaccgcga 300

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<210> 345
<211> 300
<212> DNA
<213> Homo sapiens

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<400> 345
ccccatcac ctactccagc tcccaacttt tgtggactga gggcgccgag agactgggtc 60
gccttggatt ccctctgctt ccgaggaccc caaaagacac ccccaacccc agggcagccg 120
gcctgtctct ggcgcgctcc aaatactacc tagcacaggc ctctgctcga ggcaaccccc 180
aactacctat gtatccagcc ccagagggcc tccattcccc ggaagtccct atgtatccca 240
acactggcag acaccacgca ccacctccc agaccgcgaa gaaagtgat ctactacta 300

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WO 99/33982

PCT/US98/27610

<210> 346

<211> 300

<212> DNA

<213> Homo sapiens

<400> 346

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accactactt	ggcttgatat	tgcttaata	aaagtatttt	tctgacctaa	gaaacagtat	120
tgtgaacagc	cagccaccgg	agaagcagca	ggccatgcac	ctgtgttttg	agaacctgat	180
ggaaggcctc	gagcgaaatc	ttcttacgaa	aaacagagac	aggttcacc	agaacctgtc	240
agcattccgt	cgagaagtca	acgactcaat	gaagaattcc	acttatggcg	tgaatagcaa	300

<210> 347

<211> 300

<212> DNA

<213> Homo sapiens

<400> 347

gctctgagcc	caggcgaggc	cagggacatg	gccatggacc	tgtgtcggca	ggaccccgag	60
tgtgagttct	acttcagcct	ggacgccgac	gctgtcctca	ccaacctgca	gacctgcgt	120
atcctcattg	agggaacacg	gaagtgatgc	agaccccatg	ctgtcccgcc	accggcaagct	180
gtgggtccaa	ttctggggcg	ccctgagccc	cgatgagtac	tacgcccgt	ccgaggacta	240
cgtggagctg	gtgcagcgga	agcgagtggg	tgtgtggaat	gtaccataca	tctccaggcc	300

<210> 348

<211> 300

<212> DNA

<213> Homo sapiens

<400> 348

gttctgtggc	tggcatggto	tgctgtctac	tggagagatc	tcctgagaat	tcaggtttgg	60
attgggtcgt	tcactcttct	gggaatgctt	gagaaagctg	tcctctatgc	ggaatttcag	120
aatatccgat	acaaaggaga	atctgtccag	ggtgtcttga	tcottgcaga	gctgtcttca	180
gcagtgaac	gctcactggc	tcgaaccctg	gtcatcatag	tcagttctgg	atatggcctc	240
gtcaagccac	gccttggagt	cactcttcat	aagttgttag	tagcaggagc	cctctatctt	300

<210> 349

<211> 300

<212> DNA

<213> Homo sapiens

<400> 349

gtcagctttt	gatgaagcta	tgtcatactg	tcgatatcat	ccttccaaa	ggnattggtg	60
gcacttcaaa	gatcatgaag	agcaagataa	agtcagacct	aaagccaaaa	ggaaagaaga	120
accaagctct	atttttcaga	gacaacgtgt	ggatgcttta	cttttagacc	tcagacaaaa	180
atttccaccc	aaatttgtgc	agctaaaagc	tggagaaaag	cctgttccag	tggatcaaac	240
aaagaagag	gcagaacctc	taccagaaac	tgtaaaacct	gaggagaaag	agaccacaaa	300

<210> 350

<211> 270

<212> DNA

WO 99/33982

PCT/US98/27610

<213> Homo sapiens

<400> 350

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gcaatanggn	gggcttctcg	tccccaggnc	cacccacag	tgctntntgg	cactggnaac	120
tctgctangg	agngantgna	nnnnaccant	aannnnnnan	nnatcnacan	nnnnnnnnnc	180
nnnnnnctn	tnnccmannn	ntannctncc	ntannnnanc	cnncannan	cactcncnat	240
naacgnnnnn	ttantgagan	nttctcaact				270

<210> 351

<211> 300

<212> DNA

<213> Homo sapiens

<400> 351

aaatgactcc	ctgcaaaaac	caacccatgc	tgctggctgt	gggatttttg	gtgtaagcct	60
atctatgcac	tctatcagcc	agaatttggc	atttagctct	tagttaaatc	tagtaaaagg	120
cagctatatt	tttaaagaga	aggtgcattt	gttcctcaat	caagcaagag	cacctgtggt	180
gtactgcttt	atatctcatg	tatatattata	gtaatgaaaa	gactttttta	attgtacaag	240
tttcagtgcc	tttctgtgtg	tatgaaaggc	aggtagatat	tatagccata	ggtaaaaatc	300

<210> 352

<211> 300

<212> DNA

<213> Homo sapiens

<400> 352

aagaaatgcc	tctatgtagg	tgaagtgttc	tctctgcatg	caacagtaaa	aattaatata	60
atattttccc	cacaaaagaa	acacttaaca	gaggcaagtg	caatttataa	atttataatc	120
aaaggggaat	catgattata	agtctctcag	cccttggaact	ctaaatttag	gggattaaaa	180
agaattttaa	ataattttga	acgaatttat	tttccctcca	gtttttgagg	gcattaaaaa	240
ggcattaaat	caagacaaat	catgtgcttg	agaaaaataa	aattaatgaa	aacacagcac	300

<210> 353

<211> 300

<212> DNA

<213> Homo sapiens

<400> 353

cccacactcg	gacactgtgg	aattctacca	gcgcctgtcg	acogagacac	tcttcttcat	60
cttctactat	ctggagggca	ctaaggcaca	gtatctggca	gccaaaggccc	taaagaagca	120
gtcatggcga	ttccacacca	agtacatgat	gtggttccag	aggcacgagg	agcccaagac	180
catcactgac	gagtttgagc	agggcaccta	catctacttt	gactacgaga	agtggggcca	240
gcggaagaag	gaaggctcca	cctttgagta	cogctacctg	gaggaccggg	acctccagtg	300

<210> 354

<211> 299

<212> DNA

<213> Homo sapiens

<400> 354

WO 99/33982

PCT/US98/27610

gaaggaggac	ctaggcacac	acatatggtg	gccacaccca	ggagggtagt	ggggagttag	60
atttcagagt	ccaggcccta	ggttgggacc	cactccaaat	aatctctcgt	gtgtgggtgg	120
tggttctata	gagggtataa	tgaataataa	acattgttaa	aatatacgaa	aaaaaaaaaa	180
aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	240
aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaacnmcn	ncnananaaa	aaaaaaaaaa	299

<210> 355

<211> 300

<212> DNA

<213> Homo sapiens

<400> 355

actgttcctc	ctaagttcca	ctataaacag	gctcatgact	cgggcacaga	cacttctctg	60
gtgacttttt	cctatgatgg	taatgtcctt	gcctctcgtg	gaggtgacga	ttcattaaaa	120
ttatgggaca	tccgacaatt	taataaacca	cttttttcag	cctcgggtct	tcccaccatg	180
ttcccaatga	ctgactgctg	tttcagtcca	gatgataagc	tcatagtccac	tggtgacatc	240
attcaagag	gatgtggcag	cggcaaaact	gttttctttg	agcgtaggac	tttccaaagg	300

<210> 356

<211> 300

<212> DNA

<213> Homo sapiens

<400> 356

ttcagaaaaga	aacattttaat	agggacttac	aaacaaatta	atgtctgagt	ctcagggtgg	60
agcaagaacaa	gatggtggat	ccccatgcca	ttacctgcta	gactcagggg	ttatataactg	120
tagtggagag	gtgattccga	aggaatgttg	taagacaatt	gaagagcagt	aacatcaaa	180
ttatttgacc	taagggcag	agttacagta	agtatccact	tttatacaag	aaacaataga	240
taaactggaa	atcttggagc	ccttcctgga	actgggggta	atgagaagtc	aacatggtgg	300

<210> 357

<211> 300

<212> DNA

<213> Homo sapiens

<400> 357

acaaaaccta	cagatggaga	taaaaattac	tactgttatt	caacatgtgt	tccagaacct	60
tattttgggg	agtaaaagta	attgggcaga	ggatcctgcc	cttaaggaaa	ttgttctgca	120
gcttgagaag	aatgttgaca	tgatgtaata	agaattcatt	tctgacatat	tttacatttc	180
tggcaatctc	aactcttatt	tggaaatact	ctgtgcattt	gtctgtccac	cgtaatttta	240
gaaaagcata	tccataacgt	ttacagttgt	agtacagttg	tggttagtta	ttgttagtgg	300

<210> 358

<211> 300

<212> DNA

<213> Homo sapiens

<400> 358

ggtgattaca	gaagccacga	aggttgatac	cagagccaag	aacgctgggg	ttacaatcca	60
agacacactc	aacacattag	acggcctcct	gcattctgat	gaccctgcac	ttgatggacc	120
agctggcacc	acccagatca	ataaactggc	ttatttgaat	ttcgggcccc	ccacccagga	180

WO 99/33982

PCT/US98/27610

actgactcag tgcaagaaga cagcttcgac tccctgtgat ttcattctctg accaatccgc 240
actcctggct cactggcttc cccaacccat gaagttttcc ttaaaaaactc tgcctcccgaa 300

<210> 359
<211> 300
<212> DNA
<213> Homo sapiens

<400> 359
atcagggtgtt cctcccatgg caggaggga gaaacccagc aaacggccag cctgggactt 60
aaagggtcag ttatgtgacc taaatgcaga actaaaaacg tgcctgtaga ggactcaaac 120
gttggaccac gagaacacgc agcttcagga ccagctcaga gatgccagc agcagggtcaa 180
ggccttgggg acagagcgca caacactgga ggggcattta gccaaaggtac aggccccaggc 240
tgagcagggc caacaggagc tgaagaactt gcgtgcttgn gtccctggagc tggaaagagcg 300

<210> 360
<211> 300
<212> DNA
<213> Homo sapiens

<400> 360
tctgtctggt gattttttatt ttaagtgaac ctttggatct atctttaact ctctttattg 60
tgagtggtaa attccaattc tgcagcagat cagtaaaactc acagtatttt tctctgtgaa 120
atctattcaa taaggaaaac aagacaggat aataaaaattt aaaaaaaac aactttgta 180
tccctgcctt aggtctttcca gttgttttcc agcgcatacc tcagggtatga ctttgctagc 240
cggggacaaa attagcacct tccgattctc tagtccaaat gaactttgtg ctaataaaaa 300

<210> 361
<211> 300
<212> DNA
<213> Homo sapiens

<400> 361
gtagaacaga aaatgagcat cggatttctt cactaaagga gaccaaactg ttccttgccg 60
tctagtattg aagaactgga acttgaaagt cctccttcta ccaactccac ctccaccccc 120
tcattccctt tctcccaag tactactgct gttgcattgac aaccccaaat atgttctgtc 180
aacacaaacc tgcctttggt gtataaacag ggcattacag aatggatcac cctatatatt 240
tctgttcagt atccattcac tagttcttca ttataaata tcattctccc cattctgctg 300

<210> 362
<211> 300
<212> DNA
<213> Homo sapiens

<400> 362
actaccgcgg ctacgggttc cccatgcctg gcagcttggc catgggcccg gtcacgaaca 60
aaacgggcct ggagcgcctc cccctggccg cagatacctc ctactaccag ggggtgtact 120
cccggcccat tatgaactcc tcttaagaag acgacgcctt caggcccgcc taactctggc 180
accccgatc gaggacaagt gagagagcaa gtgggggtcg agactttggg gagacgggtg 240
tgcagagacg caagggagaa gaaatccata acacccccac cccaacaccc ccaagacagc 300

WO 99/33982

PCT/US98/27610

<210> 363
 <211> 271
 <212> DNA
 <213> Homo sapiens

<400> 363
 ggcaattagc ctgccttaag ttgccttttt tacacaccaa aactttttac atgaagggct 60
 ggtttcacat gaatactata ctgaaatctg tgcctctcaag atctagcagt gaccagggct 120
 gcccgccggg ggctctcctg gcaagtcagg aaggtnnnnn nnnnnnnnnn nnnnnnnnnn 180
 canattantn nctgatcctc tntnangaan nnnngantgc tctnttggnc ntgtgnnnnn 240
 gncntnnnnt naantntttt ntntatgtnc t 271

<210> 364
 <211> 300
 <212> DNA
 <213> Homo sapiens

<400> 364
 agaggaccct gcagtttagg ggtgttactt tgtcgcccag gatggcctgg acccccaggt 60
 tcagggattc tccgcgcgct gcttctctgag tagctgggac ctacaggcttc cgctctgtgc 120
 ccgcacccct gctgtgttta ggcagcaggc ggtgaacctca ctccctccctg gctctgagctc 180
 tccgtccgcg atcccaggcg gaggccctag ggaacacttt gaagctgagc acgggggtgga 240
 cctccctccc tgagtgaatg gagaatagaa agggagagga tttctgttct gttctgtggg 300

<210> 365
 <211> 300
 <212> DNA
 <213> Homo sapiens

<400> 365
 gttcttcaaa gccaaccaag acaggcttag cagtttttaga gcttcagaac aaattgccaa 60
 aagccagagt tgtttatgct agtgcaactg gtgcttctga accacgcaac atggcctata 120
 tgaaccgtct tggcatatgg ggtgagggta ctccatttag agaattcagt gattttattc 180
 aagcagtaga aocggagagga gttgggtcca tggaaatagt tgcctatgat atgaagctta 240
 gaggaatgta cattgtctga caactgagct ttactggagt gaccttcaaa attgaggaa 300

<210> 366
 <211> 300
 <212> DNA
 <213> Homo sapiens

<400> 366
 gccagtctct acctcccta gtcctcgtgt gtatttttagg agatgcgtgg gtgtggaaca 60
 gcctctctgc tccggtccag gtgtactggg gtctgtgtgt tgtgtttctg cgtgttctcg 120
 gcagaaagtg gcattgtctc ccgcctgggt gatttgcctc ttacactat tctctgaagg 180
 cagggaacgaa tccctatcca caagttoacc actgcaactaa aggcactggg actgcagaca 240
 tcagatcctc ggctccgaga ctgcattgagc gagatgcacc gcgtgggtcca agagtccagt 300

<210> 367
 <211> 300
 <212> DNA

WO 99/33982

PCT/US98/27610

<213> Homo sapiens

<400> 367

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gaagtcacatg	tgggggtcagt	tctggtctgc	tcaccagagg	ttcttcaaat	acttatgcat	120
agcatccaaa	gttaaaaggg	ttgtgcaact	agctcgagag	gaaatcaaga	atggaaaatg	180
tgttctaatt	ggtctgcagt	ctacaggaga	agctagaaca	ttagaagctt	tgggaagagg	240
cgggggagaa	ttgaatgatt	ttgtttcaac	tgccaaagggt	gtgttcgagt	cactcattga	300

<210> 368

<211> 300

<212> DNA

<213> Homo sapiens

<400> 368

gcccgcccg	gcgacgctgg	cgacgcttcc	gcccctgagg	tagtttggcg	accgcgaaga	60
aggaaaaagg	gcggggcggg	ggctgtcctc	tcaccgtcct	caccccgaga	ggcccgccc	120
gctctcctgt	cgtggtattc	gcggcgatcc	ccccggcagc	tttttgcata	gctgcttgaa	180
actctcccca	aactcggcat	ggatacgact	gcggcgcgcg	cgctgcctca	ttttgtggcg	240
ctctctgtcc	tctctccttg	gcctctcctg	ggatcggccc	aaggccagtt	ctccgcaggt	300

<210> 369

<211> 300

<212> DNA

<213> Homo sapiens

<400> 369

gtgggggtgtg	cctcgtgtgc	gtggattcgt	gtgtgtgtgt	gtgtcttgta	tatgtgtgcg	60
cagagtgcac	cattttcaga	ctctactatt	tcogtcaagt	attctgtttg	atttggatca	120
tctcaggatc	ggattctgtt	ttagagtgtt	tctggggcag	gatccggggc	cctgccctcc	180
tctgcacctg	accacactcc	ctactcaggg	ctagtctgtt	cttcccgagc	atcttctggt	240
agcctgtcag	gagagggtcg	ggtggggcag	agggcacaga	ggggacctgg	tgtgtcacct	300

<210> 370

<211> 273

<212> DNA

<213> Homo sapiens

<400> 370

cagaggctgg	ttcagaaaaag	gaggaagagg	cccggtggc	agccctggaa	gagcagagga	60
tggaggggaa	gaagcccagg	gtgatggcag	gcacctgaa	gctggaggat	aagcagcggc	120
tggcccagga	tgaggagagt	gaggcctagc	gcctggccat	tatgatgatg	aagaagctnn	180
nnnnnnnnnn	nnnnnnnnnn	atcatgtccn	ntgcattgct	acctatccca	tatttnatnt	240
ccctnnctgt	gnnttcaatt	ncacattntc	ttt			273

<210> 371

<211> 300

<212> DNA

<213> Homo sapiens

<400> 371

WO 99/33982

PCT/US98/27610

gatgaggagt	gtttaatcat	tgatacagaa	tgtaaaaaata	atagtgatgg	aaagacagct	60
gttgctgggt	ctaacttaag	ttccagacca	gctagtccaa	attcttctc	aggacaggct	120
tctgtaggaa	accagactaa	tactgcttgt	agtcctgaag	agtcattgtt	tttaaaaaaa	180
cctctccaaac	gagtataata	aaaatttgat	ccagttggag	agctttttaa	aatgcaggat	240
gagctcttaa	agccaatttc	cagaaaagta	ccagaattgc	ccttaatgaa	tttagaaaat	300

<210> 372

<211> 300

<212> DNA

<213> Homo sapiens

<400> 372

gggcccacat	gcagctgccc	tctccagata	cctggcagcc	tcataatatca	gccaaagcct	60
ggctgcgcgg	caggggcctg	ggggaggggc	ccccgcagcc	tcccggggct	cctggctctc	120
tgctcccaag	tcacgggcat	cttcgcgcgc	ccccacagcc	cagccaccac	ctcccgcaag	180
caggcgagct	agctatgcca	cgacgggtta	catccacgtg	ggcggggggt	ggcgctgtcg	240
gccagccaa	gcccagggtc	ggttgaacca	ccctgtctct	ttggcctcca	cacagggaatc	300

<210> 373

<211> 300

<212> DNA

<213> Homo sapiens

<400> 373

accctttctg	ccttctgttt	gggaccagcc	tggtgttctt	tggtttgctt	tcttcaggct	60
ctagggctgt	gctatccaat	acagtaacca	catcgcgctg	tttaaagtta	agccaattaa	120
aatcacataa	gattaaaaat	tccttctcca	gttgcaactaa	ccacgtttct	agaggcgctca	180
ctgtatgtag	ttcatggcta	ctgtactgac	agcgagagca	tgctcatctg	ttggacagca	240
ctattctaga	gaactaaact	ggcttaacga	gtcacagcct	cagctgtgct	gggacgaccc	300

<210> 374

<211> 300

<212> DNA

<213> Homo sapiens

<400> 374

tcaaggcccta	cgaaacagggt	atgcactacc	ccggctacgg	ttcccccatg	cctggcagct	60
tgggccatggg	cccggctcag	aacaaaaagg	gcttggaagc	ctcgccccgt	gccgcagata	120
cctcctacta	ccaggggggtg	tactcccgcc	ccattatgaa	ctcctcttaa	gaagacgaag	180
gcttcaggcc	cggttaactc	tggcaccccg	gctcgaggac	aagttagaga	gcaagtgggg	240
gtcgagactt	tgggggagag	gtgttgccaga	gacgcaaggg	agaagaaatc	catacacccc	300

<210> 375

<211> 300

<212> DNA

<213> Homo sapiens

<400> 375

cttcagtgc	cacaacagga	gagaggagaa	agaagaaacg	ctagtaattc	caagcactgg	60
aattaagtgt	ccttcacag	tggttgcttc	agagtttgag	gaagatgttg	tgattgttaa	120
ataaagcagc	tccagttcca	ggacctcgac	tggtatttga	tctcgacatt	gttgacgctc	180

WO 99/33982

PCT/US98/27610

ttgatgatga	ttttgacttt	gatgatccag	ataatctgct	tgaggatgac	tttattcttc	240
aggccaataa	ggcaacagga	gaggaagagg	gaatggatat	acagaaatct	gagaatgaag	300

<210> 376
<211> 300
<212> DNA
<213> Homo sapiens

<400> 376						
gggagactgg	ggtctatttc	acccctgcag	tctcgacccat	aagagatggc	tacacccagg	60
ggggccagtt	cagagaccca	ctcccagggt	tgcatctctct	ttctcaagga	tggtctcttc	120
tgagaaaaag	aattcagtg	tatttctccc	atttgcttgt	gaaagaagag	aaatgtggct	180
ttgttccacc	tggtccaccg	gcggtcagaa	tttaagggtta	tctctctgt	ttcctaataa	240
ttgtgttat	ctgttctctt	tttcaagggt	cccagatttc	atattgtctc	aacacacatg	300

<210> 377
<211> 300
<212> DNA
<213> Homo sapiens

<400> 377						
gatcagccca	cctcggcctc	acaaagtgtc	gggattacag	gcgtgagcca	ccttgcccag	60
cccacatcat	acagtttgaa	atgaaacttt	gccacaacca	gcctttgctg	tagcacacac	120
atatatcact	gaacctgttt	gaaataaagt	ttttttctct	ttctctctgg	tattctgggt	180
tctgaagtct	ggtattctgg	tattctgggt	tcaaaagtat	gacttgagag	tggtgtctctg	240
gtattctgag	agttgctctg	tattctgggt	tctgaagatt	atttgaaaaa	taactctcac	300

<210> 378
<211> 300
<212> DNA
<213> Homo sapiens

<400> 378						
tcgtgtgtgat	ccaaggataa	aaaagtccaa	ggaagaagaa	aaagccaaga	aagaagcaga	60
aaagaaagca	aaagcagaag	ctaaacggaa	ggagcaagaa	gctaagaaga	aacaaagaca	120
agctgaattc	gaagctgttc	ggttagctaa	ggagaagaag	gaggaggaag	tcagacagca	180
agcattgtctg	gcaagaaggg	aaaaagatat	ccagaaaaaa	gccattaaga	aggaaagggc	240
aaaacttcga	aactcatgca	agacctgga	tcattttctc	gataatgagg	cagagcgggt	300

<210> 379
<211> 300
<212> DNA
<213> Homo sapiens

<400> 379						
acactataga	atacaagcta	cttgttcttt	ttgcaggatc	ccatcgattc	gaattcggca	60
cgaggcagct	tcgagccaat	ggtgagctcc	ttctggatca	gctccttcag	ctccttcttg	120
ctcaggatgc	tgaatttgca	aggctgatgg	aagacttgga	ccggaacaag	gaccaggagg	180
tgaaactcca	ggagtatgtc	accttctctg	gggccttggt	tttgatctac	aatgaagccc	240
tcaagggctg	aaaataaata	gggaagatgg	agacacccct	tgggggtcct	ctctgagtc	300

WO 99/33982

PCT/US98/27610

<210> 380

<211> 296

<212> DNA

<213> Homo sapiens

<400> 380

acctggacag	ggccagctgc	tgggggagcg	gcactgggga	ctggaggctg	gaagcgggtg	60
gtgtgtgtcc	cctgtttact	tttagctgag	ctggggtttg	gtgtacgggt	tctgttctct	120
tgagccctgc	ggcccacctg	atgtttacgt	gtgtgtgtga	gggggggcnm	nnnnnnnnnn	180
nnnnnnnnnn	ngtnatangc	ttaacanatg	nanagncnac	tnactnctga	ttntttatnc	240
atttgtgc	at	at	at	at	at	296

<210> 381

<211> 300

<212> DNA

<213> Homo sapiens

<400> 381

cagaaaagag	tatagtaggg	atgaccaagg	tcaaagtggg	taaaagaagac	tcatcatcca	60
ctgagtttgt	agaaaaacgg	agagcagctc	ttgaaaggtta	tcttcaaaga	acagtaaaac	120
atccaaactt	actacaggat	cctgatttaa	ggcagttctt	ggaaagtcca	gagctgccta	180
gagcagttaa	tacacaggct	ctgagtgagg	caggaatatt	gaggatgggtg	aacaaggctg	240
cgcagctgtg	caacaaaatg	acaatcaaga	tgaatgaatc	ggatgcattg	tttgaagaaa	300

<210> 382

<211> 300

<212> DNA

<213> Homo sapiens

<400> 382

gccaccggct	tcttccta	at	ctgcacagac	tattttgggt	atttctgggc	gggcagttcc	60
tttgcatgtt	tcgggagagg	tttgctgatt	tggggcttat	atgtcaggcc	tttggtttgc		120
gtcttatttt	aggggttgtt	tgggggcctg	ggtggctcgg	ctcacatggg	aaggggatgg		180
gtagtggatg	gggtttctgt	tgtatcttgt	gggcgggtga	ttttgctttt	gtttttgttt		240
cacattcttc	cccctccaca	agccaaagtc	gtttcatttt	gtttccactg	tgtggactgt		300

<210> 383

<211> 273

<212> DNA

<213> Homo sapiens

<400> 383

gagatttgat	attcgagtgc	tgggcttagg	tctgttgata	aactctagtgg	agtatagtgc	60
tcggaaatcgg	cactgtcttg	tcaacatgga	aacatcgtgc	tcttttgatt	cttccactctg	120
tagtggagaa	ggggatgata	gtttaaggat	aggtggnnnn	nnnnnnnnngc	cngcnttnac	180
ttnatngcnn	ctttttcttg	atcnacgncn	gmnatncnna	nnngtntata	ntaatnccnga	240
anantntttt	gnmtgtcctt	atcaantntt	cnt			273

<210> 384

<211> 259

WO 99/33982

PCT/US98/27610

<212> DNA

<213> Homo sapiens

<400> 384

aagagaagga	cctagagatt	gagaggctta	agacgaagca	aaaagaactg	gaggccaaga	60
tgttggccca	gaaggctgag	gaaaaggaga	accattgtcc	cacaatgctc	cggccccttt	120
cacatcgcac	agtcacaggg	gcaaagcccc	tgaaaaaggc	tgtggtgatg	ccctcacagc	180
taattcagga	gcaggcagca	tcccaaatg	ccgagatcca	catcctgaag	aataaaggcc	240
cgaagagaaa	gctggagtc					259

<210> 385

<211> 296

<212> DNA

<213> Homo sapiens

<400> 385

agagcctgca	agtgacaaag	gaagtgaggc	agaggcccac	atgccccac	cgttcacacc	60
ctacgtgcct	cggattctga	acggcttgcc	ctcgagaggg	acagcactgt	ctccgcagca	120
gcagcagcac	cagacctatg	gtgccatcca	caacatcagc	gggactatcc	ctggacagtg	180
cttggcgcct	agcgccaacg	gcagtgtggc	ttgctgcccc	ccaggaggcc	tgaggctggg	240
tctcactgct	ctgaaaaaga	ccmncctaaa	atgggccttg	gggctnnagg	cccttg	296

<210> 386

<211> 300

<212> DNA

<213> Homo sapiens

<400> 386

gaagaggagg	ctgtgtatga	ggaacctcca	gagcaggaga	ccttctacga	gcagccccca	60
ctgggtgcgc	agcaaggtgc	tggctctgag	cacattgacc	accacattca	gggccagggg	120
ctcagtgggc	aagggtctctg	tgcccgctgc	ctgtacgact	accaggcagc	cgacgacaca	180
gagatctcct	ttgacctcga	gaacctcctc	acgggcatcg	aggtgatcga	cgaaggctgc	240
tggcgttggt	atgggcccga	tggccatttt	ggcatgttcc	ctgccaaacta	cgtggagctc	300

<210> 387

<211> 300

<212> DNA

<213> Homo sapiens

<400> 387

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atgacctcac	tgttcgcctc	tgggaccttc	aggctggagc	tgatcggtcg	aagctgcagg	180
gccaccaaga	ccagatcttc	agcctggcct	ggagctcctga	tgggcagcag	ctggccactg	240
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<210> 388

<211> 300

<212> DNA

<213> Homo sapiens

WO 99/33982

PCT/US98/27610

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 aagagaaaaa agtgaccttt catttttttt tcttgaaact tgaggaaaca agatacatac 180
 tactgatttt ttttttctta aaactaaatg catgactgca gagcggtaga ggtgtatatt 240
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<210> 389

<211> 293

<212> DNA

<213> Homo sapiens

<400> 389
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 tccagtggct atggcggctg cagcgggtgc ggcannnnnn nnnnnnnnnn nnnatgaanc 180
 agntactect atgggnnttag cnttntanct atnacctgcn cnaactannc tnangtctga 240
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<210> 390

<211> 300

<212> DNA

<213> Homo sapiens

<400> 390
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 tgccctcggt tctgaacggc ttggccctcg agaggacagc actgtctccg cagcagcagc 180
 agcagcagac ctatggtgcc atccacaaca tcacgcgggac tatccctgga cagtgtcttg 240
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<210> 391

<211> 257

<212> DNA

<213> Homo sapiens

<400> 391
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 ctctctcttc tctctctctc tctgcccggc gctggtttcc gtctctcggc tcggggctgg 180
 aactccggcc caacctagcg gcgcagccgc cagcagatgg cgcacttccg atcaatgtca 240
 aagccgcggg ggagccc 257

<210> 392

<211> 300

<212> DNA

<213> Homo sapiens

<400> 392
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 cgcagtgtct tacgggcaag aacctgcaca cgcaccaact cccgtcgcgg ctgtccaaca 120

WO 99/33982

PCT/US98/27610

accaggaggt	gagtgccctt	ggggaagacg	gcgagggcga	cgacctggac	ctatggacag	180
tgcgctgctc	tggaacagac	tgggagcgtg	aggctgctgt	cgctctccag	catgtgggca	240
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<210> 393

<211> 300

<212> DNA

<213> Homo sapiens

<400> 393

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accaggaggt	gagtgccctt	ggggaagacg	gcgagggcga	cgacctggac	ctatggacag	180
tgcgctgctc	tggaacagac	tgggagcgtg	aggctgctgt	cgctctccag	catgtgggca	240
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<210> 394

<211> 300

<212> DNA

<213> Homo sapiens

<400> 394

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gggaattgca	cacgggaaag	ctgtgtggtt	tccttttacc	tttcagctga	ccatgaactc	180
ctgagcccca	ccaactacca	cttcctgtcc	tcaccgaagc	aggccgtggg	gctctgcaag	240
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<210> 395

<211> 300

<212> DNA

<213> Homo sapiens

<400> 395

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ttatctaaat	gcccttgaa	ggaatacaaa	tcagattctg	gaaagcctta	ctattataat	180
ttctcaacaa	aagaattctcg	ctggggccaaa	cctaagaac	ttgaggatct	tgaagcaaat	240
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<210> 396

<211> 300

<212> DNA

<213> Homo sapiens

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ggcctaggga	gcgcacctt	gtcatgtacc	atcaataaag	taccctgtgc	tcaacccaaa	180
aaaaaaaaa	aaaaacnnnn	nnnnnnnnnn	nnntntngggn	gnctnnntnc	nnaaanccan	240

WO 99/33982

PCT/US98/27610

ncttnataaa anccttngnt natttggaac aaccncann taaanngcag ggaaaaaaag 300

<210> 397

<211> 300

<212> DNA

<213> Homo sapiens

<400> 397

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ttctctcact	ctcagtgctca	gagcagaaat	gaatcctggg	gttgactgtg	tccattcgagg	180
ttattagcag	ctaagaagcc	cagacgagta	gtgtgagctg	ccttgggagc	ctcagtgagg	240
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<210> 398

<211> 300

<212> DNA

<213> Homo sapiens

<400> 398

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gcaaatgaac	tgaatcagg	gagcaataag	aacattcaca	ttgctctggc	tacattggcc	180
ctgaactatt	ctgtttgttt	tcataaagac	cataacattg	aagggaagc	ccaatgtttg	240
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<210> 399

<211> 300

<212> DNA

<213> Homo sapiens

<400> 399

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gctctctcca	aaatacaggt	cagcaaaact	gaaagcagcc	tgaacaacag	caagaccagc	180
tgtgtgaca	tgcataagat	gctgtttgag	gaacgaatc	attttgccga	gatagagaca	240
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<210> 400

<211> 300

<212> DNA

<213> Homo sapiens

<400> 400

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aaaatgatgt	gatgatcaga	aaagaggctt	atgtgcacaa	gagtgtaatg	gaagaactga	180
agagaattat	tgatgacagt	gaaattacaa	aagaagatga	tgtttgtgg	cctccccctg	240
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<210> 401

WO 99/33982

PCT/US98/27610

<211> 300

<212> DNA

<213> Homo sapiens

<400> 401

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tgagggggtg	ccggaagagc	tggtccccgt	ggttgagctg	gtccccgtgg	ttgaattgga	180
agggccata	gccccagcct	cagaggccca	gggcgctggg	tctgggtggg	acgcgggggt	240
gcccccaatg	gtgcagctgc	agcagtcacc	actaggggggt	gatggagagg	aagggggcca	300

<210> 402

<211> 300

<212> DNA

<213> Homo sapiens

<400> 402

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atttgagggtg	gaccctttca	aagaaagtga	ccatttccgt	ggctctgcga	ctgaogactt	180
cttcaagaaa	cagacaaaga	atgacccatt	tacctcggtat	ccattcaoga	aaaacccctt	240
cttaccttgc	aagctcgacc	cctttgaaac	cagtgatccc	ttttcatcct	ccagtggtct	300

<210> 403

<211> 300

<212> DNA

<213> Homo sapiens

<400> 403

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aagcatcaca	atgggaagaa	aggaatgtc	tcattcctgga	agaaatcctg	gcctaccgac	180
gtgatataatt	gtgcctccaa	gaggtggacc	actattttga	caccttcacg	ccaactcctca	240
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<210> 404

<211> 300

<212> DNA

<213> Homo sapiens

<400> 404

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aattaagaga	tgctcagcag	gatgcaagag	ataaaatgga	ggatatcgaa	cgccaagtta	180
gagaattgaa	aacaaaaatt	tcagctatga	aagaagaaaa	agaacagcct	agtgctgaaa	240
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<210> 405

<211> 856

<212> DNA

<213> Homo sapiens

WO 99/33982

PCT/US98/27610

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gagttagatt tcagagtcga ggccttagt tgggaccacc tccaaataat ctccctcggtg 180
tggttggtgg ttctatagag ggataaatga ataataaaca ttgttaaaat atacgaaaaa 240
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 300
aaaaanaaaa aatnaaaaaa annnaaaaaa aaaaaaaa aannccctn cncctaaaaa 360
nattcngggg ggntttttcc tccannccnn ntntttaata nntcctntnt tgnntcttng 420
nctcacennn tcttttggtn ggcnnataa naaaatntnn ntnttttttn ggntanaaaat 480
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caataatttc tnnncccc nannccnnat tttntttnnc ctctatntnn gnnngnnnat 720
atnantcccc tttattnttn atnantagtc ntntnttttn ttntcmtng tnatannatt 780
ttntntcccn ntntaanttc ctcanntnat ttntntnnnn ncngngntata tttntangnta 840
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<210> 406

<211> 843

<212> DNA

<213> Homo sapiens

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<400> 406
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<210> 407

<211> 743

<212> DNA

<213> Homo sapiens

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atagaggaga actagattga tggttgcttc gggatgggag gaatgggaag attagggtct 180
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atatgcttaa gaccattgaa ttacacactt tacgttggtg aattgtatgg tatgtaaat 300
atagtctcaat aacatagtaa caaaagataa tcaaaagcat gaaagcactg ttgatgtggt 360

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WO 99/33982

PCT/US98/27610

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gatattgagt cctcatcaca tctggttgct tcaaatgttg tggtgccctc cctctatctc 540
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gtttccctgc gctnccctag aacaaaactg ctgtgctctc tgnnccctac tacaggaccc 660
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<210> 408

<211> 746

<212> DNA

<213> Homo sapiens

<400> 408

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gtctagaggc agaattcagaa ggcttgggtg gaacatactg ntctctctt tctcttctct 720
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<210> 409

<211> 761

<212> DNA

<213> Homo sapiens

<400> 409

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<210> 410

<211> 748

<212> DNA

WO 99/33982

PCT/US98/27610

<213> Homo sapiens

<400> 410

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gaaaaaancag	ctttgtcctg	ggtgaaaaag	gatgccaaaa	ttgctctggaa	aagagcagtg	180
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atgcacactc	ttaggggaaa	atatggtatt	aaatcccat	gncattgtct	aacaaacaga	480
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<210> 411

<211> 773

<212> DNA

<213> Homo sapiens

<400> 411

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atgttanttt	taacagaacc	nanaaggggt	gnccatttgg	ttaaaaaaa	aaaaaaaaaa	720
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<210> 412

<211> 774

<212> DNA

<213> Homo sapiens

<400> 412

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cogagatgtc	atgggttcaa	gtgctggggc	cggcagtgga	gagttccacg	tgtacagaca	180
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gcgaagcgcg	cggagagaagc	gccagaagtt	aaaagagaag	aaattactgg	caaagaaagt	360
gaaacttgaa	cagaagaaac	aagaaggacc	cggtcagccc	aaggagcagg	ggtccagcag	420
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WO 99/33982

PCT/US98/27610

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atgacaatgt ttgccacagc ctctgcctgg aacctggctc gtgctgtgac cagaagggaa 540
aggcggtgt ttggctcttt ctccccgcga aggaccocgc ttaccocgtg gatggagagc 600
aaaggagacc ccctctcgag ccgntcaca gtctgtatt tggcaaggtt tgggaacctg 660
aaggggccaa tntncttga cacttanang cacttgcett tcagacacca ttccgngcnt 720
ctggtaaaa gggacaagaa aagcettaac cttggcnna tattttgaca gggg 774

```

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<210> 413
<211> 773
<212> DNA
<213> Homo sapiens

```

```

<400> 413
gnngnnnnnn ttttaaatgc ttgggnnnnn ngtcnatgcn taagagccan gcgngtcgaa 60
ttcggcacga ggcgggcccc gccagcggaa gccctgcgc ccgcgccatg tcaaaagaaa 120
aaaggactga gtgcagaaga aaagagaact cgcntgatgg aaatatattc tgaacaaaaa 180
gatgtatttc anttaaaaga ctgggagaag attgctccca aagagaaaag ctttactgct 240
atgtcagtaa aagaagtctc tcaaagctta gttgatgatg gtatggttga ctgtgagagg 300
atcggaactt ctactattta ttgggctttt ccaagtaaa gctcttcacg aaggaacatc 360
aagtggagg ttctggaaat tcagttgtct gagggaaagt caaagcatcg aagcctacag 420
aaaagcatgt agaagctaa aattggccga tgttgaacg gaagagcgac caggcttagc 480
aaaagacttt cttaacttcg agaccaaang ggaacagcta aaggcagaag tagaaaaaat 540
ncaaagactt tgatccccga agttgtngga agaaaatgcc aagcaaatna agtagcccaa 600
acagactgctt acagatggac tgattacata ttgcacaata aatcttngcg ccaaagaaaa 660
atttngggtt tgaaggaaaa tttaattggt tngaaccttt tggaaattcc cgaagacttt 720
ttgcctnct ngacttaaaa tatttccatg gnggtgaaag gttgtccaan ctt 773

```

```

<210> 414
<211> 755
<212> DNA
<213> Homo sapiens

```

```

<400> 414
gnagnnnnnn ntttaaatgc ttggggnnnn nngtcaatnc ctngnancna ggcgngtcgc 60
tcatccagaa angtcagatc ancaaagaag tccangaaaa antgcgaccc agctngacnn 120
tttgatccca ggcttagcac acgattgcat ggcntccct ttagccaactt naaccactgc 180
agactcaaga gaagctggac tctctcctca gtccntccag actctggcc accacagant 240
gaaaacccca ttctcaactg agctatcttt gctccagcct gataactccg actgtgtgtg 300
agatagctcat accccactgg ctttttcctt caccgaggac ttggaaagtt tctgttgcct 360
agacogaaag gaagaaaaag gggattctgc caggaaatgg gaatggcttc atgagtctaa 420
gaagactatc agagtatgga gaaacacacc aaactacctg gggacaaatg ctgtcagccc 480
ttaggcaaga cttaatttga aagaaaggtg tctgcacaa gaaaacaggca gcccctgtc 540
ctcctcaaaa catcacagga atcctggaat ggagaaaaa tagaatcagt gaaacaaaac 600
cgtatccag ttctgmgttt tctctgggata tgaagaagat gaccangac tncgtgagtc 660
aacttttcc ttgaagaatc tcaagccac cgttcaatgg ccacacactn gaactccttt 720
ttaagatga cccattactg gaattgggct taggg 755

```

```

<210> 415
<211> 852
<212> DNA
<213> Homo sapiens

```

WO 99/33982

PCT/US98/27610

<400> 415
 gnagaaannn ttctaattgct tgggnnnnnn ngtcaaacct tannaacctg gcntgncgaa 60
 ttccgcacga ggtcacaggc aggtttantg gccagtttaa aacttatgct ntctcggggg 120
 cnttctagat gatggtgagt gtttccctgg gctttgtctca tcacttcggg acatcgtgga 180
 ctttaccgtg cgcntttggag tgtgtgatgg tgcttgagta gatctgctgg cagagtagtt 240
 tgagccagct ggactggcct ggccgctctg cgtcttttga ggggtggaaga ggggtgctct 300
 gagaagacac tcaaggcagca gactctgcct ctacttagga ggtgcccccc cgaccccgct 360
 ccaccatagt caaggctgca ggtgcccccg ggagaagtgg ctccccctct tgcgcctgtc 420
 ttccattcgc ttcaccgggg gganaagacn ttgggcttgg ttggcacagc ntgacacctt 480
 tgcacctctt naaggcganc ccggaantgg gaaaaatatt tctttaaattg gtggcctttn 540
 nttttttttt nctttnaaag ggggttgaagt tccannaatg natttcccaa tctccttccc 600
 gaattgggnc ccaaaaggccc ccaatggggc antcgggtct ttaaaaagna acctttttgg 660
 acctgggaag aagaaaaatca ccagatttgt tgggaaatat ttggncattt aaaaataant 720
 aatggaaaaa ctnaaaaaaa aaaaaaaa aaaaactcgag ccnnttaaaa accttttagtg 780
 agtcnnatta ccnttanatc canacnttga tangaanctt tggataattt tggngcaaac 840
 cnnaacttng at 852

<210> 416

<211> 754

<212> DNA

<213> Homo sapiens

<400> 416
 ggnnnnnnnng tnaaaccttc cnaannaggc tnggcgtcac tgncccggt caacaaaccc 60
 acctttatga cagtttttct ccgcagcttg gctnttaaat tttactggca ggtgtatggt 120
 tgtttggagg ttcctagtag gtggggggac ctggcantan agctgcttgg ttggagggaag 180
 tgaanctggc ttantaccag cagctgatct ctccacgtg ctgctgcttt ttttccact 240
 ctgatactaa accagagaaa gctgcaggtg gataaagaag ctgtggtctg tttttgctt 300
 tgggttgcaa tgagaaagag tcacagtgtg ggttaaaagg atctgcagtg gggccaagga 360
 tgccacccca cctcagctg tangcaagct tgacataaaa taaccccccg cagtggaagt 420
 ttogggatgc agggggcant atagtgttct tggactttgt ccgtcctggg gcagttttta 480
 agttctttat atttaagtgg ggtcagtgcc aagtgctacc accttcccaa taaangaatg 540
 ggggaccocan aaggtcgggg tccctggcta ccttgttatg aaggttttgn tntttctctg 600
 acaaganttg ctttggaaa anccgttttt taggggatta ttttttgnat accccgatgg 660
 gganccaggg ttcctnctcaa aaccttaca acccttagga tcatagggaa aagggggccc 720
 tnttttctg ctggttnc ccaacttaaaa acnt 754

<210> 417

<211> 755

<212> DNA

<213> Homo sapiens

<400> 417
 ngntatagc ttntaatgc ttctancga attcggancg agagaagccn tgagcagcaa 60
 agtcntcgc gacacctctg acgaggcgtt ggggaagtc ctgcacggga nccagcgcaa 120
 gcgcgcgaag ttctcgaaa cgttggaagt gcagatcagc ttgaagaact ntgatcccaa 180
 naaggaacag cgttttccg gcacgcctag gcttaagtcc actccccgcc ctaagtctct 240
 tgtgtgtgtc agcggggacc agcagcactg tgacaggctg aaggcgtgg atatcccca 300
 catggacatc gaggcgctga aaaaactcaa caggataaaa aactggctaa gaagctctgg 360
 caagaagtat gatgcgtttt tggcctcaga gtcttttagt caagcagatt ccacgaatcc 420
 tcggcccagg tttaaaatag gcaggaaagt tcccttctct gtnacacaca acgaaacatg 480

WO 99/33982

PCT/US98/27610

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gtggcctaaag tggatgagnt gaagtcacac atcaagttnc aaatgaagaa ggtgttatgt 540
ctggctgttan ctgtttgggc acgttgaaga tgacnngacg atgaancttg ggggtataaca 600
ttcacctggc tgctcaactt ttgnggttca attgcntcaa agaaaaaact tgggcagaaaa 660
tgttccnngc cttatntntt caagaacmc catggggcna agccccaaag cccttnttt 720
aaaggcnatc ttggaattaa attcntnttt ncccg 755

```

<210> 418

<211> 757

<212> DNA

<213> Homo sapiens

<400> 418

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tggggnntnn nttetaatgc tgggatgttc taaangntgg gctactcggt ctttcgcgac 60
gancccntcg attcgaattc ggcacgagga aaggtggcgc gcttctcacg gctgagttgc 120
tgccgctgca gacggaagct cccacaggc agagctgctt ggtatgtgtga gtcatagaagc 180
cagagaagcc cgcctccatg agcagtgact cccacaggccc tgtgacctcc ctctctgttt 240
gcagctcctc ctggcaccag tccccagggc tctctgtgtg gtatgtcttc cttttcttct 300
tggaaattcc cgttgagact cgagatcttt accctaaaat agttctgttg aatttcaccc 360
ttgacatgta aattgtatgc ttatcttcac agatgcagga caatggacaa ctacccatca 420
gtcctctgct cacctgagac aaatgcattg ctgattgtct cctctgacct attgnttatg 480
tgaaaaatgca gattcactga gccagactaa ggcattcagt actgttccct tactgectct 540
cacatggaga ttgtgtattc agtgaaggc tgatcaaaga ccccaaagga atgcaccagt 600
ttatctctta tctactctac acctgcgagc tgnccaccac ccccgattgt tgcgctttc 660
cagacagaac cagtgctcat ttacacgtat taattggatg tctctgngct tccttaatat 720
gtatcaaaac aagctngcct tgaacacctt gggcactn 757

```

<210> 419

<211> 738

<212> DNA

<213> Homo sapiens

<400> 419

```

gnnngnctt cnaattncgn ggnntctttc tngccnanna nnnnnngcgt gngngaattc 60
ggcacgagac tgttccatcct aagttccact ataaacaggc tcatgactcg ggcacagaca 120
cttctgtcgt gactttttcc tatgatggta atgtccttgc ctctcggtga ggtgacgatt 180
cattaaaaat atgggacatc cgacaattta ataaaccact ttttccagcc tcgggtcttc 240
ccaccatggt cccaatgact gactgtctgt tcagtcacga tgataagctc atagtcaact 300
gtacatctgt tcaaagagga tgtggcagcg gcaaacctgt tttctttgag cgtaggactt 360
tccaaagggg gtatgaata gacatcacag atgcgagtg tgttctgtgc ctgtggcacc 420
caaaagctga ccagatcatg gttggaactg gaaatggatt ggctaaagtc tattacgacc 480
ccaacaagag tcagagggga gcaaaattat gtgtggttaa aaccancngg aaggcaaaaac 540
aagctgagac tctactcagg actacatcat caccctcat gccttgccct tgttcccgtg 600
agccccgnc aaggagatca aaggaaacag ctggagaagg acagactgga tccctgaagt 660
cgcattaaac tgaacctcct gtancangcc cangtctgtg tggccgattt ggaaccacg 720
ggggcactnt tttttctt 738

```

<210> 420

<211> 739

<212> DNA

<213> Homo sapiens

WO 99/33982

PCT/US98/27610

```

<400> 420
gcgntntat tagcgtgggc tcnctctcgc tcnacncanc nngnctggg cgaattccgtt    60
acgagaatca gaggaggctt cttcatcctt caactccatg atgaactcct atatgaagtg    120
gcagaagaag atgttgttca ggttagctcag attgtcaaga atgaaatgga aagtgcgtga    180
aaactgtctg tgaaattgaa agtgaagtg aaaaataggcg ccagctgggg agagctaaag    240
gcatttgatg tgaactctg ctgttgatga agtctccca gggaagcctg tgcagatgca    300
gtcacctgga aagaacagag attccttttc acctacctca gcaaaaacaaa ctttcaagtc    360
ttgatagact tagccttagta attttatagt gagagtttca aactatata caagtgtcta    420
tagcatcaaa aactctctggg ggcgtggggg aaagttagaat accaagtata atagttaacat    480
tcactttcaa agagcatcta tgaatttgcc ttttgaact tactgtggct ttaaacatat    540
tcagaaacga tgcttgaagt atgcacttag caacttgggt ccacatctgt ctgggttaaac    600
catgaagaaa atgaagctgc tgccctcaatc gancccgagc agcagccata ggcagataaa    660
gatttnggtt cacccttggt ggtgggaggc atcgtgtgtg cctttttttc ctctaataac    720
aattttacag tccgggaan

```

<210> 421

<211> 727

<212> DNA

<213> Homo sapiens

```

<400> 421
gtgatctttt tgagtggggg cctnctnctgc tctannanatt aggttngngg ggcctagcgat    60
ttctactctgc gctactacgt agggcacaag ggcaagtttg ggcacgagtt tctggagttc    120
gaatttcggc ccgagcgga agcttagata tgccaacaac agcaattaca aaatgatgtc    180
gatgatcaga aaagagctta tgtgcacaag agtgtaatgg aagaactgaa gagaattatt    240
gatgacagtg aaattacaaa agaagatgat gctttgtggc ctcccctgat aggggtggcc    300
gacaggagct tgaaattgta attggagatg agcacatatc tttaccaca tcaaaaatag    360
gtctcttat tgatgtaaat caagtcaaa gactcctgaag gccttcgagt attttactat    420
ttgggtacaag acttgaaatg ttagtttttc agtcttatg gattacactt caagattaaa    480
ccaatttaaa ttgtatgttt tcaagctggt tgnatattta attaaagga tgggaagggg    540
ttatttgc tttacagtat tggggtttta tgaatgtgaa gcaaccaaaa aaattnnaa    600
tctaaacctg gaaaatagga aaattcatta ncaagcttaat gggatcctt acttgatnctn    660
gtggggttgg aagtcaccac acacattaaa tctgtaatga aancnctttt ggttaaaatt    720
tctctat

```

<210> 422

<211> 753

<212> DNA

<213> Homo sapiens

```

<400> 422
gtntngnng nngttnnatt atatggntcg nctnnctcna nnanenango ttngnctgac    60
aacttgatgt ggtctcctt caggtttgaa gcgcctcna gaagtgtcta aaggagacag    120
ttgatagcca aacaacagtt ttggattcac tgactgatta tgaagaagc agtagactgg    180
ttcaagaat cagtcagcaa ggaggccctc accagacgcc agtgccatgt tcttggactt    240
ctcagcctcc atatttcata actaagtttt tggaaatcctt aggcttcacg agtggaag    300
cctgagctaa cctactggag gatgagccat cactctggag agattcaggc catcctagtt    360
gaagcctccc tagggcaagg aacogtccaa ctaccagaca ttgaccatc agccttgaa    420
attcgcgaca aagcaaaaac agaccagacc agaagagtc cccagaaatg gggaaactat    480
tcagagaaaa cttaaagcac taagttttat ggtgtttgt tctttagacc aagcctatag    540
gcatactgac caatacaaac cgaaatcctt ctaacttant ggaccctttt caggccagca    600

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WO 99/33982

PCT/US98/27610

```

ttttttccct tgaaaaacctg ggagccttgt attccatctt attagcagaa gatcactttc 660
accaatgggt tgggctcttg atttggaaat gatgatgtaa tgagccctnta ttenanatgn 720
gaactaatac ctctgcgaat tgactggatt ccn 753

```

```

<210> 423
<211> 844
<212> DNA
<213> Homo sapiens

```

```

<400> 423
nggnnnntnn nnnnnatncc ntgatcgtgt ntogttcttt ctncaggatn nnnctogtttc 60
gaattccgga cgagggaaaag ggagccgcgc agngcctacg ggagtnccgc gccagcagcc 120
ggtaccggca accacgggca gctctcaggc aatctccgtc gttgaggcca naggctccag 180
tccccgcgag tccagatgcc tgtccagcct ccaagcaaa acacagaaga gatggaaagca 240
gagggtgatt ctgctgctga gatgaatggg gaggaggaa agagttagga ggagcgganc 300
ggcagccaga cacagctcaga agaggagagc tccgagatgg atgatgagga ctatgagcga 360
cgccgcancn agtgttttcag tnagatgctg gacctggaga agcagttctc ggaagctaaa 420
nggagaagtt gttcaaaagga acgacttgga tcanctgccg gnttgcggct tggaaaggaaa 480
ntggggggggc ttgaanaaga agccccctga atnccacccg aagccccctt ttggggggggg 540
gccttgcaaa ccgggaancc ctttnaaagg aatttcngcc antttcaang gttggggccaa 600
ggggaatcnt accnaagggg ccttctnggc cttggnatgg tgaatccang gnaaattaag 660
gtncccaatt gntgaanctc tccaanggga ancccaaac agcacccctg naanaagttg 720
agaaaaactg cttgcntctt ntgcaccccc tncnaggggg aacttcaagg aaccgggttc 780
tnaggcttgg aaggaggacc cccanancct tggancctaa attnttaaat gggtnggacc 840
accn 844

```

```

<210> 424
<211> 799
<212> DNA
<213> Homo sapiens

```

```

<400> 424
ggagnnnnngn ntccnaattn nntgggnnnn nngtccaaan nctngctact cgttcttttc 60
gcaggatccc atcgatctcg aattcggcac gagcccagac ctatggagtc agacagtagg 120
tttgaggccc agcaatctat ggtttaacaa gccatccagg tgtttctgat gcacagtga 180
attgggggtac cactgggtatt aggttttgga tggcaacttt ttcatacatt gttttatgta 240
gtgtctctgat caattgtgaa aacataatga atgttgga aaagaaacagta aaataacgaa 300
agcacaacttt tttttttttt tttagagcgg agtcttgctc tgtcgcccag gctggagtg 360
agtggcgga tctcggctca ctgcaagctc cgctccctgg gtcacgccca tctctctgcc 420
tcagctcccc gagtagctgg gactacaggc gcccgncacc acgcccggct attcttttgn 480
atatttagta gagacggggt ttcacggtgt tagccaggat ggtctcgatc tcttgacctc 540
gtgatccacc cgctctnggc ttccaaagtg ctgggattac aggcgtgagc caccggggccc 600
gggcacaaag ccaactcttt atgcctagaa aatatgtgc accctatgac ccaagcccat 660
tgaatttttn cngggaatatt tatggtaaat tattgaaatg gatggtaact ttaaaaagtt 720
atttggcaca ttcctcttgg gttacctttg gnatggtttg ccagggaatt naaaactttg 780
ggnntnaaac ttttttann 799

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<210> 425
<211> 750
<212> DNA
<213> Homo sapiens

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WO 99/33982

PCT/US98/27610

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<400> 425
gangeccggat tccaattntc nggetnctct naaannctgt ntaatgettg gteccganga      60
nccatgcgga ttogtggagg tctcctttcg ccccgccca ggtggccaag cccatcctgg      120
cctcagaaca ttctgagcac attttgtagg gtggcacctt tttatccaag ttaactagcta      180
cacatcagtg tttaaagaga aaaaagtgcac ctttcatttt tttttcttga aacttgagga      240
aacaagatac atactactga tttttttttt cttaaaacta aatgcatgac tgcagagcgg      300
tagaggtgta tatttttcat actgtggggc aaagtatttt tgctgctttt tggagatgga      360
ctggaaagctc tggtttctgt ccccgggccc ggcagctacg tctattttct gtagaagggt      420
ccacagtgag acctggagcc accccttctc gcttggcgcc gtttanagct ggggagccctg      480
ggactccggc ctgtttctac cttctattca accactctga cgtggggaga caagaagaaa      540
tagaactttt tgatagtgtg gtaaaaaacat tggattttga actatttttag taaaaggagt      600
taccacaag aatgtnatag gtgctacttt gagctagata aataaaggct ctttgtgagc      660
ctcctgaaaa aaaaaaantt nnnnnnnnnn atnannnnnn annaaaaaaa ctggnccttt      720
aaaaacttan gggngcttta cctanaccct                                     750

```

<210> 426

<211> 819

<212> DNA

<213> Homo sapiens

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<400> 426
gnagnnccgn ttcttatgat cgtggetnct cntctanngg ttgtgtaagt ctnggtcmnc      60
anganmncnt goganncgaa ttccgcagca agggggggtc ccaatagtag aaaaggggtc      120
ccatttccctg tcagcacgcg acctctctac cccccacag acacacatgc agacacacac      180
atgcagacaa cagcgagaca cacacatgca ggccactcaca tgcaggccca tgcacacaca      240
cgtgcacaca catgcagaga catgcagaca cgcaggtcaca catgcacaca tgcacaagaca      300
cgcatgcagg cacacgcaga cgcacacaga gacacacatg cagatcacat gcacacacac      360
atacacacac tggccctctgt ttttctgtgg tgtcactggg tgccagcaac tcggtatctn      420
ccaccttcca ctaaaacctg ggccttaatt tctctcccgt cccccccctt aaatttctga      480
tggatgaacc tagagctgtc ctgtccactc caggccgggac tgacgtancc tatgggcccc      540
cgaggtccag ggcccacgtt ttaatttctt tttnaaaagc tttaggtctt ggcncggccg      600
cgggtgggtc acgccttggg agttcccagc atttttnggg aaggccnaag gcccggttgg      660
attcacaaag gtcaagcaag ttccaaggaa ccaagccttg aaccaggcca ttgggtgagg      720
aacccctggc ttnttactng ggnaaattcc aaaaaaaaaa ttggccttgg gccnaagggt      780
gggcaagggc acctctgttg gggctcccaa antttaacct                                     819

```

<210> 427

<211> 750

<212> DNA

<213> Homo sapiens

```

<400> 427
gagnnngatt cmaattnctg ggctnctctc ttnttatnta atgctgggtc cgcangancc      60
nntgcgattc gaattcgcca cgaggtccaa ggacaacttc gagacatttc tttttgcccac      120
cgatctaac agggagcag agatctctg ccgaggaatt gtcacgcttc gcttcaatga      180
gcaaaagccaa cagctgctag cagaggtcca gccctctgac tctttctcca tggtagagac      240
aactgcatac tttagggcct acagggcagct cctggaagga ctccaggagg tccaggagga      300
agatgttccc ttccagagga atatcgtgga gtgtaatctc catgtgaagg agccaaggtta      360
cttgttaagt gggggcagat atgaacttac ccccttaata gagaatcctt gaccactggt      420
ggaatttcta agaaatgtcg aggggttgag acatcccaga attaatgtct tagactctgg      480
ccagtggccc tcaaaagaag ccttgaactg gatgatcca gatggaagcc ttgcagtttg      540

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WO 99/33982

PCT/US98/27610

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ctctccacaag ggaactggct attattcaag gaccttctgg aacaggcnaa acctatgtgg 600
gtctnaaaaaa ttgttcaagc ccttctacca acgagctctg ttgggcaaaa ttaaccttca 660
gaattcccca tcttggtgtn gtgtatacta atcatgcttt ggaccanttc tgggaangctt 720
ttccattgtc agaaaaacan atttggccgg 750

```

<210> 428

<211> 943

<212> DNA

<213> Homo sapiens

<400> 428

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gnngnccggg ttctattct cnggcancct tcttctctcn acctattanc tggactctaa 60
anaaaagmnt gnngcggttg gctcaagggc caccanaaca tttcttattt attattattt 120
tttaacctgn acatgcntta aagggtctat tacctttctt tccgtctgtc tcaaacgctg 180
aaatggggcc nccaaggagt gccttctctt tgctccctcc tactgggact gacggntggg 240
antgntntgn cccanntggg ggtgtctctt gntgggaag ganggaaagg gaggcanagt 300
tttgcggggg ttgcannng acancangct gnanaggana tggctaataa ctgtttaaag 360
gaaacctgct tgggcttgga nggaaccttag nctgaatttt cccgactctc ctgtgccagt 420
attgcacacn tctctttnta agacangaaa taaactaaac cccaccccaa ggnantnatn 480
ncangcngaa aacmncnat ngcccacatt nctnatccc ntanccnn ctontnttt 540
nncccaanac tntctccan nctnccent ttaccentan nctnntttt atccnctaa 600
tncctnann centntntt ccnnatnctt acnccnccn ntntnnccn nntcttntn 660
cccaaanctn nctcncntt tcnctnaac cntntnnca nnanacccc tctnntnn 720
ccannctcn cccnntnmnt ntctcnnnt nnnccnccn ntctnnnnna nancntntn 780
nanancnct ctnntncnnt cnantnnnt tcanctcan ctctnnnnnn ntanccnat 840
tancnctnn tnnccntta nnnctnnnn nnnnaantct nnnnnctct nennnccnt 900
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<210> 429

<211> 775

<212> DNA

<213> Homo sapiens

<400> 429

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gnangnnnnn nntttctaan tncctggggn nnnngtcann gattnngeta aaggttngga 60
tcnccgcag naangctgtg gcgctccatt gtgaaagatc caggcatttt tccgagccag 120
gaaaagccca agatgactac aggatattag tgcattgccc ccacctctct ctccagtgtg 180
tacgcagatt tgcccatctc ttgaatcaaa gccagcaaga cctctctgtc gctgtgatgt 240
gcacaccctc caacctgggc agggactggg gggatgcagt gtgtgttagt gccatgtgg 300
cattgtggca ctgttgcccc ccatggcggc atgggcaaga tgacctcca ttagcttcaa 360
gtctgtgtct ctgtctctgt gtctgtttaa tatgtgggto actagggtat ttattctttc 420
tccatctctt acactctgga tcatgtgca gacttaatca gggttttaac gcttctatn 480
nnnnnnnnn ttttttgag tcaagaaaag ttctcatttt cctattcca ctaataccca 540
tgccgmgttt tttaacttgg atttaaaagg accttangtt ggggcaacag attctcactc 600
atgtttaana cctggnatcc ancttctaaa gaccaaaag ggagctttcc cttctctctt 660
accctnagg attctcatcc tttaacannn gactttttcc aggccaatat cccatnnaat 720
ctgcanccc cngccttttg ncccaagctt ttntgntngn cccccattt acccn 775

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<210> 430

<211> 763

<212> DNA

WO 99/33982

PCT/US98/27610

<213> Homo sapiens

<400> 430

ngggtgnnnn	nntttcta	nctgggggnc	nnnnnnnnnn	ntttccta	nettagngnc	60
tcgttcttcc	tccangcagn	nnngcgttcc	gcgcagctcc	tccaatactc	agggttaatgc	120
tgaaaaatca	tccaagacag	ttattgcaag	agtttaattt	ttgaaaaactg	gctactgctc	180
tggtgtttaca	gcgctgtgca	gtttagggca	tgtagctaca	ggacattttt	aagggccacg	240
gatcgttttt	tcccagggca	agcagaagag	aaaatgttgt	atatgtcttt	taccocggcac	300
attccccctg	cctaataata	agggctggag	ctcgacggg	acctattaga	gtattttcca	360
caatgatgat	gatttcaagc	gggatgacgt	catcatcaca	ttcaggggcta	ttttttcccc	420
cacaaaccca	agggcagggg	ccactcttag	ctaaatccct	cccogtgact	gcaatagaac	480
cctctgggga	gctcangaag	gggtgtgctg	agttctataa	tataagctgc	catatatttt	540
gtagacaagt	atggctctct	cgtatctctc	cttctctagga	gaggagtggt	aacaaggagc	600
ttagataaga	caccccttaa	accatttccc	ttttccagga	gacctaccct	tcacaggcac	660
agggtcccaa	atgagaagtc	tgctaacctc	tttctcatct	ttttactaaa	ctcaaaangca	720
ntgacagcag	tcagggacag	acatttcattt	cttnatacct	tcc		763

<210> 431

<211> 761

<212> DNA

<213> Homo sapiens

<400> 431

tggtgtntnn	ntcctaagtc	ttggnnngnn	ggtannnctt	ctaattactt	tggggctcgt	60
tcntntctma	cmnnngcnn	cggttncgaat	tcggcagcag	cttgaagcgc	tggtttttct	120
ogaagcactc	cttattatat	tgtaaaacaa	ggaaagatca	accagatggc	aacagaccca	180
gattctcaga	gattaaagct	attaagagaa	gtagctggta	ctagagtgtg	tgacgaacga	240
aaggagaagaa	gcattctcct	aatgaaagaa	acagagggca	aacgggaaaa	aatcaatgag	300
ttgttaaaaa	acattgaaga	gagattacat	actctagagg	aagaaaaagg	agaactagct	360
cagtatcaga	agtgggataa	aatgagacga	gccttggaa	ataccattta	caatcaggaa	420
cttaacgaga	ctcgtgccaa	acttgatgag	ctttctgcta	agcgagagac	tagtggagaa	480
aaatccagac	aattaagaga	tgctcancag	gatgcaagag	ataaaatgga	ggatatcgaa	540
gcgcaagtta	gagaattgaa	aacaaaaatt	tcagctatga	agaagaaaaa	agaacagctt	600
aatgctgaaa	gacaagaacn	gattaagcag	aggactaant	tggagcttaa	agcccaagat	660
ttacaagatg	aataccggcg	aatagtgaac	aaaggaaaac	gtttttttaa	agaaangccn	720
aanctgcttg	aaaaaaaaaa	aaaaaaactc	ggcctntaan	t		761

<210> 432

<211> 748

<212> DNA

<213> Homo sapiens

<400> 432

gnngantnng	tcttattatc	gtgngctct	nactnnctct	aaatanaatt	gtgttngngg	60
aattccgcac	gaggccaccg	aagcttcagg	atgacatctt	agactctctt	ggctcaggnga	120
ccaatgagtt	aaagactgca	gaacaaatca	acgagcatgt	ttcaggcccc	tttgttcagtt	180
tcctttgtcaa	gatttgtggc	cattatgctt	cctatatcaa	gcggggaagca	aatgggcaag	240
gccacttcca	agaagaatcc	ttctgttaag	ctctgacctc	caagaccacac	cgccgatttg	300
tgaagaagtt	tgtgaagaca	cagctcttct	cacttttctc	ccagggaagcc	gagaagagca	360
agaatcctcc	tgacggctat	ttccaacaga	aaatacttga	atatgaggaa	cagaagaagc	420
agaagaaacc	aagggaataa	actgtgaaat	aagagctgtg	gtgaataaga	tactactagag	480

WO 99/33982

PCT/US98/27610

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ctacacaccca ttcttggaact tcagccccctg ccagtggtggc aggatcagca aaactgtcag      540
cttccaaaaat ccatatccctc actctgagtc ttggtatcca ggtatttgtt tcaaaactggt      600
gtctgagatt  tggatccctg gnattggatt tcttaaggac ttttggangg ctcttgacac      660
catgcttcac  agaacttggg cttcanaagc ttcanttttt tgcanaagtg ccccgaggtta      720
ggaaaacagt  tntncttgtt ttgtannt

```

<210> 433

<211> 769

<212> DNA

<213> Homo sapiens

<400> 433

```

gggnaaaagt  ttnnnannng ggnagnnnng ntinnacntt cctattactt tggagctcga      60
actcgcncca canannmagt gncntgngct gttttgcaga tgaggaaaac tgagggtacag      120
aattcttagg  gaacttaccg aaaaatggctt ttctgcactc tgccttttgg tattgtccca      180
tgtgaattgt  ttaaaaacta tgtgtatagt ggcatgagta ggtgatcca gaaacagaaac      240
tcacttttgt  tgttttgtct taaaatttagg aacttttctt catctgggct tcaattccct      300
gcaccttccc  agcttttctag tcatgcaagc cacatgtctc cacgtgaggg gttcatttga      360
aagcagccac  agagccaccc cctggctggg ttcttcccca gctctgcttc ctctctcccc      420
aagtctctga  gctgctctct ccatggcaga accacttctc ccttacttgg aggggaggtc      480
cactgaacaa  atccaggaga ggaatcattg tgttttccac agaagagaaa gtacacttga      540
ctttctgtgc  aacctgtttc tacattttca caganactca tatttgtgca ntgttaacta      600
atttgaacc  cagcaaaaat aggtccctgt gtctccataa aaggccacca tgatggtaac      660
cgttggaact  caccttgtgt ttnggacana ngctgattgg attttacca tcatcacanc      720
cgtgtcttac  attctcnttt cctgggcttt ggacccctgn tanaaaaaan      769

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<210> 434

<211> 764

<212> DNA

<213> Homo sapiens

<400> 434

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ctanccttcc  taaannctng gctactcngt cttctnnnan ganncnnttg cगतncgaat      60
tcggcacgag  caccttgctt ggccaagggg ctagacctcc caggctaagc ctcagattca      120
gtgcaggaca  caagctcatg ccccgctctt gccagtgaac ctgaagcct cccgacttcc      180
acagagtgtt  tcaggacaca ttttgagtgg tattttctt tcttttttt tctctttttt      240
tttttgagat  ggagtctcgt tctgttgccc aggcctggagt gcagtggcct gatctggct      300
ccttgcaccc  tctgcccacc aggttcaagc gattctctct cctcagctc cagcttagct      360
gggactatag  acatgcacca ccaagccagg ctaatttgtt atttttggtc gagacggggt      420
tttgcatgt  tagtcangct ggtcttgaac tntgcacctc aagtatcca ccaactggcc      480
tccaaaagtgt tgagatgaca ggcacgagcc accagcccaa cctgagtgtt attttctta      540
gggacacamt  agacttttaa acgagggtaa gagaaaaagc ccagtgtgtt tttctgagg      600
taataaatt  tctgcccagg aaacmttnc aagccccaac cagcaagcca acccttaaaa      660
aaaaaatcac  tctgtgtccc ccaangggan cttntttaa gcttggggg cttccagyna      720
aatcatcttc  cagtnaant  ttggaagaat tcannagnat ttnt

```

<210> 435

<211> 755

<212> DNA

<213> Homo sapiens

WO 99/33982

PCT/US98/27610

<400> 435
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 tncagatncc ntgcatttga attcggcacg agggatcctt tccagacaga agacccttcc 120
 aaatctgacc catttaaaagg agctgacccc ttcaaaagcg acccgttcca gaatgacccc 180
 ttgtcagaac agcagacaaac ttcaacagat ccatttggag gggacccttt caaagaaagt 240
 gaccatttcc gtggctctgc cactgacgac ttcttcaaga aacagacaaa gaatgaccca 300
 tttaacctcg atccatttcc gaataaacctt tccttacctt cgaagctcga cccctttgaa 360
 tccagtgatc ccttttcatc ctccagtgtc tcctcaaaag gatcagatcc ctttggaaacc 420
 ttagatccct tcggaagtgg gtcccttcaat agtgctgaag gctttgcccga cttcagccag 480
 atgtccaagg gtgcctgggg aagagccact gcgcattgta tctttgggtg tactccagt 540
 ttgaacanaag agctggctcag aggcagtcca tcgcanagag acattataaa gggaaacctt 600
 tgaatcccta ancagcanca gcttttctga nggggccnat gatgccagtg acctntcan 660
 ggnaagctcg ggaacttggg accaccctgg ggggaagaac ttgtgggatg tggcttttct 720
 tttatgaata aagtactttg agttgggtgn aatcn 755

<210> 436

<211> 760

<212> DNA

<213> Homo sapiens

<400> 436
 aaggctggnn nngnnnnntgc nnnncttent attantctgg gggctcgtnc tctctcnann 60
 nagmnaggcg ntngaaattc ggacagagct caagaaaagg agaaagtttt ttgtatgaa 120
 atttggaggaa atattgggga acgtgcctt gatgatgaca cttacatgaa ggatttatat 180
 cagcttaacc caaatgtctga gtgggttata aagtcaaaag cattgtagaa gacttaacaa 240
 gctgcagata accatgtgga cttctgtcat aattcttgct gagtcaagag tgtaataaa 300
 agaaaaggga ggactcatat tattcagttg tcccaagtat ttaaaaatga ctctcttaag 360
 ccttaaaaag tcatagattt gtgctgctgc cagaattata ttaattatta ttaattggtat 420
 tattagaaaa aaaattttctg gagtgaagat naagangctt aattagtttg tgggcagttt 480
 tcatatgtct tgtgaaatgt gtccagatgt gacataagtt ttttttttta atatggngga 540
 aatgntctct ctttccattt ctttctcctt aaaaatcata tatactggga ataatgcct 600
 cntntacctc tattaccctc ctccacattt ccctttccca gttinggtttt gctttttnac 660
 caaaaagatt ccaatncnca ggtattggca agtntnaaa accegccmtt aaaaatccct 720
 aatttcnag nattccnnnc ttgccaaatn tngntctenn 760

<210> 437

<211> 748

<212> DNA

<213> Homo sapiens

<400> 437
 ggnnnnnngnn ngntnnctgt cccatttant caggngctcg ntctntctcn annnanenng 60
 gcgtgtncga attcggcacg aggattttcg aaactcttca gctaactgcc cttttttatc 120
 tgaaaccatc atacccttctg aaagaaaaaa gcatatcttc attgacataa cagaagtggag 180
 atggcccaat cttgatacag atggtccatg atatatatgg agagtggcat tgtgaagata 240
 acatctttag atggtcatgc ataccctctgc ctgcccagat ctgagcatga atttaacagta 300
 cattttttct gtaagattga ccagaagtca gactcatctg cagtgtgttc agaaacaaat 360
 aataaagccc caaagatgaa actagttgaa aaaactggca aaatctgtaa acgtggaat 420
 ttaccaggac agagactgaa gaataaagaa aatgagtttc attgccagat catgaaatcc 480

WO 99/33982

PCT/US98/27610

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aaagaaactt taaagaagat gagttgtgta aatggaactg aaggggagggg aagaactgcc      540
ttcgccctggg acaagacaca catgtgtata cacatgggtc aagcagtgtct ggtctgtggc      600
tgnctgtcca gangaattgga aatatccttg gctttagcac ttcattttca taataaaatc      620
agcaattntg tctaaaaaaa aaannnnana aaaaactnga gcctntanaa ctntagtgag      660
tcgtattacg tagatnmcna catgataa                                     748

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<210> 438

<211> 823

<212> DNA

<213> Homo sapiens

<400> 438

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taatcctttnn tattgntcgg gtactngntc tntctcnaag annntntcgt tncgccccagg      60
tagctgagac taccacacac ttggtcccag ctacttggga ggctgagggt ggaaaaatcac      120
tttgcccagg aattcaaggc cgcagtgagc tatgattgca ccactgcaact ccaggcaaca      180
gagtgagacc ctgtcttaaa aaaagaaggg agaagtgctc agatgggtgat gaggctctggg      240
ggggaaatag agaattggga tcaggagtggt ggaatgggtgt attccctcac caagaggtga      300
catgttgagc agggaaacttg ggaggtgagg gtgtgacccg tgtggaaatc aggggaaaagc      360
attncagcct gagggaacagc caatgcanaag gcctgagcgt ggccagtgcc actgagcagt      420
gagcttggga tagggggcan gtgangaggc tggagagcgg ggtcagacaa accaatatgc      480
ttatttataa caaggttggt ncagcacccct tgccttaaaag ccttgagcct gnaantnga      540
aaaaatttggg cacnttcaaa agcanggang gaaccacaaa gaagattggg aggggaaaagc      600
ccttncttc ccttancagg aaatgaagtt nccacccttn aaaaacaggnc caggaccttt      660
ttgggaacct ttgggccttt tggttcctta gaatcctctt ggtngcctnn gaatnaaaag      720
gnaaaagggg cctttaaggg gggatcccat tntttccaaa attcaaaggg ggccttccct      780
gggcttacc ccaatttctt ggncttaant aaaaaattt ntt                                     823

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<210> 439

<211> 767

<212> DNA

<213> Homo sapiens

<400> 439

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gnnnnnngntt ctaatgtctg nnnnnnnngg taccctttcc aaaacctggg ctctcgnct      60
ttctnccanng agccnnngca ttctgtctgc ttggtgattt tattttaagt gaaccttttg      120
atctatcttt aactctcttt attgtgagtc taaattccaa ttctgcagca gatcagtaaa      180
ctcacagtat ttttctgtg gaaatctatt caataaggaa accaagacag gatantaaaa      240
tttaaaaaaa ancaactttt aattccccg cctaggtctt ccagttgttt tccagcgcat      300
acctcaggtg tgaacttgct agccggggac aaaattagca ccttccgatt ctctagttca      360
aatgaacttt ggctaaataa aaaattatta tactacataa taaagttnca gatagcagga      420
aatgcaagag ctaggagatt cctagattat atcttgccaa gccaaatacc ttaaacatcc      480
acctggaaat cctctacccc ctctcttgag ataatttgc ccagcccttc tctccacaca      540
ctcaactcaat gtcacccctt tctaactccc aaaaactgtt ttgtggcctt ggtagcctat      600
agtagttact cacacttttt cccctanact tttctgtttt cagtttcaga ccaaaaaaac      660
ttctcaactt ttttccagt gggcttctct taccagtaac ttaccactt gnaactctat      720
ttcattgaaa aaaccttaaa tgggntggga aaaggcttgc cnnccann                                     767

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<210> 440

<211> 752

<212> DNA

<213> Homo sapiens

WO 99/33982

PCT/US98/27610

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<400> 440
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ttttccaag atncnngcgn tncgaattcg gcacgaggat ggatgagact gttgctgagt      120
tcatcaagag gaccatcttg aaaaatccca tgaatgaact gacaacaatc ctgaaggcct      180
gggatttttt gtctgaaaat caactgcaga ctgtaaatct ccgacagaga aaggaaatctg      240
tagttcagca cttgatccat ctgtgtgagg aaaaacgtgc aagtatcagt gatgctgccc      300
tgttagacat catttatatg caattcatca gcaccagaaa gtttgggagt ttttccagat      360
gagtaaagga ccaggtgaag atgttgacct ttttgatatg aaacaattta aaaaatcgttc      420
aagaaaaatc ttcagagagc attaaaaaat gtgacagtcg gcttcagaga aactgaggag      480
aatcgagtct ggattcgaat tcctggggaa cacagtacac aaagccaaac cagtacaaac      540
ctcctacgtg gtgtctactc ccagactncc tacgccttca cgtnctcctn catgctgang      600
cgcaatacac cgcttcttgg gtcangaatt agaagctact gggaaaaatc accttccgac      660
agaagagatc attttagatn tacccaatga anaaagcttg cattagtgcg attgaaaggg      720
aaataaaat tcctacagtc naaaaaaaa at                                     752

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<210> 441
<211> 775
<212> DNA
<213> Homo sapiens

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```

<400> 441
gnagcngat tccaaaaacct gggnnccgat ccaatgettn ccaattactt gggagctcnn      60
actngcnma ncaanctncc cntgcgaatt cggcacgaga agnaggcgga gcttgcaagt      120
agctgagatc ggcgcactgc actccagcct gggcaacaga gtgagactct gtctcaaaaa      180
aaaaaaaaaa aatgggaagc cagggcaga aactcgtntt ggaaggagat gggggaaagg      240
ancggtatta taccatgttt gnatttgcag gcaaatgaga tgganccctc tctgtaaaga      300
agagtcattt gtgcaagtag acggggtctg tgggtgcang ccttggaggg gcacacaatt      360
gcctgnangc ttcgtgtana tcggggagang gaggagaagc agtctcttga caaaataaag      420
tatttttatt catnngtatt tatttaatag aaaaacaatc ccatggtgtc ccttggtgt      480
ggtggaacct aatgactggt gaaataaagt ctgmgttttc ccttcaaaaa aaaaacnmcn      540
anaaaaaaaa ctgcagccct ntaaaacctn tngnagtcce gnattacnt anattccnga      600
cnttgagtag gatccattga tnaantttgn cccaaaccca actnngaagt ccmnnaaaaa      660
aaattgcttt atttgggaaa tttgcnaatn ctttgcetta nttnnaccce antttanctn      720
cannnccaa gttacnancn ncaatgcnt tcatttangg tccaagggtg aaggg          775

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<210> 442
<211> 804
<212> DNA
<213> Homo sapiens

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<400> 442
gagnnngntt ctatacctgg gnnccgatcca aancttnccct attacettgg atcttnngct      60
atctcnaann aaaangcttn cgaattcgcc acgaggccac ctgcaactgag gtctgggccc      120
ggggacaggg tgcttagacc aggcctgtct gcgcctcagg gaagggtgag cagcccaggg      180
accagatgca agtgtgtggy ccctccacc cmtccnagc cactccccag tgtgtggggt      240
cctaaacagt cgtccatggy gagcagttag cctctctctc ctctccaggg cagctctccc      300
acctgctant ccccgacacag agaacctcat tgctctgagc agtgtcttat taccaggttg      360
gtgaaaaact agcatgtgan ggccgggggc ggtgggtcac gctcttaate ccaacgcttt      420
ggggagccaa ngcgggtgga tcatgangan aggagatcaa gaccatctgt gcttaacacn      480
gtgaaaacct gtctctacta aaaaataaaa aaagtancca ggcgtgggtg tggccctctg      540
agtnccaann ntactgggaa gctnangan gaanaatggc ntgaacccaa tgaaggagaa      600

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WO 99/33982

PCT/US98/27610

cnttgcantg	aancttaaaa	ttgcgcccac	tggaatttca	aaccttgggc	cnanaanaat	660
tgaagaatcc	cgctcttaaga	aaaaaggaaa	aaanttttnc	ntntnnaaag	gcccgccac	720
aanntngcct	taacgcctcg	gtaaatnccc	aancactttt	tggggaaggc	ccaaaggcaa	780
ggccnggatt	caatttttna	aggg				804

<210> 443

<211> 786

<212> DNA

<213> Homo sapiens

<400> 443

gnagccggat	cttattattg	gcmncgnttt	aatgtcggtc	aatntntcgt	aatncttggt	60
nncccaamn	annnaggngg	ggngaattcg	gcacgagcac	cattttttatt	ttgatgctta	120
cactcattta	ttctgttttt	gtaaaacagt	ttcaagaatt	taaaaatcct	tccagttaat	180
agagcttttg	ttattatatt	ataattttgt	aaacccactt	tgttttttccc	actttaaaagc	240
cacagggctg	actcatggat	gatacctcta	ttgctgctgc	atgatgttca	agacoggccc	300
ttggctgttg	ttacagagat	gttgggcaga	gctatgcagg	tgtttcaattg	ngaactctag	360
ctttgatcat	ggtaaaaagt	taaccccttc	tattttttaa	tggaatgttat	accaactatt	420
cagaggactc	atacttcaaa	aatattagga	aaactgtctc	tatagtcttc	tcaataatat	480
ctgaaatctc	aagtacgaca	tgaagaatg	tcagaccatt	gntattgggtg	aaagtcattt	540
gatgaatggn	aaattctatg	aaaagtaagt	ggatttgcat	ggattaatat	cagggaaaaa	600
ttagccttc	ccaagtgtga	ctgggccaaa	gagagccaga	tgccccagct	gcctgtgccc	660
ataaagttcc	cgaaatcccc	aatggggctc	nttttcaaaa	acttggncca	gacccggaag	720
ataaaanct	tctcataaaa	tcaannngg	gncctcanga	aacaanttcc	cccancaacc	780
cttngg						846

<210> 444

<211> 760

<212> DNA

<213> Homo sapiens

<400> 444

gnagncoggt	tcmnangent	nggctnnatc	caatgctggc	taaagttcna	ananctggca	60
acnccaggan	ncangcgttg	cgaattcggc	acgaggagga	attacaggtta	gcgaattatg	120
gagttggagg	acagtatgaa	ccccattttg	actttgcacg	gaaagatgag	ccagatgctt	180
tcaaaagagct	ggggacagga	aatagaattg	ctacatggct	gtttnatatg	agtgatgtgt	240
ctgcaggagtg	agccactggt	tttctggaag	ttggagctag	tgtttgcccc	aaaaaaggaa	300
ctgctgtttt	ctggtataat	ctgtttgccag	tgggagaagg	agattatagt	acacggcctg	360
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acaagaattc	gaagaccttg	tacgttgtca	gaattggaat	gacaaacagg	cttccctttt	480
tctcctatng	gtgnactcct	atgtgctgat	atnccatttc	ctagtcttaa	ctttcaggag	540
tttacaatng	ctaacactnc	atgatngatt	cantcatgaa	cctcatccat	gttcatctgn	600
ggcaattgct	taccttgggg	gntcttttaa	aaagtaccac	gaaatcatca	tattgcatca	660
aaacccctaa	aagttctggg	gggnatcaca	gaagacaagg	ccnaanttna	aagnggagga	720
attttattat	ttaaaagaac	cttttgggtn	ggatnaaaan			760

<210> 445

<211> 761

<212> DNA

<213> Homo sapiens

WO 99/33982

PCT/US98/27610

<400> 445
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 aaagaacttg gtcataaata tgataatgag aagacaaagt atttatatta aaacagttta 180
 gttagcctta gttttgtgaa aatagttttc agcacagaaa ctgactcttt tagacaaagt 240
 tttaaacaaat gatgggtgtt gcttcttagga tatacacttt aaaagaactc actgtccacg 300
 tgggtgtgcat tgatggcctt tagtaaatg gagctgctta atcatattga tatctaattt 360
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 agtgccagtg gtagtaactg tgtaaagtgt ctaattcaca acnttaattc ctttaaaatn 600
 cacanccttc tgcctctgna tttggaagtt gtcagtncaa ctcatcaag aaaactgcct 660
 aatntnaaaa tcatattntg ggaataattt cctctctttg tagtctgcc aagatcetta 720
 aagattggat ttttattact atttaacca gtaggaatat n 761

<210> 446

<211> 770

<212> DNA

<213> Homo sapiens

<400> 446
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 tgactcccca gctcctcctg gcaccagctcc ccaggggctct cctgttggta gttcctgctt 180
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 ttccacctgg caatgtaaat tgatagctta tcttcacaga tgcagacaaa ttgacaactc 300
 accatcagtc ctctgtctac ctgagacaaa tgcattgtctg attgcttct ctgcccattt 360
 ggntatgtga aaatgcagat tcaactgacc agactaaggc atcagtgact ggtcctctac 420
 ctgcccctca catggagatt gggatttcag tgaaggctg atcaagacc caaaggaaatg 480
 caacagttta tctcttatct acctatgacc tgcgancctgc caccaccccc agntggngcg 540
 cctttccaga cagaaccagt gtacatctta cactatata atngatgtcc onggggctcc 600
 cnaaanngna tcaaacacgc ngggcctoga ccactctggg cacataatcc nanggacatc 660
 annctggagg ctngmgncac tggcattggc cctnacccctn ggcaaaatca accttctaaa 720
 attggnaaaa aanaaanaaa aaaaacctng nncctntna naacnntacy 770

<210> 447

<211> 757

<212> DNA

<213> Homo sapiens

<400> 447
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 gggagaggtt ncattgagcc gagattgcgc cactgcactc tagcctggcg gacagagcaa 180
 gactcgtctc cgaagaaaag aaagagaaa gaaattcccc aggggaagtac ctggccttat 240
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 tatttgggcc gtggcatctg aaattttctta ttccagagc acccctttga tgaccttggc 360
 agtgaactgc agtcatctgt tttaggccttt ccatggccca cgtcaatgcc ggtatttctg 420
 ttgtttgcac atttgatttt cttgtgtgtg gcatttgaa gggcccccggt tccccagatc 480
 accccacggg catggacacc agagattgca tctgtgtagt ctgtagaatt ggtcaaggcc 540
 ttgtcctctc ttaagtcacg agctcangtt aatgcaaaat tttnccggnc atctgtgtgtg 600

WO 99/33982

PCT/US98/27610

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aaatcccttt  ggggaagctc  ctggctgggt  tctgttaggt  aggacagcta  cacgtncctgc  660
cctttattgg  cttcttttca  tgaagctcct  gccatntacn  aaacatgtct  ccctctttga  720
atcacatctc  tggttattgna  actctanaat  cgcccg      757

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<210> 448
 <211> 770
 <212> DNA
 <213> Homo sapiens

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<400> 448
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atcttaccca  gtggaacctc  agaaattaaa  ttctccagaa  gaaactgtct  ttccagacac  180
aaaaactcag  cagatgcctc  ggccttcagt  gccaccatta  gttaaaacat  cactgttttc  240
ttcaaaatta  tctacacctg  atgtttgtgag  cccatttggg  accccatttg  gctctagtgt  300
aatgaatcgg  atggctggaa  tttttgatgt  aaacacctgc  tatgggtcac  cgcaaagtcc  360
tcagctaata  agaagggggc  caagattgtg  gacatcagct  tctgatcagc  aaatgactga  420
attttcatt  cctttcccat  ctacctctat  tagtgctcag  ggtaagacaa  tgagcaaac  480
cagtgtaggt  tttcatgatt  ttcagaataa  acgtgaacag  attaagaatt  tcttgtcaaa  540
acgggtgctg  ataattgatt  ttttcagtaa  gcacccagag  gccncaatc  aggtgttttt  600
ttcagatgcc  caaatgcata  tttgggcatt  agaaaggctc  gtgcacatta  gtagcagcat  660
cattttacag  aggatagatt  tggagttgtc  cagacgcac  taccagctat  ccttaatact  720
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<210> 449
 <211> 792
 <212> DNA
 <213> Homo sapiens

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<400> 449
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atnacttgnt  cncanccgnc  tggcatcnac  ncgncacacc  tacntnagcg  cnttgtagcg  180
caaatnccac  ctntntnaaac  cmnnnagtc  cagggtctctg  cmnnnnnact  gntcaactga  240
cnaacnacen  nctancncaa  cntnnnnnta  nccnctgnc  tgnctctatg  gcaacctnnc  300
tnctcncnc  cntnaccnc  tacgctcagg  gctatataca  atgggaacct  tncccaactg  360
aanccntgga  tctnaggnat  ggcctctgnc  tggcggatca  cagccttnna  gntatcagn  420
attctgagga  agacaccatt  ccgtcccnga  tnttgacca  ncncctcggat  gtgncatgg  480
gctcnattga  ggnacaacaa  ctnncactgc  nnataggcca  tccctennan  nctacacatg  540
ngactttncn  mnncatntna  aatgmnnaa  tgtctctcnc  aagcatcacc  cncgtctcc  600
ncgntcncn  ggaagacctt  ctgnncaact  ganctccttc  ntgnnnccnn  ngatnttnc  660
nnncnnaata  tncntncccc  aatgnccttg  tmnnngnatt  atnaggsgnt  ttccaaattg  720
ggntaaattc  ntncncnccg  nannctannn  nccatnaac  cntcngncc  tctctgnaac  780
cttttnncc  gg          792

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<210> 450
 <211> 848
 <212> DNA
 <213> Homo sapiens

<400> 450

WO 99/33982

PCT/US98/27610

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annctgggng ntcgcaactc nctcmanaca gnaaggncgn gggctttgct ctctccattc 120
caagtgtmtc tctgttctag aaagcagatg tagtagacat ctactgttgt tgctggaaca 180
gaatcccttt gtcccttttt tgntaaaagt actcatccct aatattcatt gtntctggaag 240
gactgaaaat acagaaactca caccatgatc ggccggggaca atcagattat ttccattcmc 300
agcaaacgga gatcganccg aaaagtggaa anatgagcmc ttctttggng ttggcatatg 360
gaccttgaga gaaagaaactn tnatnttttc tcttggactg caataaagta tagctgccta 420
aaatacgnnt cctgacactt ggaggnttgt ccacaatcgg ngaataaag gcgagaccgn 480
acactggatg aaaaaaaa gnnnccngnn gaanaaccac tnnnccannn nccnnnccnn 540
tnnccannng nngancennn tannccgnnn naggcennng cmntngcnnc nnngecnnnn 600
nnnnnnnggn aaaccennnn gnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnccnnng 660
nnggnnctnn nnnnnnnnnn cccnnccncc cnnccnccnn nggnaanncc nnnnnnnann 720
annnnngggn nnnnnannnn cennnnnnnn cannnnccnn cnnnnngggn nnnnnccnnn 780
nnnnnnnnnn nennngngnn acnnnngngn nnnnccnnnn nnnnnnccng nnnnnccnnn 840
nnnnccccc 848

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<210> 451

<211> 765

<212> DNA

<213> Homo sapiens

<400> 451

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gcttnggcnna ctgcgtctctn ctncangcag nnnntgcgtn gncgaattcg gcacagacat 120
tctccttttg ttaacgaagc aacatttaca caagatggac attacattat tagtgcatcc 180
tctgatggca ctgtaaaagt ctggaatatg aagaccacag aatgttcaaa tacctttaa 240
tccctgggca gcacgcgcagg gacagatatt accgtcaaca gtgtgattct acttctaaa 300
aaccttgagc accttgttgt gtgcaacaga tcaaacacggt tggatcatcat gaacatgcag 360
gggcagattg cagaagcttc agttctggta aaagagaagg tggggacttt gtttgtctgt 420
ccctctctcc cgttgtgaat ggatctactg tgtaggggag gactttgtgc tctactggtt 480
cagtcatgca ctggcacaact ggagagaact ttgacagtgc acganaagga tgtgtattgt 540
attgcacatc accctcatca gaacctgatt gctcctacag tgaagatgga ctctaaaagc 600
tctggaaacc ataattcaac ttttcttttt taaatcaact cgaaagcatg tncctaaatg 660
aacatattca tgtaangctt tttttttttt tgncactttt ctaagcaaat agatggctga 720
attagtcaen gaataaattt gngaaaaatca tggttaaatn ccaac 765

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<210> 452

<211> 765

<212> DNA

<213> Homo sapiens

<400> 452

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nnnnnnnnnn ntttctctaa tgettggggn nnnnnngngn nnnnnntctn atgttcttan 60
ngcnnngngn ctgcgtctctn ctncacngnn cngtgcggt gncggtctga ttgaaagctg 120
ttcaggttta tcatgcaaat cctcgccctc ggctacggct ggctgaatgc tgcattgtgt 180
ccaataaggg gactctctga caagaaacta aaggccttc cagcaaaaaa ggaattgttnc 240
agtctattgt tggctcaagt atcatcgtaa aatagttttg gcatcacagt ctatacagaa 300
tactgtttat atgtgagggc agtctctggc cattcctgta ccagatgga gtttgagacc 360
atatgtctca gaaatgcctt gttgtgctc ctgaagaaca gcaagatcca aagcagaaaa 420
atggggctaa aaaaatgcat caattaggtg ggaacacaga gagcacgaaa cgagtgtaac 480
ttgcagcagt naagcatctat atggagatna attcattcca gcttcacctt ctctgcaatt 540

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WO 99/33982

PCT/US98/27610

gagaaaaacag	gaattagaaa	acttaaagtg	ctccatactt	gcttgacgtg	cctacgtggc	600
tctggctttt	gggtgatacc	tcatggcttt	gaatcatgcn	gatnaacttc	ttcagcagcc	660
caagctgcag	gattctctaa	gttttgggac	atttatatgc	tcgagaaccc	ttatcttctt	720
cgacngaatt	tctgtgcctt	tctcacttga	ccccgagaat	gtncct		765

<210> 453

<211> 833

<212> DNA

<213> Homo sapiens

<400> 453

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ntgcgattcg	aattcggcac	gagagaaacg	ttctcaggtt	gaccagctgc	tgaatatctt	120
tttaaggagg	gaagaactta	gtaagtcatt	gcagtgcatg	gataacaatc	ttctgcaagc	180
ccgtgcagcc	cttcagacag	cttatgttga	agtcaagagg	ctacttatgc	tcaagcagca	240
gatactatgg	agatgaatgc	actgaggacc	catagaatac	agattctaca	ggggattaca	300
agaaacatat	gaacctctct	gagcacccca	ggttttggca	ttagaaaaag	ggtagccctt	360
ggttcaaaaa	tcagcaaaaga	aagccttaga	tttggatggg	ggaacctgat	ctgtccagtc	420
tagaaggatt	ccagtgggga	aagtgtttcc	atttccttng	tcccctggct	tggtccaggga	480
aagcgaaagc	cctttcttga	anagcaaccg	tggatcattn	gaccaggaaac	ttccttctgg	540
ggtattaagc	ttcttttcaa	tggaaagggaa	aggttccang	gccaaaaggaa	aaatggaagc	600
ccccaaacng	atgggtttca	ccctaantaa	cctcaattgg	aagggcttgg	accaagaacc	660
cnggaagagc	nanccattgc	acccttaaaa	ncaaggaaag	tggaccacct	ttggggcttg	720
ncnttcntt	ccgaaccagg	ttgaaaangg	gcttgaaaaa	tggttgctta	cccaaaaggg	780
cgnaamttaa	tggcaccaat	tattcctntg	gacctntttt	aatanccttt	ngn	833

<210> 454

<211> 737

<212> DNA

<213> Homo sapiens

<400> 454

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ttcggcaaaa	tcaatgtgga	ctgaacataa	atcacctgat	ggaaggactt	actactacaa	120
cactgaaacc	aaacagtcta	cctgggagaa	accagatgat	cttaaaacac	ctgtgcagca	180
actcttatct	aaatgccctt	ggaaggaaatn	caaatcagat	tctggaagcc	ttactattat	240
aattctcaaa	acaaaagaat	ctcgcttggg	ccaacctaaa	gaacttgagg	atcctgaagc	300
aatgatcaaa	gcttgaagaa	agcagtaagc	aagaagagtg	caccacaaca	tcaacagccc	360
cagtcctctac	aacagaaaat	ccgaccacaa	tgagcaccat	ggctgctgcc	cgaagcagca	420
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gcttccactt	ctgcttctaa	tactgtcagt	ggaactgttc	cagtgtgttc	tgacctgaag	540
ttacttccat	tggtgctact	gntgtagata	atgagaatac	agtaactatt	tcaactgagg	600
aacaagcaca	acttactagt	acccttgcta	ttcaggatca	aagtgaggaa	agtatncagt	660
aatctggaga	agaaacatnt	taaccaggaa	actgtanctg	attttacttc	caaaaaagaa	720
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<210> 455

<211> 718

<212> DNA

<213> Homo sapiens

WO 99/33982

PCT/US98/27610

<400> 455
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 ataatagtga tggaaagaca gctgttgtag gtcttaactt aagttccaga ccagctagtc 180
 caaatctctc ctcaaggacag gcttctgtag gaaaccagac taatactgct tgtagtctgt 240
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 gacgattgcc atatgaactt caggactatg ttgaagatac atcggaatac ctagtctctc 540
 aggaagggaaa ttttggttat aagttatcta gccctgcaaga cctgtgtgtc tctgtctgtc 600
 agtgttcnaga ggatagagnc agaccacgtt ctaaaaacnga gaaatcagaa gacatttnca 660
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<210> 456

<211> 739

<212> DNA

<213> Homo sapiens

<400> 456
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 agccaagatc atgccactgc actccagact gggccaacaga gggagactcc gtctcaaaaa 180
 ctcaaaaaaaa aaatnctatt agtataccgg ggggtggggg ggagaaataa tgttatttcc 240
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 gctctcttgg tncattttatt ttacccttta cngaataatt tcttgtaaaa tccntaaaaa 660
 tntttggcat ttaaaagctc nntcttggan tnaananann mnnaaaaaa ancttncccc 720
 tttanaactt tngngggct 739

<210> 457

<211> 743

<212> DNA

<213> Homo sapiens

<400> 457
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 tggttgncga attcggcacg aggnnanagg gnagctacat gnntnacnt ntngnnctc 120
 tcagccangc tcnctnnnnn ctggtctctac tgctacatag aacacttggt ntncnnggna 180
 actnnntatc gtncnncnga ntctctgnna ctngtttaaa tgctanttga taacaggcta 240
 tgcaaggncg gnaagtggan agcgtcatca ttcactatnc ntnttanctn gantnnntgt 300
 actctacatg ctttgattgg taaatgncm tcagactggg actctcaata aatgnatata 360
 ganganctcg ctgtggaaaan ctgtctctct ntatctntnc atgngnaant tccactncag 420
 ntgaactcc aaatgcmntn atngngnanc cctncttgta tagtgggtgc catccaanc 480
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 cngtnttnc ctgcancctac cataaaaatg gnttacccea gctttatcat ggaattgnta 600
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WO 99/33982

PCT/US98/27610

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<210> 458

<211> 906

<212> DNA

<213> Homo sapiens

<400> 458

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aatcaaggat cacaaaactnc acatttngca cnttggtctn cacaatcmtg gttngggcgag      180
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gggacccann ntccmnatc ncgnnttncc tccnnnatng gagngctnct tngnccannnn      300
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naaanggtct ntccnccnga nccccnnnnn cncetaacan ngnacctcgc aaaggggcccc      480
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nannaagggy nggnnnnnnn nnncttncc nngngnagcc cnnnnnnccn nncntnnenn      840
aaaaattcnn cnttgnanen cccctnnntn nangngnccc natnnnnnnn nnnngnaaanc      900
nnacco                                           906

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<210> 459

<211> 765

<212> DNA

<213> Homo sapiens

<400> 459

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ttgattgggt tgtttaaagt acctaaagtac taccttttga ctccctacca aaagtctctt      180
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ggtcttatct ttaaccctta ttactcagt ttccatctg aatgactcta tctctaataa      360
aaggatttaa taaatgctgc aaattgtcca ctttgcaaat ngtcctaaag ctttagtttt      420
ggaccttngc aacttttttt ttaataaacac attatttggg cccggtcgtg gtggctcaag      480
cctgtaattc cagcactttg gaatgcctag gcagacagat cacttaangc ctggagttcg      540
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tancaagcta tggnggtgca gcctgmaat ctacgtact tgagangcaa atcnggagaa      660
atgcttgacc ngggangcan anatangann anattgcaac actgcattcc acctggggan      720
nanantgaga anctggctca aaacccaaaa acccaaaaaa aaaa                                           765

```

<210> 460

<211> 677

<212> DNA

<213> Homo sapiens

WO 99/33982

PCT/US98/27610

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<400> 460
gttttcgctg ggagccacca acatagcaga ttaccatgtg aagtgtccac tgctgcattct      60
cctgaaacct ggctgagggg agaggtctca tttgtgtctt gagaatgtcc aggtgtgtctg      120
cagacacact cactgatttc ccattagcag ttattatttc ctggccattt ctctctgaag      180
gttttgtggt taaactccct gtctccaata ttttatccgc agtagggctg tcattcttct      240
ggttatcaac ctctacatta tgaagtaagg ttcaaccctt ctgcttttct caggccccca      300
aaacggttcc tatccaatgc aacacaaaaa cgggtattga gaaggaaatt gcagggtctca      360
gtggtctgtt cegtgtctcc taccctcatg agactcttca tcatgtctga tttattgaga      420
ggaacttctaa ctgaccactc acccccaacc actcttatgc agtctgttca ttcttgaaaa      480
caccacttct atccctctct cacaacaacc atgaggggatt gctacttctc ataatgattcc      540
tcagtgaacc ttatagagtt gctgcgagaa ttacatttgg tcatgatgtc aagtgtctgg      600
tatgtagctn atgtctattg aacacatagt aatttattgg aataattgnc atgatcactg      660
gatgagaata tagcccn                                     677

```

```

<210> 461
<211> 787
<212> DNA
<213> Homo sapiens

```

```

<400> 461
gnnnnnnnnag ggnnnnnngg ggccctcncaa agccccngcn acaggtccce gtcccaaaagc      60
ntggngnanc gcnncgcccc ancagnaagg cgggggaang cggcacgagg acatcatcnn      120
cttattctag taagagaaaag tacacagatt caactttaga gaggaacnggg gggnnnnnng      180
gagcmaaatc aaggaaaggn tatcacngng cccccnnga atataannnn gaagctgnga      240
acagnacatc cagnaacann nnatggacag ctctgatggg gnnaatacca cggcactctn      300
cnnacnnngn gnggaagcna tccggagcna tgactgangn gnnaagnggn nnatgmnag      360
aanccngngn ngctaggann ctgggagagn cactttcang aagnnacngn gcgagagcnc      420
atcanaagaa cccgganaag ngagaagacn ggaaaaagnn cncanognac ngagcccagn      480
nannnnctct gagccanggg ctncgaaang ccccacnga agcmccatca canggnacaa      540
ggnnnnggaa aaggaaacna cnnngcngac angnccnccn aanagnacca anacacngcn      600
nngcccnctc gcccaagaa naacnggacng cnggcncnna ncanaaggag cncnanggcc      660
cnnngnaang aaactcnag nagcccaanc ccaaaggccc cnanggannn cncncaaggg      720
gaaaacanna nncacccaag gggcctgggc naanaaggcn ncccacnngn gccnccmnc      780
nnnaccg                                     787

```

```

<210> 462
<211> 747
<212> DNA
<213> Homo sapiens

```

```

<400> 462
ctaattggctt ggnnnnnnng nnnnccgntt ctaattgnc ttgggcnct cgtctntct      60
ccannnagnn nntcggttng cgaattcggc acgagcctca gccccacacc agctctattt      120
caggggtgag agtcagagag cactgcaata tgtgcttcac gggatttcca ttccgaagac      180
ctagaccagg gagacactgt gagccagggg tacacaaaaa tactaggtaa gtcatcgag      240
acogacctcc ctgcagtttg ggaagaagc ttgggttttg gagaatcaga gcatcttgac      300
atgactgctg acctaaagat ccctggcatt ggccagggat cctgtggaac ctcttctaagt      360
tcagggggtg gagcattaga ctgcagtttg tctagtgaac tctgatgctt gctgtgaact      420
tttaagatcc cgaatcctg agcaccctca tctttaattg cctgtatcc cgaagggtta      480
tataatttat ctgagtggaa attttaaga tgaatcccc tttttctct tctnctctct      540
tttcttctct tctcctcttc ttctttgctt tctaaatata ctgaaatgat ttanatattg      600

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WO 99/33982

PCT/US98/27610

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gtcaccaatt aatgatcttt tattcaatct aagaaatggn ttaagttttt ctctttagct      660
ctatggcaat tcacttcaac gggacagggg aaaaagtaan tgccatnngc tcacaagaat      720
tnntttatgt ttagctattt taaaaaa                                747

```

```

<210> 463
<211> 750
<212> DNA
<213> Homo sapiens

```

```

<400> 463
tncctttcta angcnmntng nnaanngtcn cegtcttaan tncctgggca gnnccgtctn      60
tctncanmca gmcnmtgcgt tgcgaattcg gcacgaggcg agatgaagct acactgtgag      120
gtggagggtga tcagccggca cttgcccgcc ttggggctta agaaccgggg caaggcgctc      180
cgagccgtgt tgagcctctg tcagcagact tccaggagtc agccgccggg ccgagcccttc      240
ctgctcatct ccaccctgaa ggacaagcgc gggaccgcgt atgagctaag ggagaaacatt      300
gagcaattct tcaccaaatt tgtagatgag gggaaaagca ctgttcgggt aaaggagcct      360
cctgtgggata tctgtcttaag taaggattcc atatggtctc catatcatcc cattccatct      420
ctgccaagat ttgataccgc caaaaatttg tgttngngga agattctgnc tgaactcttt      480
cattcaagga actactacca tgaatctgca tctctngtgc cacactgagc ncttagtaga      540
taattgggtg gttctgaataa cctattatct cttatntctg gtctctange tggnatgtta      600
attcctctga aatgntaaaa gtaatgggtg anaccngaaa aagaaatttc aatnacagat      660
caanmtgggg ngcatgtatn attttcaagc gtcaaaaatgg aataagggaa gantnctgga      720
tacctgcttg gaaaaggaag natgtgtatn                                750

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<210> 464
<211> 748
<212> DNA
<213> Homo sapiens

```

```

<400> 464
gnnngtctct tgnaaaagcct ttggggaann gmcncttct aatgcttggc tatcngtctt      60
tacgcagmnc ccacgattcc gaattcgcca cgaggccggc cggcgacgct ggcgaogctt      120
tcgcccctga ggtagtgttg cgaccgcgaa gaaggaaaaa gggcggcgcg gcggtgtctc      180
tctcacctgc ctacccccgc gaggcccgcc cgcctctctc gtogtggatt tcgcggcgat      240
ccccccggca gctctttgca aagctgtggtt aaacttctcc caaactcggc atggaacga      300
ctgcggcggc ggcgctgcct gcttttgggt cgtcttctgt cctctctcct tggcctctcc      360
tgggactcgc ccaaggccag ttctccgcag gttggntgct tctttcgttc tctcctctgg      420
gggctctgaa gtttcaccag gtggacgctg gggagcgggc tcccagagcac ttgtctacct      480
nccgcacgct ctgacaactt ttctggccaa cctaccagc ttgccttggc tggcgagcgc      540
atctgtctgt ggggttcgcy gtgcaaatgg agacgcagtg gtggccagag ggtgatggag      600
aagacgggaa aagcgacagc cagctnctgt gcttgaagcc gcaggacgca aataaectac      660
tttgacactg acagttctac gttgntgttg angccctgtt tcctggaaat aaaactcaaa      720
atggtggttt tttggaaaaa aaaaaaat                                748

```

```

<210> 465
<211> 863
<212> DNA
<213> Homo sapiens

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<400> 465
gggnnnnnnnn aangnnnnnn ggnnnnngtc cegtctccaan gaccnnngaga tcgnnngcgc      60

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WO 99/33982

PCT/US98/27610

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tccanaagaa aggcgggtgng aattcggcac gagacctgta ccgcctggcc actggctgtc 120
accggcggtga tgagctgcgc gtgtttgaac cnggcacttt ccgggcanaan 180
nggcnnnnaan atggcnccca tncaggaagc cgcacagaaac ctccctngnnn acacnaacttn 240
agngccttcn agtcocgttg naccocggnc aagcccccgg aancnctgcc ccgggtcncc 300
gttcccaagg ccaaccagcc ctgggnaccc ccggggagcc gaaacnctgg ggctnggana 360
ccngantga gagncncaact tttcnmtgta nacacgggcc cagganacan ctntgctcgt 420
ggccccgggg naaannnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 480
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 540
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 600
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 660
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 720
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 780
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 840
nnnnnnnnnn nnnnnnnnnn ncc 863

```

<210> 466

<211> 713

<212> DNA

<213> Homo sapiens

<400> 466

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ngtctttcga gcntggngmt cgttctngct cnannanatt ggttgnggga attcggcacg 60
agcctcagcc ccacaccagc tctatttcag ggtgagagat cagagagcac tgcaatatgc 120
gcntcatggg atttcgattc gaagatccta gaccaggag acactgtgag ccagggatagc 180
aacaataatc taggttaagtc actgcagacc gacctccctg cagtttggga aagaagctgg 240
gtttgtggag aatcagagca ctttgacatg actgctgacc taagaatccc tggcattggc 300
cagggatcct gtggaacctc tctagtcca ggggtgtgag cattagactg ccagttgtct 360
agtgcacatc gatgcttgc gtgaactttt aagatccccc aatcctgagc acctcaactc 420
ttaattgcc tgtattcoga agggtaatat aatttatctg gatggaatt ttaaatgatga 480
atcccccttt tttcttttct tctctctttt ctctctctct cccttctctc tttgcctctc 540
aaatatactg aaatgattta gatattgtgc aacaattaat gatcttttat caatctaaga 600
aaatgggtta attttttctc tttactctat ggcantcac tcaantggac aggggaaaaa 660
agtaattgcc atgggcttcc aaaagaattg ntatatgntt tagctatttn aaa 713

```

<210> 467

<211> 732

<212> DNA

<213> Homo sapiens

<400> 467

```

gnnnggtntt ctaatncttg nnnnnnnntc ncccttctaa gccntggntc cgnctnnccn 60
acnannnggc ttncgaattc ggcacagagc gagatgaact acactgtgag gtggagggtga 120
tcagcccgca cttgcccgcc ttggggctta ngaaacgggg caaggcgctc cgagccgtgt 180
tgagcctctg tcagcagact tccaggagtc agccgcgggt ccgagccttc ctgctcatct 240
ccaccctgaa ggacaagcgc gggacccgct atgagctaa ggagaacatt gagcaattct 300
tcaccaaat tttagatgag gggaaagcca ctgttcggtt aaaggagcct cctgtgggata 360
cttgtctaac taaggatttc atatggctct catatcattc cattccactc ctgccaagat 420
ttggatacgg caaaaatttg tgtttgtgga agattctgtc tgaactcttt cattcaaggat 480
actactacca tgaactctga tcttgntgcc cacactgtgg tcttagtaga taatttgggt 540
ggtctgaagc acctattatc tcttatttct ggtctctagg ctggtatggt aatcctctga 600
tatgtcaaaa gtaattgggtg agaccngaaa aagaaatttc aatacngatc aantttgggg 660

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WO 99/33982

PCT/US98/27610

tgcatgttga atttgaacc tcaaattgga gtaaggggaan attctggata cttgtctggaa 720
aggaggaatg tn 732

<210> 468

<211> 748

<212> DNA

<213> Homo sapiens

<400> 468

gnnagnnttc taatngcttg tnnnnnnnna gacgttctaa nnetttggcn ategtntttt 60
ctncagnann cntcgattc gaattcggca cgaaggccggc cggcgacgct gggcgacgctt 120
tcgccccctga ggtagttttg cgaccgcgaa gaaggaaaaa gggcgggcgg cggtctgtcc 180
tctcacgcgc ctccccgcgc gaggcccggc ccgtctctnc gtctgtgatt tcggcgcgat 240
ccccccggca gctctttgca aagctgcttg aaactctccc caaactcggc atggatacga 300
ctgcccgggc ggcgcgtccct gcttttgttg cgtctctgtt cctctctcct tggcctctcc 360
tgggatcggc ccaaggccag tctccgcag gttggtgtct tctttcgttc tctcctctgg 420
gggctctgaa gtttcaccag gtggaagcgt gggagcgggc tcccgagcac ttgtctacct 480
tcgccagtc ctgacaactt ttctggccaa cctaccagc ttgccttggt tggcgagcgc 540
atctgtctgt ggggttctgc gtgcagatgg agacgcantg gtggccagag ggtgatggag 600
aagacgggaa aaagcgacag ccaagctcct ggctgaacc cgaaggacgc aaaataactt 660
actttgnacc tgacagtctc tncagtttgt tgtggangcc ctgtttctctg ggaaaaataac 720
tcaaatgtgt ggtttcttgg aaaaaaaa 748

<210> 469

<211> 776

<212> DNA

<213> Homo sapiens

<400> 469

ggngntota atgottgnnn tgattctcgc ttctataacng gntaatnctt ggnccctacna 60
aaaggctang ngaattcggc acgagacctg tacgcctgg ccactggctg tcaccggcgt 120
gatgagctgc cgtgttttga acgcaacctc tgctggactc tcccggcaga ctgcctggat 180
atggtcgcca tgcaggaagc cgcgccagcac ctctcggca cacacgactt cagcgccctc 240
cantcgcgtg gcagcccggt gccgagcccc gtgcgaaagc tgcccggggt ctccgtttcc 300
ccaggccaag ccagccccct ggtcaccccc gaggagagca ggaagctgcg gttctggaac 360
ctggagtgtg agagccagtc ttctcgtgat agacaggtac ngaggatgac ngctgtgtcg 420
gtggcgcgtg ggtctnaann tnnnnnnnnn nnnccnnnac caantctncc nannnnnnnn 480
cnnacnnnta aaantnnccn ncnnnnnccn nnnnnnnnac cnnnnanncc nnnnctnnn 540
naannnnnnn nnnnnnnanc nnnnnccnna nnnnnnnnna nnnnnnnccn nnnnnnnccn 600
nnnnnnnnnn nannccnnnn nnnnnantnn nnnnnnnnnn nnnnnnnnnn aaannnnnnn 660
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnccnnccn nnnnnnnccn nnnnnnnnnn 720
cnnnnnnnnn nnnnnccnnn nnnnnntnnn nnnnnnnntn nnnnnnnnnn nnnnnn 776

<210> 470

<211> 765

<212> DNA

<213> Homo sapiens

<400> 470

tatgnnttn ctaaaatncc tgggcaanac gtccctcnct tctctaanagn ttnggcanaa 60
cccttgccaa nacgcctgn acccanaacc agnnnggcg tggcgggcga gcggcgcaaca 120

WO 99/33982

PCT/US98/27610

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gctcttgagg agtgagactg cnggagatnt gggccgtgcc aaagagatgg atgagactgg 180
tgctgagttc atcaagagga ccatcttgaa aatcccatg aatgaactga caacaatcct 240
gaaggcctgg gattttttgt ctgaaaatca actgcagact gtaaatttcc gacagagaaa 300
ggaatctcga gttcagcact tgatccatct gtgtgaggaa aagcgtgcga gtatcagtga 360
tgctgcctcg tttagacatca tttatatgca atttcatcag caccagaaaag ttggggatgt 420
ttntcagatg agtaaaaggac caggtgaaga tgttgacctt ttgatataga aacantttaa 480
aaatctgttc aagaaaaattc ttcanagagc attaaaaaat gtgacagtga gcttcagaga 540
aactgangag aatgcannct ggattccaat tgcccggggc acacagtaca caaagcccaa 600
ccagtcacac ctacctacgn ggggggactcc tccagactcc cgnacnctct cagctcctcc 660
tccatcaatga ggcgcaatca cgccttctgg gncacagaagt tanaaacnct gggaaaaact 720
acctnagaca agaaggggan catttanatt taccnnaaat gaana 765

```

<210> 471

<211> 820

<212> DNA

<213> Homo sapiens

<400> 471

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cnnnnngggg nnnngggcgn cntcnaaaan cggggggcgc agnccnnngg ttccaacaga 60
ccngggnggc cgnccnggcc ccanacagca ngggnggggc nnnnggggnn cncnncnnn 120
cnnancnaca aagaaactca caagaaaaaa acnaacccca caagcgggca aaggacngga 180
acagacantn cccaacagaa gacatacaag caaccnaaaa taatcnaaaa taagnnncaa 240
aagaaaaaaa ngcnagacag agnnngngana gnactnagna aaaagngana tctagcgggn 300
annagnangn nngnnnncag ncngnnncna agaaanagnc nctggnnccc aagcnggggn 360
acagcggcgc aagcnnngcn cactgcaacc gcgaacnccc gggctcaagc gaacncnagc 420
cctcagcctc ccaagnngcn gnnaaaggca ngcaccacca caccgccna aaatanccng 480
nancaanaac ananaanggc nccccnggc nnnncnagga aanaaacacn cnnangcnnc 540
ngaaaaaan naancncnnc cnnnacaaaa aaacnnnagc cnnagaacaa nnnnggaggc 600
ggaanacggn nnancccgac anganaanga nacnanngan gganganngg gaccnaacn 660
cancccgga anggcnnngn aaaaaaaang cnnnaaanm ggggggaaaa ncgngnngan 720
ccnaaagggc cnaaaanggc gaaccnncn naaaangccg ggcannannn aaccnagcnn 780
nancnancn nccaangggg nannncnnc nncnagccg 820

```

<210> 472

<211> 738

<212> DNA

<213> Homo sapiens

<400> 472

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gnngtgctc taatgcttg ctactngtgc ttctcgccga acncttgcta atgcttggn 60
ntgcttctt ctccacnnac nnnncnntnc gaattcgga cgagggtaca ganatnaaa 120
tccaatcata ggggctggnc cnacntctnt gctnntccct gcangantca tangatcagn 180
nanaccgtgc gnntttgnaa gcntttcaaa tegtntacca tcgngttact tcnngnggca 240
cctgntgann tnggttgnaa tnnncnggat nctccaaanc caccnnnnnc atgggntng 300
tgngcatgng ntggnnncan nacagannna ganactttaa ngaannngnt gtatcaaccn 360
tngnnctag caancntgan antnccaggg nnggccacna agctgaaatc nnatgtana 420
cnnaatngt naatctctag natgacttcc ncannnancn aaactnangc anggctgcna 480
tgtagaanc tanaggcna atttctntc ntntatgctt ttaagacnct ttaagacnct 540
caactgttnc natgaagccc atntacatna ttncggtaat agcgctatnc ttaaanntaa 600
ctgctgaaaa tnatgatna nctacgaat cctnncancn ncatntggct naatcattac 660
caaccatttg acaccnncat ngnetaccca cntgcattnc catgaacnan tccantgcca 720

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WO 99/33982

PCT/US98/27610

ccgcgcagca tntacett 738

<210> 473
 <211> 752
 <212> DNA
 <213> Homo sapiens

<400> 473
 tatgnntncc taanagagtt ntgnnacacg gccgccttc tnaaancttc ctaatncttg 60
 ggcgcctcgt ctnctncaac ncagnnnttg cggtncaaat tcggcacgag gtccctttga 120
 accaccceaa agaactcaac atggcaaaagc aaatggtaaa agcttcccga ctgtctact 180
 ttgggtccgc gcgaagccca ctcacgtgtg atctgtgttg cccctgggag gcccgggcg 240
 accggaaaag ggctctctca agttctgaaa agagaatctg ccaccagatc gaattctgac 300
 cctcgagctt gttcggagct atggtccaaa ttcagattaa ggtgtgtcacc caaccggaga 360
 tgtcaggaaa ggctttctgc agagaaaaatg tcccccaacc gcgcattctgc agccagggtg 420
 gtgccacacg gcagccttcc cgaacaatag tatggatttt aaaaatgtgt ntatttttgg 480
 ttctcaacca ctttataacg tattttttaa tttattttgt aatgtcttgt tttgaagtat 540
 gtctgctatc cttggtatcc tccccactgg ttttatcaat gantatttt gngaagtgt 600
 ncactaatgt tctatgtcaa aatcaaaaat atttaatgaa atactanntc tatttaatgt 660
 ggnatggaaa ccagctggaa acacaaaaca aacagtatt gacancaagc tgggcccacg 720
 agncaggtca ttttgnacat atgccataaa ac 752

<210> 474
 <211> 752
 <212> DNA
 <213> Homo sapiens

<400> 474
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 ctcgntctnt ctccacnagn nnttgogttn cgaattcggg tctnagccca tgccgggatc 120
 ttcccacacc cgtctctaca gatccagccc cagccctgtt ctccccaggc catctctcag 180
 cagcacctgc aggatgcggg caccggggag tggagccctc agaaacgcatc catgtcggag 240
 tctctctcca tcccagcttc cctgaaacgac gcggccttgg ctcatagaa cagtgaagtg 300
 cagctcctga ctgaaaaggg cctgatggag ctgggggggt ggaagccgct tccgcacccc 360
 cgggogctgt tctgtctcct ggatggcagg tccaaacgtc acgttagaca ttcatacatt 420
 gatctccaaa gagctggaag gaacggaaat aatgatccca gtttggactc tggcgtagat 480
 atgaatgaac caaaatcanc ccggaaggga angggagatg ctttgtctct cgacgagaac 540
 taccgncgcg tccaagagga ccancagaaa gancctcanc cccagacagc accgntcaca 600
 cgcancctgt gnacctggat gacntggaac anaatggtan cnaatgtggg accacngnct 660
 tgtanccma ggacaaggcc ctnmcangct tngtggangg gtcnantcng anaaatggng 720
 gccactgcc aaccgcgag aaganaacaa nn 752

<210> 475
 <211> 742
 <212> DNA
 <213> Homo sapiens

<400> 475
 gntttctntt aatncttttn naaangcggn ntttacntt ctangnntgn gntcgttct 60
 ttcccacma nnnncggtg cgaattcggc ncgaggtgaa acagaaagtg gagatgcttt 120
 ccttgacctg aagaagctc ctgcctccaa atgcccccat cgtatataca aagaagaact 180

WO 99/33982

PCT/US98/27610

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cttgatata aaagaactcc cccattccaa acagagcctt catgccttcc tgaataatat 240
gacagtgat gtgtctggga ccttgagaag tggcatgcct ctctctaccc agcttcaggg 300
cggagctcac cagtggaaag tctgaagaaa gaggttgata cagaccggcc ttcctcggtg 360
cgcagagatg tagatccacg agagcgtgtg aaagaagatg acttanaagt tgttctcagc 420
cctcagagac ngagctttgg agggggctgc cacgtgacag ccgctgtcag ctcccgccgc 480
tcangaagtc cattagagaa agatagtgat gggcttcgtc tgcttgggtg acgtaggatt 540
ggcagtgtga ggataatct tgcccggaac tttagaagg atcacgcctt aacgataagg 600
acctgcggga cttgagagac agagaccman anaagactt caaggacaac gtttcangan 660
anaanttttg gagaaagtaa ncntgtcttt tgggtgancgt anaanaaat gattcttactn 720
cnaanaaaga acccgaaatg tt 742

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<210> 476

<211> 1122

<212> DNA

<213> Homo sapiens

<400> 476

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gnnnggggnnn ttctaaaagc tgggnnnnnnn nnnngaggnnc ttctaatnct tctaatgggt 60
ggctctcgtt ctctctnccac gcagcnnngc gnnnccgaatt cggcagcagc ctgcagccac 120
taatgcattg tgtatgataa caaaaactct ggtatgacac attttctgng atcattgnta 180
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ggggtgtatn cctcngggga nggnnnnnnnn nnnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnn 300
nnnnnnnnnnn aannnnnnnnn nnnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnn 360
nnnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnn 420
nnnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnn 480
nnnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnn 540
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<210> 477

<211> 747

<212> DNA

<213> Homo sapiens

<400> 477

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gnngtgccct tgaannccn ttggnnnng nggcccttct aatgctnttn cgtcngggg 60
gtcgaaactg ccccaactcg cnaggcgggg gctncaagcg attctaaac acctatgagt 120
attctcttta gggctcactt aaatacatgt ntgngnntac ttggggctag ccgaataat 180
tttagatcgt atcaggtngn ngctnaaatt ngaaaaaan cnnntngatg cttaagaagt 240
tngctccatc ttttgagctc aaatctctta aaatnactg ngatccacat ctagnagaat 300
gtcmgtgtca anatatctn gatnatcgct naaatccnca ttaatactcn ctngggggttn 360
nnnatagngg aaectctnag nnnntcncaa agcacatngn ctctcgtmct ccgctgctcc 420
cacagnnggt nttgnaactg ggnaaatcag nnnnnngata gcgngngnnt ntnaganaaa 480

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WO 99/33982

PCT/US98/27610

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ntngatncac acatnctttn nnctcagnnc ncacatngat tgaacactct ggccaagatg      540
ctgngngnga tgaagtggga gtctgannga agaagccngc gctggcctgg ctctnaagac      600
cmnngncttt cccntnccct cnetngaaaag ctgcccngac ngaggccnaa ngnaaatggg      660
tganngnnnc gtcnngcccn cttcngcnnc ttngaaacmn nnagngggnc tnnnngnacc      720
cnnngnnntn cngnaaacgg nncnngc                                           747

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<210> 478

<211> 746

<212> DNA

<213> Homo sapiens

<400> 478

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gnnnnnnngcg cgncccttcta atgcttenta attnnctngg atactcggtc tttctncagg      60
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ccctcctgcc ctctgggttc acaatacgtg tacacttgac tgtgaagtgg ctgtgagagt      180
gggtggagag ttcttctttg accctcagcc tgcggatgcc tctagaaacc tctgttgtat      240
tgcagaggga gtccggaatta accctctgct tccatcctg cggcacgacg cagatctcct      300
cagagagcag ccaaacaaaa gaaatggata tgagatagga acaataaaac tatctcacag      360
tgcaaaaaat accagcgaac tctgttttaa gaaaaatatc cttgatttag taaatgaatt      420
tcttgagaag attgcatgca gtttgcattg taaaaaacag actacacaaa tcaatgcgga      480
actcaagcca tacatcacgg aaggaagaat aacggagaag gagataagag atcatattc      540
aaaagagact ttgttctata ttgtggccc accctcaatg acagactttt tctccaagca      600
actggaaaac aacctgtac ccaagaaca catttgcttt gagaagtggg ggtaggaggg      660
aagaccaaag cagggaaaaa attaangagg tgagatctac tcaaggagag ctcaaaaaaa      720
aaaaaaaaa actngggccc tttaga                                           746

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<210> 479

<211> 750

<212> DNA

<213> Homo sapiens

<400> 479

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gnnnnnnnnn nngngnnnnnn ttctannntt cntattnnct nggagctcgt tctttctnca      60
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gttccacgta gcaacacctg ctgagttctc tgggttttct tctgcctca tgtagcccag      180
acttggagct gaagaagctg gaaacatgga aacaccaaca gctacagacc aaaaaaagt      240
ccaacaaagg cctgtcagtc tgcacagcctg ttctgtggat ttccaactca agattgcagc      300
atcaactcac acctgaagtt ctggcttccc tacaactttt gaacttgcga gtcccacaa      360
tggcataagc caattcctta aatatgaatg ctagtcttag ataattgtgt tattctactg      420
gttctgttct tctggagaag cctactaata gatcatttgt cttagtcaat tcaagctact      480
ggtacagatt accatagact ggggtgttaa aactaccaat ctattactc acagtttttg      540
gagtcgtgaa agtctgagat cagggttcca gcaggattga gttctttggg gaacatnctc      600
ttctctgmct acagaatact gggttacttt aagtnggaaa aagtaggggt aagctgggtc      660
ntttggcctc ttcttttaag ggggactaat tcatgaaggg ttccaccctt attgacctat      720
tttaccttnc caaangntt ccattttccn                                           750

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<210> 480

<211> 714

<212> DNA

<213> Homo sapiens

WO 99/33982

PCT/US98/27610

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<400> 480
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tattttgaac cctataccaa tatctgntga tcaatgacca tttttgtcca gcatggagaa      180
acagtccctt gcatgaaggg tagtgagaat aaaaaggatc ttaccacttt tatcatgagg      240
gtggcttttg tctctccatt ccaagttggt ctctgttcta gaaagcagat gtagtagaca      300
tctactgttt ttgcctaaac agaatccctt ttctcttttt ttgttaaaag tactcatccc      360
taatatatac ttgttctgga aggaactgaaa ataacagaac tcagcaccat gatcggaccg      420
ggacaatcag attatttcatt tctcancaa acggagatcg atccgaaaag tggaaaatatg      480
agctcttctt tgggtgtggc atatggaccc tgagagaaag aactttaatt ttttctcttg      540
gactgcaata aagtatagct gcctaaaata cgtttcctga ccttggangt ttgnccacaa      600
tcggtgaaat aaangcaaga cgtacacttg gatgaaaaaa aaannnnnnn naaaaaaaaac      660
tcgaccttta nactatnnga gtcgatacnt aatcngactg atagatcatt gnta          714

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<210> 481
<211> 742
<212> DNA
<213> Homo sapiens

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<400> 481
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nactcgtttt ttctncaagc acccatcgnn nogaattcgg cacagggcat gaaaggagtc      120
ggaagcgga ggggtagccc ggaacgtgct gtgggtgcaag ggcttgtgga aaaattggag      180
aaaaaccaag ccttgcccca gcagttgaca agggaggcca ctcaagcgga aattgaagga      240
gataggtctt atcagcacag tctccgcctc ctggattcag tgtctcggct tcaggggagtc      300
agtgtcagtt cctttcaggt ggaagaagca aagaggatca aacaaaaaag ggatttcaatc      360
tcaagccttg taaccaggca tatggaatag ttcaagcgta cacagaagaa tctgggaaac      420
tggaagaag aagcacagca gctcttaacag aatggaaaaa gtgggagaga gaaatcagat      480
cagctgcttt ccctgaccaaa tcttgctaaa agcagancac aagaagcact gagtatgggc      540
aatgccactt tttatgaagt tgagagcctc cttaaaaaac tcagagagtt tgacctgacg      600
gtggacaaca gaaaacagaa ctgaagaacc atgaagagac tctnctacat caccagaagg      660
ttcagancca atgacaagac ccancaagca naagagccct ggggagccct ctgtgatgcc      720
caaaanggcaa aaaaatggggc cn          742

```

```

<210> 482
<211> 752
<212> DNA
<213> Homo sapiens

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```

<400> 482
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ngctccttgt ctttntgcag gatcccatcg attcgaattc ggcacgaggc caagcctcgg      120
cctccactgc acctgctcgg gagtggcacc ttgctcgca aggccctcta ccccatggcc      180
cagtgctcat tcagcagggt ctttggccac tcaggaggcc ctttgtgtgg gttgctcagt      240
ctgtccttcc ctcatgagaa gctactgctt atgtccacag accaggagga gctgtcacgc      300
tggttaccca gtctgcactg ggctatcagc agccagaaaa actagaggaa tcttatagat      360
tcagaactc aggatccctc agggataggt cacagcgaag agtcaaaagg aatcttcagt      420
actgaacaaa acagaacccc tcatgattg acaaaaggtc ctttctgttt gctctgacca      480
agctactcca gatcattcga ccaactctta aaaatcacgg ccaggcagag tggcctatgc      540
ctgtaatccc agccatttgg gaagcaaaag tggcaggatc attccagccc aggagtttca      600
agancagcct ggcaacacag tgagtgagac cctgtctcta ttaagaaaaa aaattattaa      660

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WO 99/33982

PCT/US98/27610

gaaattttat	taaaaaagga	agaatcagga	aaccaaagtc	aacccaact	taaccctcaa	720
tgaaccagcc	ctaacacaga	tgangggatt	tg			752

<210> 483

<211> 849

<212> DNA

<213> Homo sapiens

<400> 483

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tttggaaocgn	cgactnctnn	atatatcnng	gataataatg	gtgataagtt	ctgncaatta	120
gtaacatcng	gaaaaaacag	ctnnngcctg	gngaaaaaag	gatgccaaaa	tngcctggaa	180
aagagcagng	gagaggagtc	cgggagatgn	ngatgcato	gggacgcanc	atngntnaac	240
attcactggg	tctgccaaaa	atgtggattt	nggggctgct	tagatngtta	caaggcaaaa	300
ggaaaggaaa	gagttctaga	gataaaagaa	ctatatgctt	ggatgaagtg	tgtgaaggga	360
cagcctcatg	atcaccaaca	tttaatgccc	aacccaaaat	tataccnggt	tctgntttga	420
cagacttcta	gatgccatgc	acactcttag	ggaaaaaata	ttgggattaa	ancccatngg	480
catggacta	acaaacagga	atttacaagg	tnggaaaantt	ttncnaccaa	tgaagggggg	540
gatcncaagg	ttttccagaa	nggntcntaa	tcnacagtnaa	taaaaattnc	tctngggcaa	600
gcctcagtc	ttaaacagca	aaaanactcc	tcccgaancc	tgnagaaaaa	agggggggca	660
gccaggcccn	naaaanggaan	gtnaggcccn	agatnaacaa	ngtnaccttc	ncccagnaaa	720
cccannnccc	caactcgnac	cnsggnaacc	cacaaacttt	gcngaagnc	aaaaaagnc	780
nnnagangga	aaaaaaaaaa	naananaaaa	aacctnnnag	ccctcaagaa	accttagggg	840
nggccnccc						849

<210> 484

<211> 1098

<212> DNA

<213> Homo sapiens

<400> 484

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cgggcnccca	ggnccgggna	aaggcccccc	ttggggcgcc	cccgngcggc	cccaatgggt	180
tccaaaaagg	gaaaaaaaaa	aaagggggaa	cctgggaagt	tggccccanga	aaangnaaaa	240
aaaggnaagn	aaaccttcgc	ccaatgggaa	tggggaaaaa	taattttttc	tggaaaaacc	300
caaaaaagga	atggttattt	ttcaaattta	aaaaaggaa	nttgggaaga	aagaattggc	360
ttcccacncc	cagaaaaggcc	attactggct	atgtcaagta	aaagaagtcc	ttcaaaagctt	420
agttgatgat	ggtatggttg	actgtgagag	gatcggaact	tctaattatt	attgggcttt	480
tccaagtaaa	gcctctcatg	caagggaaac	ataagttgga	gggttctggaa	tctcaagttg	540
tctgagggaa	gtcaaaaagca	tgcaagccta	cagaaaaagca	tttgagaaag	ctaaaaattgg	600
ccgatgttga	aacgggaagag	cgaaaccaagg	ctntgcataa	agagcttttc	tttcactttc	660
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ctgggantaa	aaacantata	tttcccccc	naattnnaaa	aaattcnttt	nggggncccc	900
naaaaangna	aaaaaatttt	nggggggttt	tggnaaggna	aaaatttnaa	atttgatttt	960
ngaaactttt	ttngggattt	ccccagaaag	aacttttgac	cttcctntng	acctnaaaaa	1020
ttttcccttg	ggggggtgna	anggatgttc	ccaagctttg	tggnatattg	gtaaaaattt	1080
naaccttttn	tncttacc					1098

WO 99/33982

PCT/US98/27610

<210> 485
 <211> 798
 <212> DNA
 <213> Homo sapiens

<400> 485

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gnnnnnnnant nnnntttnaa atccttnntg aatcctttga antaccatcc cnttttnnca 60
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aagctgcccc caggcgagagc tgcttgagat tgtagtcat gaaccagaga agcccccgctc 180
catgagcagt gactccccan gccctgtgac ctccctccn ctgcagctc ctccctggcac 240
cagtcgccag ggctctctctg ttggtagtct ctgctttct tcttggaaat tctctgtgga 300
cctcgagatc ttaccctaa aatagtctct ttgaatttca cctctggcaat gtaaatgtat 360
agcttatctt cacagatgcc agacaatgga caactcacca tcagtcctct gctcacctga 420
gacaaatgca tgtctgattg ctctctctgc cctattgntt atgtgaaaaa cgagattcac 480
tgagccagac taaggcatca gtgactgttc ctctacctgc ctctcacatg gagatttgt 540
attcagtgaa aggtgatca aagacccaaa ggaatgcaac agtttatctc ttatctacct 600
atgacctggc aactggccaa caaccagtt ttgncgctc ttccagacag aaccagtgct 660
atcttacacg tatnaaatg gatgtcctgg ngctcnccta atatgtattc aaaagcaagc 720
tggggcctng accaccctn ggacacatt cctcangac atcattctcg angtctgttc 780
actggcatgt ccttaanc
798
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<210> 486
 <211> 785
 <212> DNA
 <213> Homo sapiens

<400> 486

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ggagacagtt gatagccaaa caacagtttt ggattcactg actgattatg aaagaagcag 180
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ccttgaacat tcagcacaaa gacaaaaacg accagaccag aagagtccca cagaataggg 480
gaaactattc agagaaaact taagccaata agttttatgg tgtttgttct tgtagcagaa 540
gcataggcat actgacaata caaacgaaa tcttcttaac gtatggacc ttttcangcc 600
agcatttttt ccttgaaaaa ctggagcatg tatccatctt atagcagaga tcactttcac 660
aatgggtggg ctcttggtat tgaattgatg atgtaatgag ccctcttnc ngattgnaac 720
ttaattacac tgggnatttg ntggattccc aacctcttaa tatttacctt tctcttttan 780
taanc
785
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<210> 487
 <211> 797
 <212> DNA
 <213> Homo sapiens

<400> 487

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cgaattcggc acgagnnngg actacctnnc aaaaacnngt ngggaagcmt gttacagaa 120
tgatntctan tcccctnagt tctggatgct gcagaccaac acctgcncac aanaancana 180
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WO 99/33982

PCT/US98/27610

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cacacacann caancantat catgtaagac agnncgntna ntntnnnnatt ntatncttnt 240
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gananangac ganantctga atcttaagca tatgetccat cntntnatat gctntgggtgg 360
agaggctngc cntnatctcat nttnnecatg agncaagttt aatgcctcta gantacattc 420
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nctnagtggg ntcaagacaa ctttngtggg ggttttgntc acaatcatga aaatggtttn 540
gccagataaa tattttgata ttagnntttn tttttnatnt annccggtag gtttgaattg 600
nacnttnaaa tgnntngggg tgtnaagaca ntggnttnca atnnaattta tnatcatgat 660
tggnngnctcc cctttggnga aaccttaagc aantntngna tacttcttca taaaagggtg 720
tgnngattng naantttcgg ggggttttnaa ttttntntga agcttatctc ntganaatnt 780
aactggntta ccaagcc 797

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<210> 488

<211> 762

<212> DNA

<213> Homo sapiens

<400> 488

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ctgggctactg cctctgtggtt acagacgtgt gcagttgtag gcatttagct acaggacatt 180
ntannnggccc caggatcggtt ttttcccagg gcaagcagaa gagaaatgt tgatatatgct 240
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agagattttt ccacaatgat gatgatttca gcaggggatga cgtcatcatc acatcaggg 360
ctattttttc cccacaaacc caagggcagg ggcactctt agcttaactc ctccccgtga 420
ctgcaataga accctctggg gagctcagga aggggtgtgc tgagttctat aatataagct 480
gccatatatt ttgtagacaa gtatggctcc cctgtatctc cctcttccct agggaggag 540
tgtgaagcaa ggagcttaga taagacaccc cctcaaaccc atctcctctt caggagacct 600
acccttcaca ggcaangtc ccccaaatga gaagctcgt accctctt tcttnatctt 660
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<210> 489

<211> 822

<212> DNA

<213> Homo sapiens

<400> 489

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ttntnnnnnet nnnngnnttt cnaatncttg tttctcgncc tttctgcagg atcccatcga 60
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ccatcatacc ttctgaaga aaaaagcata tctctcattga cataacagaa gtgagatggc 180
ccagctattga tacagatggt accatmntnt atatggagag tggcatttgt aagataacat 240
ctttagatgg tcatgcatac ctctgcctgc ccagatctca gcattgaatt acagtaactt 300
ttttgtgtaa agttagccag aagtcagact catctgcagt gtgtgcagaa acaataata 360
aagcccccacaa agataaaccta gttgaaaaaa ctggcaaaat ctgtatcagt ggaatactac 420
cangacagag actgaagaat aaagaaaatg agtttcatgt ccagatcatg aaatccaaag 480
aaacttttaa gaagatgagt tgtgtaaatg gaactgaagg gagggaaagc ctgcctctgc 540
ctggtacaaa gcacacatgt gtatacacat gggctcaagca gtgcgtgtct gtggctgcct 600
gtccagagga atgggaaata ttctttgtc ttttagcaatt catttttcta aataaaaate 660
anccaatatg tctaaaaaaa aantttntnt atataaaacc tngaagccct nttnaaacct 720
tntntnggag gtectnnttt acmtatgat tcccggaact tggataagga atccncttg 780

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WO 99/33982

PCT/US98/27610

gattgganatt ttggggcna aaaccncna ncttggaaat cc 822

<210> 490

<211> 789

<212> DNA

<213> Homo sapiens

<400> 490

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acnctgcang	anggaanaaa	ggctggccnn	cngntgtacn	ctnacgctcc	taaccccgcg	180
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aaaaagcaac	nnncaangct	tttggctnaa	agccgatang	acncaaat	ntncttttgg	660
accttganaa	tttctccaan	nnttttnagn	annctcttt	ttntctggan	aaanaacttaa	720
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annaatnnt						789

<210> 491

<211> 790

<212> DNA

<213> Homo sapiens

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WO 99/33982

PCT/US98/27610

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<213> Homo sapiens

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WO 99/33982

PCT/US98/27610

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WO 99/33982

PCT/US98/27610

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<211> 773

<212> DNA

<213> Homo sapiens

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WO 99/33982

PCT/US98/27610

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WO 99/33982

PCT/US98/27610

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<213> Homo sapiens

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<212> DNA

<213> Homo sapiens

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WO 99/33982

PCT/US98/27610

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<210> 506

<211> 796

<212> DNA

<213> Homo sapiens

<400> 506

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ttttaataaa	gcctgcgaagt	tactaaattg	tagtttcata	aattctgtag	taaagtatca	180
tcttggcagt	gtgccaaagg	tgaaaatgat	gctttctcta	acagagaaat	tcttagtgac	240
tcagtcgta	gaaaaacgct	tttacaacct	gaataagatt	gaagaattgt	gaacatacca	300
tgccctattg	gatgaatcat	ttgcgtagg	ctaaatcaga	ctgtagggtt	tgtgatggat	360
tatgtgagta	tgtaggtata	gaaatcatga	atctagcatt	tgttttcaga	gattcaagca	420
tagtcttaag	ggatanatcag	aaatgacaaa	tgaattcaaa	acctagcagg	tgcattgtna	480
atgtgtgccc	agttntgttt	tggaatggc	agttcccttg	gggtcatgtt	ctactggcaa	540
aatttgcaat	antgtntcat	tgtngtgaat	ttcaaaattt	ataagattat	cccccgttcg	600
cccaagtaaa	acctgtntctg	cccaatanaa	tcttggaatc	gnngagaaat	cgntccatt	660
cgnnnttcaa	ctcgggatnc	ntcgncttaa	naaaatnttn	tcnnggancc	cnctcatnan	720
gaanaacacc	anactattnn	gggnacctgn	aangctcaat	ngcccnngcc	cnmngnncn	780
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<210> 507

<211> 774

<212> DNA

<213> Homo sapiens

<400> 507

WO 99/33982

PCT/US98/27610

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ctnntttntt ttngaaneet tngctcttgt tctttttgcy gateccatcg attcgtgaag      60
aggagacggt gacctgggct ccttatgtgc ctgaaagagt ttgagtttcc tgttaactcc      120
aaatcaacag tattttcaac aagaaatgtg caattgaaat caagtgtctg ttaagtgcag      180
ctaggatttc cacaggaaga cacttgcagt gaacagagtt atggagcagc aaaaacacag      240
atctatttgg aaaaagagaa aacatatgcy ttgtattttg cttcaattat aaaataccat      300
cctctcaaaq gtgggtcttaa attacaaggc actttgattt ctaggtagat ctggggtaga      360
gacttccttt catattgagg cattaatgac accotttaa cttgggaagca atatgactgc      420
agttgtactt tgagaagatt aatcagggttt ggttgcagaa tgaagagaaa gatgaagtca      480
agagatttgt tttagaggctc tagcagaagc ttagtcatat ttcaaaatga tcaaatatca      540
agaaaaatcc tgagctgcac aacttgtata aagtaatttt cagtgtattt ttcatggtta      600
tgatnaaaga actggattta nccagaaacc ttacctgga ttcaagattt aatttttctc      660
ttgagctca tccctaaagg attttcgggg aaacattaaq gggagccaaa nccnattggn      720
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<210> 508

<211> 724

<212> DNA

<213> Homo sapiens

<400> 508

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cttgcctttg aaanccgttg gctactngtt ctttttgcag gateccatcg attcgaatcc      60
ggcacgaggc ggcgtgtgacc cggccggccc cacaccgcct ctccctcttc ttgtccgcgg      120
actcccttcc ctgacctcaaa gacctgggtg ctcccaactgt gagccccagct gtccccacagg      180
cagtccecat ggacctagac tcaacctccc ctgtccctcta tgaacctctg ctggggccag      240
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agcgagcgcc ctgagccacc gccctccctt tcttccgggc cctgctgtca ggcagctttg      360
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tctctcatca ttgtcatggt tgtcgggggt gtggggctgn nntggggccc gtgccccacac      480
cangmanccc cctgtatggg atcanaggcn cgaagangca ntgnangctg ntggcanntn      540
aantactgnc tgggctggaa nangaaactn taaaagctmt ngcccnatc cactctggna      600
ccmanntn nnccntant cnnngggntn angtggtlann nctnggggac agntcnntnt      660
ggntnncma tngnncnnaa gnanacttgg ggttcannaa ncntttccnn atgnaancng      720
ngtc          774

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<210> 509

<211> 803

<212> DNA

<213> Homo sapiens

<400> 509

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tnnnntttta tttctntogt totngntttt attacatcag ctcttttctt ttgtcgggtcc      60
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aagaaagaga gaaatttgag aaagaaacgga gagaaagaga gagggagcgt gaaagggaaac      180
gagaaagggc agaaccggaaa cgagaaaggg aaagagaacg tgaacgagaa aaggagaaag      240
aaaggggagg ggaacgagatc cgggataggg accgtgaccg gacaaaagaa gagaccgaga      300
tcgggatcga gagagagatc gtgaccggga tagagaaagg agctcagatc gtaataagga      360
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gagagagaga gaaccgagag cgagaacgag aacgggagcc gagagagaga cgcagagagg      480
gaaccgggag cgagaaagag aaaaagacaa aaaaagggac ccgagaagaa ga tgaagaag      540
atgcatacga accgaaaaaa aaaaaaaa aactcgagcc tnttaactat agtgagtcgt      600
attacgtaga tccagacatg ataagataca ttgntgagtt tggacaaccc ccaactgaat      660

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WO 99/33982

PCT/US98/27610

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gcagtgaaaa aaatgctttn ttgtgaaat ttgngatgc tnttgctttt ttgttaacca 720
tttttagctt gcaataaaca agtttnccac caaccanttg cnttcatttt ntntnttcan 780
gttcaagggg aagtttttgg aag 803
```

```
<210> 510
<211> 789
<212> DNA
<213> Homo sapiens
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```
<400> 510
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gaggggagact ggggagagg gaaaagagag aaggcaggga gagtagggag agaaaaacctt 180
ccagcagccc agtaaaactgc gggcgaagag atctaccctt ctccctccct cccacagtta 240
ccattggcct tgtcatcgca agcatttgac aaagacttgc ttgtttgggc ctgtcacctc 300
ctgaaggcct gcttttagctg tggatgacct tgattaaggg agagagcgcc taggagctgc 360
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catgcagctgg aaagtgtctta gctctctccc tcctgacctc tgggcagcca gtcatcaag 480
cagagagcgc ttgctggcatg tgggcagcat gccacggttc cttgctgact cagcacttat 540
ttctgtagtt ttaaaaaaga atttaattgt tttggttgta tttttttggg ggggtgaggg 600
tgggcaaaaa catggggggtg gttctgagtt gttagaaatg tttctgaatc aagtttgttt 660
gaaaacacgt tgtgcctttg tacccattat aagatggtca taanacccaa gaactgataa 720
gctttggggt ttttttgggt tggtttgggt ttttgcttca ttttaacctat tcatgcctag 780
ggtttccat
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<210> 511
<211> 776
<212> DNA
<213> Homo sapiens
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<400> 511
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cactgggttat tccactttat taaaatgtcc agaataagca aatctccata tagaggaagt 120
agattagtgg ttgcttcggg atgggaggaa tgggaagatt gaggtctttc ttttgagtg 180
ataaaaaatg cctaaaaattg actgtagcga tgggtcacaca actctgaata tgcttaagac 240
cattgaattc cacactttac gttgttgaaat tgtatggatg taaattatag ttcaataaca 300
tagcttaaaa agataatcaa aagcatgaaa gcactgttga tgtgnttgg atctgtgtcc 360
tcaccgagtc tnatgttgaa atgtaagccc cctgggtggga ggcgatggga ttatggggga 420
gantcctcac aaacgggtta gccaccgccg tcaggctgtt ctctgatata tgagtctcca 480
tcacatctgg ttgcttcaaa gtgtgtggng ccttccctct atctcctact gctctggcca 540
tataagangt gectgcttct ccttcgcttt ntacatgatt gtaaagtctt ctgagcctcc 600
tagaanaaaa gctgctgngc tttctgtcca tctacangan cgtgagccca attaaacctc 660
tttttttttt ttngagggnn nttntntnnc nntccnncca ntttnanann cctngnang 720
gttttnnaaaa anaananngn naannnnnnn ncccccncc ccttttaaaa taaaaa 776
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<210> 512
<211> 917
<212> DNA
<213> Homo sapiens
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<400> 512
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WO 99/33982

PCT/US98/27610

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tcgcagggtt tcggcttttg ctctcgatat gcagcgacag aattttcggc ccccaactcc 120
tccttaccct ggtccgggtg gaggagggtg gggtagcgga agcagcttcc ggggaacccc 180
gggcgggggg ggaccacggc gcgcctcccc togagacggg tacgggagtc cgcaccacac 240
gcgcgcgtac gggcccccgt ctaggccgta cgggagcagt cactctccgc gacacggcgg 300
cagcttcccg gggggccctg tcgggtctcc gtcccctggc ggctaccctg gctcctactc 360
caggtccccg gcgggggtcc agcagcaatt cggctactcc ccaaggcagg annanaanca 420
nccmcaagg tntncaagga catntacacc atttggatca nggcgtntta naaaaaaaan 480
aatgttaagt anttggaaaa ntatttnaaa gcctttnaat gntnnnnna atccttnggg 540
nttggcctta naaanccaan attntngtng gngggntntt aannccnnnc aantnccnnn 600
nnattncntt naaaacnttt nnccganggn cnnaaaaaaa nggggnaann aaaaaacttt 660
ttntnttnaa nnantttttt tggaaaattt naaancntng gaaaancntt tnnntngttn 720
ntnangggaa annantnttt tgggnncaaa aaaaactttt naannntnn ngggtnnnan 780
nnrttaaaaa nttnnnccc ccaannnnnt nnanngnanc ttttnnantt ngggantaaa 840
nttnnnnnna nggggnnttt tttnnnnnaa atttnnnnnn annnnnnnan nnanggggnt 900
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<210> 513

<211> 780

<212> DNA

<213> Homo sapiens

<400> 513

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tnnnnnnttt aaatccatta gctacttgtt ctttttgcag gatccatcga attcgtgcgg 60
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cacgagctgc cctgcgcgtc gcggagctcc caggtctaca caggtccgaa aaagtaccag 180
cggctggttc gcgcctcccc ggccttgac tatgcagagt tcgagccgca catcgtgcc 240
agcaccaana acccgtangt ggtccnccgc ggccggggga ggcccagggc aatnngacag 300
nccctcognn tgaactccgc agtgcgtcag nccctactct tcanagtty ggagccctgg 360
gacccaggca ccaattgttc ttgcaaaetc accctgcggc acatcaacaa gtgcccanaa 420
caogtctga ngcacaccca aggcgggggg taccagcgag cttttgtgta aatatgaaga 480
atgtctnaag caaggggtgg agtacaatgcc tgctgcctgg tgcaacccgan gangaagang 540
gaaggacaaa tggacnctga acggccttcg cccgcgggaa agcttctggg agcccaactt 600
caatgatgaa gggggagctg caagtgatga cagcatgaca gacctgtnc cctgaacttt 660
caccagaagg accttgaaca cngaggatgg ggatggactg atgatttttg acaacaaaga 720
ggttgaaagg caaancccca aaaaaaaggc cttgtgaagg cagganaaan acaacctntc 780

```

<210> 514

<211> 793

<212> DNA

<213> Homo sapiens

<400> 514

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tttnnnngnt ttannnctt ttgctactng ttctttttgc aggatcccat cgattccgaa 60
ttatagattt gaogtgaatc ccactgtggt atagattcca taatatgctt gaattatagt 120
atatagccat ttaataacat tgatttcatt ctgtttaatg aatttggaaa tatgactga 180
aagaatgtta aaacatttag aatagctcgt gttatggaaa aaagtgcact gaatttatta 240
nacaaactta cgaatcctta actnttttac acagcatagg tgaatcata ttgggctat 300
tgtatactat gaacaatttg taatgtcttt aatttgatgt aaataactct gaacaagag 360
aaaaggtttt taactanag tagccctaaa atatggatgt gctatataat gccttagtt 420
ttggaactgt atctgagtaa cagaggacag ctgtttttta accctcttct gcaagtttgt 480

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WO 99/33982

PCT/US98/27610

```

tgacctacat gggctaatat ggatactaaa aatactacat tgatctaaga agaactagc 540
cttgtggagt atatagatgc ttttcattat acacacaaaa atccctgagg gacattttga 600
ggcatgaata taaaacattt ttatttcagt aactttnccc cctgtgtaaa gttactatgg 660
tttgggggta caacttcatt ctatagaata ttaagtggga agtgggtgaa ttctactttt 720
tatggttggg gtggaccaat ggctatcaag agtgacaaat naagggtaan ggatgattcc 780
caaaaaaaaa aaa 793

```

```

<210> 515
<211> 770
<212> DNA
<213> Homo sapiens

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<400> 515
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gttgatttgg aaagcagtag tgtggacgaa ttgcgagaga agcttagtga aatcagtgagg 120
attcctttgg atgatattga atttgctaag ggtagaggaa catttccctg tgataatttct 180
gtccttgata ttcatcaaga tttagactgg aatcctaaga ttctaccctt gaatgtcttg 240
cctctttata tctgtgatga tgggtcggttc atattttag ggataaaaaa gaagaattaa 300
tggaaattgac agatgagcaa agaaaatgaac tgatgaaaaa agaaaagcgt cgactccaga 360
agactggaca tctgttaaaca tactcacctc gtaaaagagaa agcactaaaa atatatctgg 420
atggagcacc aataaaagat ctgactcaag actgactctg atagtgtagc attttccctg 480
ggggagtttt ggttttaatt agatggttca ctaccactgg gtagtcccat ttgggcgga 540
catggttggg gtaacccactg gacaccacac tgattggact gccctacacc aatcagaact 600
cagtgtccaa tgggccactg ttttgactcg gaatcatggt gtgcactata gtcaaatgta 660
ctgtaaagtg gaaanggatg tgccaaaaaa ttaaaaaaaa ccnccaaaaa agcttccaaa 720
aaaaaaaactt taaactatag tgagtgtnt acntagatcc aacatgataa 770

```

```

<210> 516
<211> 825
<212> DNA
<213> Homo sapiens

```

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<400> 516
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gcntgctnan tgcntgttag nncctttctg nacnntagc attgtctctg gagaacnnga 180
tgtgtcttnt ntnaaanggc anaccagnn tgnnctgnnt ttaatgatgc agancctnac 240
tttaacgcga cctggccogt ttnacatttn agtaangnac gatatttggc tgatggctga 300
acantttctg aaatacacnt ttagtgtatg gaantacaag accnntaaag gnetgccagg 360
ttancatctc atctngcatt cnntctctt ggmanaaaag gganatntca gaattatatt 420
tcttgatggg gtcttttcaa tcaantgtatc tgtcgaaann tcttaganaa anctatgtgn 480
tcnogggtgt gtctaaaaan atnctttcaa anatgacccc tggaaatncc tganananagc 540
ttaaacgtga gaagcanggt nggcacaaaca cccnncnaag gttnttggna angcccnant 600
ntgttttgc tggcccatat aancttngcn ccattnaagc cnoggnggag ctttgnatnt 660
atattngng ngttacttct tttgnnccct tgcggggaac ancttnnata atgctntntn 720
nccnannnt gacntttgtc ttttgnnccc nnaccccccc aaaggngcn cactcccant 780
gaaaagctct ttttnnaaaa gggctccttn ctnaaaaaaa nnmnt 825

```

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<210> 517
<211> 1444
<212> DNA

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WO 99/33982

PCT/US98/27610

<213> Homo sapiens

<400> 517

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ccnctattnt	cntntntntc	ntctntcnnn	antnctnnnt	ctctnctnnc	cancnttcca	180
tnntntactn	tctntntntc	ggctntnta	ntnggggggt	ctatttntn	nettaaactg	240
actngttcca	agctctntan	cngctctnt	ctnnctntct	ntgcncntcn	ctggggcntt	300
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cggnncccc	tgaattttnn	ancnngganc	nttaaatnnt	ntngnggtac	ganncncnn	540
ncgnnnnnnc	gnntannccn	canngttaan	tgcncccnna	nnnantcaac	tctntnttcc	600
tnntnnaacn	nnmttantct	annatnnta	cnnntnagnt	tttctcnc	nacnctctg	660
tnctntntnn	atctntntct	tctcncctna	ttntatctc	ntntntntnc	tnccctnate	720
tatctnctac	notctnttcc	netctctct	nnctctctc	atcatatccc	acgcnaactna	780
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cttctctctn	ctctcctnnn	nnnactactc	tcaactctc	nnctntcnc	ctacnnntnn	1020
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ntntctctac	tctacactc	tnntctccac	tcatatnana	cttctatant	ntcatactca	1140
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ngngcanaat	nnaacmcan	tcncctcctt	ttagctctct	ctctanaaac	ccccnttttc	1320
acacggnaacc	ccccntntnc	tcnaaatcct	catcncncta	ctttatatnt	cnccaagcct	1380
cnctntgtga	anagcatctc	netntccncc	aatnnaanac	tcctctctcc	natanatntn	1440
anat						1444

<210> 518

<211> 706

<212> DNA

<213> Homo sapiens

<400> 518

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caagtttggc	ttctctatg	ttttccagaa	atgactctag	tatctggagc	atcctcagaa	180
aatgtattgg	aatggaacta	tccaagatca	cgatgccagt	tatatttaat	gagcctctga	240
gcttcttaca	gcgcctaact	gaatacatgg	agcatactta	cctcatccac	aaggccagtt	300
caactctctga	tctgtgggaa	aggatgcagt	gtgtagctgc	gtttgctgta	tctgctgtgt	360
cttctcagtg	ggaaaggact	ggaaaaacct	tcaacccact	gctggggagag	acttatgaat	420
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tcagtgcatt	tcagtctgaa	ggattaaaca	atgacttcat	ctttcatggc	tctatctatc	540
ccaaactgaa	attctggggg	aagagtgtag	aagcagaacc	caaaggaaacc	atcaccttgg	600
agctccttga	acacaactgag	gcatacatc	ggacaaatcc	cactctgtgt	gtgcataata	660
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<210> 519

<211> 734

<212> DNA

WO 99/33982

PCT/US98/27610

<213> Homo sapiens

<400> 519

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gataaaagag	tgaggcgca	tcgaaaactt	gtggaagaac	agaatgcaga	gaaggcgagg		180
aaagccgaan	agatgaggcg	cgacagagaag	ctaaagcagg	ccaaactggt	ggagcagtagc		240
agagaacaga	gctggatgac	tatggccaat	ttggagaag	agctccagga	gatggaggca		300
cggtagcaga	aggagtttgg	agatggatcg	gatgaaaatg	aaatggaaga	acatgaactc		360
aaagatgagg	aggatggtaa	agacagtgat	gaggccnagg	acgctgagct	ctatgatgac		420
ctttactgtc	cancatgtga	caaactnttc	aagacanaaa	atggccatga	agaatcacga		480
gaagtcnaaa	aagcatcggg	aaatgggtggc	cttgctaaaa	caacagctng	angangaacg		540
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agaaatgna	aagatgcacc	aaaaacaana	agctttctac	acantnaaat	ccnannaact		660
ccatecntct	anaactatnn	gtgagtcctt	nttaentcna	cccagacatg	antancnata		720
cnattgatgg	aacc						734

<210> 520

<211> 701

<212> DNA

<213> Homo sapiens

<400> 520

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catgtaccag	gttgagtttg	aagatggatc	ccagatagca	atgaagagag	aggacatcta	120
cactttagat	gaagagttac	ccaagagagt	gaaagctcga	ttttccacag	cctctgacat	180
gcgatttgaa	gacacgtttt	atggagcaga	cattatccaa	ggggagagaa	agagacaaag	240
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gaagagctct	ttccagaaga	agtgccagaa	gagacagtag	tctgcataca	tcgctgcagg	360
ccacagagca	gcttgggttg	gaagagagaa	gatgaaggga	catccttggtg	gctgtgcctg	420
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gtttggtcac	caaaaaataca	aaatacaccc	aatgaattgg	acgcagcaat	ctgaatcat	540
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gtgaaaggaa	atactagtga	atcacccaca	aggaaaagcc	actgccacag	aggaggcggg	660
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<210> 521

<211> 784

<212> DNA

<213> Homo sapiens

<400> 521

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cccaccatgt	cccagggtgat	gtccagccca	ctgctggcag	gaggccatcg	tgtcagcttg	180
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cagtgcttct	actacacccac	ggaaggctgg	ggagcccagg	ccctgatggc	cccgtgccc	300
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gaacttctac	tggaaggccct	caatcagatg	atcctgggaac	tggagccccc	cttccagctg	480
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WO 99/33982

PCT/US98/27610

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aagaaggagg aatctgaagc cttgggtaag gatttggggc acagtaccag gaggggggct 600
tgggtgccaga cctcatgagg aagaaggatt ttcctatgta cagagaaggg gacccctgtc 660
ctgttgaggan gtgctgtgca aacctaacca aagtactata cccctctggt tcttgnsggt 720
acacaaaangg ggataaatac aaagctttnc ctnaactagc caattctatt tggggtttcct 780
gagt 784

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<210> 522
<211> 719
<212> DNA
<213> Homo sapiens

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<400> 522
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ctcatataca cattgtgtcg attggacacg tagattcggg caagtccacc actactggcc 180
atctgatcta taatgcgggt ggcacgcaca aaagaacat tgaaaaattt gagaaggagg 240
ctgctgagat gggaaaaggc tcttcaagt atgcctgggt ctgggataaa ctgaaagctg 300
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catctcagcg tgaactgtct gtccgtattg ttgctgctgg tgttggtgaa ttTgaagctg 480
gtatctocaa gaatggggc accogagagc atgcctctct ggcttacaca tggggttgta 540
aacaactaat tgtcgggtgt aacaaaaatg attccactga gccaccctac agccagaaga 600
gatatgagga aattgttaag gaagtcagca ctacatttaa gaaaattggc tacacccocg 660
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<210> 523
<211> 710
<212> DNA
<213> Homo sapiens

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<400> 523
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cagagagaca agatggtgaa ggaactgagc ctgatgaaga gtcaggaaat ggagcacctg 180
ttcctgtacc tccaaagaga acagttaaaa gaaatatacc caagctggat gctcagagat 240
taatttcaga gagaggactt ccagccttaa ggcattgtatt tgataaggca aaattcaaaag 300
gtaaagggtca tgaggctgaa gacttgaaga tgctaattag acacatggag cactggggcac 360
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gtaaaaagga agttcagacc tgtttaaaac gaattcgact tgatctcctt attttacatg 480
aagattttgt tagcaataat gatgaagttg cyggagataa tgaacatgat gtcactttcta 540
ctgaattaga tccctttctg acaaaccttat ctgaaaatga gatgtttgct tctgagttaa 600
gtagaagcct aacagaagag caacacaaa gaaattgaga gaaataaaca ctggcccttg 660
aaagaaggca ggcaagcgtg ctgagtaata gtcagacctt aggaaatgat 710

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<210> 524
<211> 730
<212> DNA
<213> Homo sapiens

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<400> 524
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WO 99/33982

PCT/US98/27610

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aggccctaaa	gaagcagcta	tggcgattcc	acaccaagta	catgatgtgg	ttccagaggc	240
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gtaaaacctc	ttttcatttt	ggaaaaatatt	tatgaataaa	tagtttttata	tgaaaaaaat	660
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attaccttag						730

<210> 525

<211> 711

<212> DNA

<213> Homo sapiens

<400> 525

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gcccgaatac	ctggggccctg	ccttagcatc	ccccatagct	tccacagccc	cagggtgatc	660
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<210> 526

<211> 692

<212> DNA

<213> Homo sapiens

<400> 526

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gaaaagagtc	aaaccttttt	gggaaaatca	gagggaagta	ctggaaagca	agaagatcat	180
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gatggggggc	ggctgggggc	agtggggaag	gcgaggagca	gggaagagga	gagtaggcat	300
catggggcct	caatgcccgc	tctgatagcc	cctgaggact	ctctcactgt	tgcactgttt	360
ccaggtgcct	catatctcgt	gactcagatt	cccgggactc	agacagagtc	cagggctgag	420
gaactgtccc	ccgcagctct	gtctcccttg	ctagagccca	tcagatgtct	tcaccagccc	480
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gtactttgat	tgtctacagt	ttcatgttta	tccagttcaa	tgatttttta	aatttttctc	600
tgagacttct	ttgactgata	gattatttgt	aatgtgtttt	taaatttcca	aatgtttang	660
gattttcata	tctttcttat	gctgatttcc	aa			692

WO 99/33982

PCT/US98/27610

<210> 527
 <211> 769
 <212> DNA
 <213> Homo sapiens

<400> 527
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 atggtanttt aaccaggggt tttgcnmtt aaggaggcct tngtgggtggg tngttaatct 180
 ggcctttccn tattgaaaag ctccctgttat tgtcca caga ccagaaggac ttgtaacctt 240
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 tggaccaagc tactncagat catctgacca actcttaaaa atcacggcca ggcacagtgg 480
 ctcatgcctg taatcccagc actttgggaa gcaaaagtgg caggatcatt ncagcccaag 540
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 ttaagaaatt tatataaaaa gaagaatcag gaaaccaagt ncaacccaac ttaacctcaa 660
 tgaaccagcc cctaacacag atgangggat ttgggactga taagctctgt gctgngtcca 720
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<210> 528
 <211> 757
 <212> DNA
 <213> Homo sapiens

<400> 528
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 nngnattctg acagtgaagg tgacananag ntaancagga aaacaagatn gctccagaaa 180
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 gcnattttta aggcaaaagt ctaattgata ttanagaata ttgnatggat cctgaaagtg 360
 aaatgaaaac aggaagaaaa ggtatttctt taaatccana acantggagc cagctgaang 420
 aacagattct gacattgatg atgcagtgaag aaactgtgaa attcgagcca tataataaaa 480
 acctgtactg tctagtgtnt ntaatctgtc tttttacatt ggctttgttt nncntaatgt 540
 tctccangct attgtatgtt tggattgcag angaatttgn angatgaata cttnntttta 600
 atgngcatta ttaaaaaat ttagtggaag tnatngtcaa ctttattaag gattactttg 660
 ctgocaccac ctagtgtcaa ataaaaatc gtaatacaat cttataaac nttaaaacta 720
 taaaaactcg acccttagac ctatantnag tgggtn 757

<210> 529
 <211> 821
 <212> DNA
 <213> Homo sapiens

<400> 529
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 gaaagcaaa acgcaaacag atgcctgtgc accaaagtgc acgggcaaac atccttcggc 180
 cttaatgggc agcatctcgt cgtccaaagc gggcattcat cctttcatca atagcgggca 240
 gcatttcgct gtcacaaagc ggcagcattc ctttcgcac aagcgggac catcttgctc 300

WO 99/33982

PCT/US98/27610

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gtcacaaagc ggcagcatcc ttgcgcaaaag cgggcaagca tcttcgtca tagcggcagc 360
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aaacatggcc agtccaggca ctggaatcca ggcgcgtaga acggcgccca cggtcataaag 480
gaatgagacc ctgatgcact gggcgacaca gacggcgac acagacttgg agacatcatg 540
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gaatggcgca gttcagaggg aagaaggagg atggcgcttg ccggtgcccg gggacngggg 660
ttgggagcga cggttgctg ttgggggttt ctttctgggg ttgangaantg gttttgatat 720
ttggmccgtt ggtgatgttt gcatacctct gaatatgctt aagancaca gaattgacca 780
ctttaaatgg atgaattgna tggatttggg aattacccaa n 821

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<210> 530

<211> 765

<212> DNA

<213> Homo sapiens

<400> 530

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tgggcccggc cagcaacaaa acgggcccgtg acgctctccc cttgcccgca gatacctcct 180
actaccangg ggtgtactcc ggcccattat gaactccttt aagaagaagc acggtctcag 240
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acagataccc caggttctat ataaggagga aaacgggaaa gaataaaaac ttaaaaaaaa 480
gcctccggtt tccactactg tgtagactcc tgcctcttca agcactctga gattctgatt 540
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aaaattttgt agtgactcgg tgtaaaacca tgtagttaa aatgaccaan aaaaaaaa 660
ttgttaaaaa caggaaaaaa ataagtgaag gtctgttga aatgaccaan aaaaaaaa 720
aaactcngcc tntaaactnt tntgagtcgt ntctgtaaat ccaan 765

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<210> 531

<211> 768

<212> DNA

<213> Homo sapiens

<400> 531

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tcgaacaaaa ttgcccataa ccagagttgt ttatgctagt gcaactgggt gcttctgaac 180
cacgcaacat ggcctatatg aaccgcttgg catatggggt gaggggtact ccatttagag 240
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gctatggata tgaagcttag aggaatgtac attgctcgac aactgagctt tactggagt 360
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gancaacgaa tgaagaagtn catgtgggtg cagttctggc tgtcaccaga ggttcttcaa 540
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aatggaaaaa gtgtngtaat tggctgcagt ctccaggaga gctnnaacat tagaactttn 660
gaagaaggcn ggggagaatt gatganttgg ttcaactgag aaagtgtgtg cantcaacta 720
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<210> 532

WO 99/33982

PCT/US98/27610

<211> 761
 <212> DNA
 <213> Homo sapiens

<400> 532

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tgagccacct	tgccacacca	catcatacag	ttgaaatgaa	actttgccac	aaccagcctt	180
tgctgtacac	acacatatat	cactgaacct	ggttgaaata	aagntttttt	tcttttctct	240
ctggtattct	gggttctgaa	gtctgggtatt	ctggtattct	gggttcaaaa	gtatgacttg	300
agagtggtgc	tctggtattc	tgagagttgc	tctgtattct	gggttctgaa	gattatttga	360
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cacattttan	gggcatttgg	taatcctgag	attttactca	ntaaatcctg	atggtaactg	720
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<210> 533
 <211> 735
 <212> DNA
 <213> Homo sapiens

<400> 533

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ctccagttcc	tggggtcaag	ccatccctcc	tcctccagcc	tcctccagtag	ctgggaactac	180
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aaggtataatt	gaggtgggtac	ttatcatctt	tactgngtct	catgttttgt	atatttttgt	420
ttcatcaact	aagatgcact	gtaacatctc	tgaaatctgg	atatattatc	aatggtttat	480
catagttttg	ttagcaatac	actgtctttt	agtggtgcct	aaaaataatg	tatagttgtg	540
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atataaaag	aagaagtatt	ttttttttgt	aatgactgaa	agctgtctgt	ggatgacctc	660
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aaaaataact	tgagc					735

<210> 534
 <211> 735
 <212> DNA
 <213> Homo sapiens

<400> 534

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agataaagtc	tttaataaat	ggtgctggga	aaactggntn	tccantntgc	agaagaatga	180
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agacctcaaa	ctatgaaaca	gctaaaaaga	aaactcgggg	aatctctcca	ggacattgga	300
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WO 99/33982

PCT/US98/27610

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atgggatcac atcaagttaa aaatcttctg cattgcaaa gaaataacaa agtgaagaga 420
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gtctacaaag aaataactga gactgagtaa ttataaaga agagggttaa ttggctcacc 540
gttttcagg ctgtcaggaa gcatggtgct aacatctgat cagcttgtag ggaggcatca 600
gggaagttcc acccatggtg gangcaaaa ggggaataag ttctccatgg caggtgcagg 660
gcaaaaanan ggggggaagg aagtgcenca caaccagatc ttgtgagtn cagatttgn 720
ggngggngct tgnng 735

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<210> 535
<211> 735
<212> DNA
<213> Homo sapiens

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<400> 535
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agaatgagtt ggagcaatct tttcatgtga cctccttaac agatatttac tgaagggaac 540
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aaggcaacag aaacagagg agaagccoga gagaatgttc tgcgtgctgc cagcatctg 660
anogattgct ctgtgaagg gttgtcact gaacattttc agggaggagct gtttaccagc 720
cnatgtctn aacan 735

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<210> 536
<211> 785
<212> DNA
<213> Homo sapiens

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<400> 536
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ttgggctggc cctctatnat gctntgaggg gagctgggac agatgatent nccctentca 180
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<210> 537
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WO 99/33982

PCT/US98/27610

<212> DNA

<213> Homo sapiens

<400> 537

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<210> 538

<211> 892

<212> DNA

<213> Homo sapiens

<400> 538

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<210> 539

<211> 751

<212> DNA

<213> Homo sapiens

<400> 539

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WO 99/33982

PCT/US98/27610

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<210> 540

<211> 761

<212> DNA

<213> Homo sapiens

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<210> 541

<211> 748

<212> DNA

<213> Homo sapiens

<400> 541

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WO 99/33982

PCT/US98/27610

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<212> DNA

<213> Homo sapiens

<400> 542

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<210> 543

<211> 764

<212> DNA

<213> Homo sapiens

<400> 543

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<210> 544

<211> 755

<212> DNA

<213> Homo sapiens

<400> 544

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WQ 99/33982

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<210> 545

<211> 767

<212> DNA

<213> Homo sapiens

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<210> 546

<211> 989

<212> DNA

<213> Homo sapiens

<400> 546

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WO 99/33982

PCT/US98/27610

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<210> 547

<211> 781

<212> DNA

<213> Homo sapiens

<400> 547

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<211> 735

<212> DNA

<213> Homo sapiens

<400> 548

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<211> 812

<212> DNA

<213> Homo sapiens

WO 99/33982

PCT/US98/27610

<400> 549

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<211> 742

<212> DNA

<213> Homo sapiens

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<210> 551

<211> 736

<212> DNA

<213> Homo sapiens

<400> 551

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ngnctggcaa	agtcacagtt	gttacactgn	gctttaaaaa	aaatcttata	tgcactgtatt	300
gttaacttag	agaccatgag	atctatttat	caggaccagg	aagatncaca	cttcagggttc	360
attgcaactg	actttttttt	tggtttttct	aaaacccctg	tggagcctgg	gaagggggccc	420
tccacaattc	tgtggcttct	atattagccc	caattttaca	agcacataca	agccccataa	480
ttgccgcagg	aaaaacaaag	atggaaaaat	caataaccca	tgcactgaga	cttagaaaaat	540

WO 99/33982

PCT/US98/27610

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catccttact aggcaaaatg tattatgatg caataagtgc cactggggnat tttnacgttg      600
ggactggnca ggaactgctg caaagaaaaa taacagctcc ttctccatta ttacacatta      660
agatgttggg ggggggaagg ttgggagaaa ttagttctga gggatcata tgcctttttt      720
aaagaaaatg ggaata                                     736

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<210> 552

<211> 733

<212> DNA

<213> Homo sapiens

<400> 552

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ctntccaagc ntgttggggg ggaagggaaat tgggtcccgag aaaatgggac tggagttagg      180
aatatctttt cttttgagag tncctccagt taattntnnc tgtgcttnat tgcctnctgt      240
ctttattgtg aatgtgttaa cattttaaaa atgttttgcc ntactctttt aggcacttgg      300
gttaaaaggag ccagtgggtc ctctgggtgg gtnctataat gagttattgt gaccacagcag      360
tgtgtgctga ccaatccact tgttaataac acaactctta aagtaaccca tctccagagg      420
gggtctcttc atgtgtccac tctcttttaa nggacaaact caggcaaggac gcatgttttt      480
tngtnattta caaaatctan cagactgtgg gtatccatat tnaattgtc ggggtgacaca      540
tgtttcttgg aactaaactc aaatatgtct ttctcatata tgtgctgatg gttttataaa      600
atgtcaaaag tctcctgtta aaaaaaaaaa aaaaaaaaaa tctgagccttt anaactntnt      660
gagtctgnta cntagatccn gacatgataa gatcatgatg agtttggaca accncactng      720
aagcagtgaa aaa                                     733

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<210> 553

<211> 870

<212> DNA

<213> Homo sapiens

<400> 553

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agganacctg gatntntng cccgntntng nttttaccgt ntgctcaant ttntgcagtn      180
acttentgcc ancctgtttc nttacntnca anagggaaag acantccttg gccagcctag      240
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attaacacat cttgagcacc tgcnatgttc caggaaacagg agatggcanc gtgcaagata      360
aagtccctga ctctcagaga ctgcatgtta gtggcaatcg gcgtntaccg gcccttnaat      420
aaactactga atgaaggaaa attctacctc caccagacac aattactggg gttttctaaa      480
tggaattatt ccccccggccc cntgcatcca gcagcctgnt gcaggggaaac tctctcnaaa      540
ggctgttaag gcaaggaaanc cgggacaatg gcntggctat ttaagcttnc aacaagatgg      600
ttaccctcaa gtnccatatt ccttaacacc aaggggggccc ttaccaggga aacccaaacc      660
aggttaaaaa accccaaggg tgggnaaaaa gccatttgc anccggggcc nttttaaaaa      720
aaacctttna aaacaccttc ccttttaaaa ctttaccttc aagntaaan ttttaagggga      780
atgggnccaa nttttttaac canccccaaa aaaaanttng gnaatttttt ttcccnnaat      840
tttttnaant tcccnaaatt tnggaaaang                                     870

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<210> 554

<211> 766

<212> DNA

<213> Homo sapiens

WO 99/33982

PCT/US98/27610

<400> 554

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cagccttgac	ctccaggaca	agtgatctcc	cacctnagcc	tccggaatag	ctgggactac	180
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ttntntcmaa	ncnnggttan	tagggggcna	aagctaaccg	natttttngt	cccntnaggt	540
tagggcngaa	attaaacngg	gtttaaagaa	cncattgant	aaagccttgc	ctnngccaat	600
tcocgggaaaa	gggaanagcc	tccttgtttt	acanatggg	aaaaattggc	cccaangggg	660
gttaaccang	tttgcctntt	aataactnaa	anggattttt	gncaaaacct	gggtccaagg	720
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<210> 555

<211> 770

<212> DNA

<213> Homo sapiens

<400> 555

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ggccttccctg	gttggtagcc	cagnaggagt	ccaggctttg	tacogtggac	accatgggct	180
atggcaacac	cttccatacc	atccttccat	gaggacctcg	gnaganagt	gacatgaaac	240
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ganaaaagt	tacctgtcat	gggggctgga	tcagtcaca	ttgannantg	gggtgtgtat	600
aaagcaagac	tnactcetta	tgacaccttt	ntttgcatat	gccccctcgg	gggnancttc	660
tttggctgct	aacatttttg	gacccaaccc	aatgggcctt	naccagaaaa	ncocgaaacaa	720
aatgcnnnnn	gccattcctt	tnngganctt	tccaaactnc	canaataaat		770

<210> 556

<211> 756

<212> DNA

<213> Homo sapiens

<400> 556

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ctggancttg	aaagtctccc	tnttaccac	tccacmtcca	ccccntnatt	cccntntccc	180
caaaagtntca	ctgntgtctg	ntgacanccc	caaatntgtn	ctgtcaacac	aaacctgcct	240
ttggngtata	aacaggccnt	tacagaaatg	tnacacctat	atatattctgt	tcagtatcca	300
ttcaactagt	cttcattaat	aaatatcacc	ttcccaccat	tgtgtgtgaa	tgcccacacat	360
ccatccagtc	tgagaaagtg	agagaggcaa	tcatgccaag	aaacaagccag	caaaactcctt	420
tcaccagatg	tagactgtag	ccctgctgcc	ttccctccag	cgagtctgcc	agcatgcttc	480
ttcatccttt	taatatgtcc	tttgccttcc	acttccctgn	cttccaacat	actgtcactt	540
actctggcag	tcttctgctt	ttcattaagc	ctcaaaatct	cctctgtcta	cttggcacca	600

WQ 99/33982

PCT/US98/27610

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caagctatgt cctatatatg natttctgga ctggcangg atagtccaag gggctctggc 660
aagtttttat ttaccttcatt tatttaaaan gggccttttg gggatgttgg cctntttaag 720
gagccttttt ggggaaatca atactctctc taanaa 756

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<210> 557
<211> 742
<212> DNA
<213> Homo sapiens

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<400> 557
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cactantttg acttttttaag taaaaantgt aggggggttt aaanctactt tctnctncc 180
aaaaantcag aaagttttcta nctttntaaa ttgggaaagc aagcantgtt ttaaaancac 240
tgaaggaaac tctttnttcg ngnccttttg ttaaaactcg ttaagctgt agacctntt 300
taaaantaaa ttaccacag aacaggaaat agaantctg gaagactcga aatacacctt 360
tgtntctctc tgttcttcac ctgctctctc gctgtctcta cacacacaca cacaacacaca 420
cacacacctt tatttgcatt aaaaatgggt agtaaaagca gtgaaggcca aacagaaggt 480
catttncatc aagtaagagg ttgaatataa actgggaccaa gtcttaattt tttatttctc 540
tatttcggat ncgtttacta atttctttgc tagctttaag acttttaaaa cattctttgg 600
ccctggggag gagttgttta cccctaaaact tggagaatcc tggccctaga ataaatgttc 660
cttttaaac ccangggcg gaaaattgaa tncngctgtg ccaaaaagga aaaaannnaa 720
aaaaaaactc gnggcctnta na 742

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<210> 558
<211> 730
<212> DNA
<213> Homo sapiens

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<400> 558
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gtggatcccc atgccattac ctgctagact cagggttnat atactgtagt ggaaggtga 180
ttccgaagga atgtgtgaag acaattgaag tgcagtanca tcaaggttat ttgacctaa 240
ggcaggagtt ncagtaagta tccactttta tncagaacac antagataaa ctggaaatct 300
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tggagttgct tagtctcccc ttcaagatgg agtttcttta gctccattg ataggagatn 420
tttaacaaaa ncangaaata agtctttgat ccattgaaac tctaagagtg agcctttgat 480
gactcaggtt taacacagtc tgagacaatt taggagatag ttttgaagnt caatttgaat 540
tgtaaaaagg caggattttt taacttttcc acatctttga anaaaagccc atagagcgca 600
agttttcagg aagancctgga aancnatatt nctatggaat taaatagctc ctacggggcaa 660
tcaattnggc ctggganaac ataatgcttc aanggtctgan gnaatctgga atttctatgg 720
gatttcttca 730

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<210> 559
<211> 743
<212> DNA
<213> Homo sapiens

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<400> 559
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WQ 99/33982

PCT/US98/27610

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cggcacgaga ggaacacccc ccttataaaa ccatcatntc aggcctgggtg atctgacaga 120
gctagacact gtcaaacaaaa caaacaaaaa ccccatcaca tctcatgaga 180
cttattttact atcatgagag cagctcagga aacaccocact cccgtgattc agttacatcc 240
cactgggtct gtcccaaaaa ttgtggggagc tacaattcaa gatgaggttt gggctggggac 300
acagccaaaac cctatcacca tgtaaaataa tatctaattt gttagagatta aagaacaaga 360
taacttaaat ctggatgta agttaagaga gtgggtgtca gagttaaatc attttaaggt 420
tcattttatt tctggacaag aataaaattt tgattatcag gaaatacaag taaaaccaca 480
gggagacatt tcttatatcc aaattgtcaa aaattacaaa gtcttataat accaagtttt 540
gctgaggggt gggagcaaca gaaacttttg ttactgggtg ggtatataaa ttgaataatt 600
tcagcttgga cattacctag caaaattgaa ggctgtatac gtacataacct accaatctag 660
caattcactt ctatagatta agtcttgaaa aactcacatg ttccagaga cgtgttaaaa 720
ggtggttaaa tcatntngn aat 743

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<210> 560

<211> 833

<212> DNA

<213> Homo sapiens

<400> 560

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atcngttctc ntannnnngtc tngttcttct tncacgatcn nntgcgattc gaattcggca 60
cgaggggctc tgggtggagt tccatccagc agtgagtgc aTTTTcccc agagcagtta 120
agggtcttat taaaagccac cactttgtct aggcctgtac aggcctctggg ggttttggga 180
agagaantaa ggcaggccact tgctccctca gggagggaact tgctcmtact gggaggtttg 240
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taagcttgac tgcaagggca agctgcaggc ctctctgtgc ttccccgtca ttcaccaagg 360
acaagttaga ccaagaagtc aagggaaaag tgccaagata gatctattcc catttcttct 420
ttccacctgg agaattctct agctatgctt caaacctctt ttgggccagg gaaagactgg 480
gggacatttt ttagtcaagg atgctttaag aaagtaaat cctgcttggg gggccaggcc 540
ttctttttca agggctgtct tgtgaatgcc caacccaaaa aaaggggccc ccaaggccca 600
atcccttact tcttnggtcc ccccaaaaaa ggatnccaan ttggggaatt gggaaaaact 660
gggcanncac cnaaanccca ctttggtagg anttnaccaa cccaaccaac ccaaaaccan 720
cccaccacaa ttnaaaaaaa ggccaaaacc accaaccaac cnaaacccnn annnnnnnnn 780
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<210> 561

<211> 773

<212> DNA

<213> Homo sapiens

<400> 561

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agccccact ggtgcagcag caagggtgct gctctgcaga cattgaccac cacattcagg 180
gccaggggct cagtgggcga gggctctgtg cccgtgccct gtaagactac caggcagcog 240
acgacacaga gatctccttt gaccccgaga acctcatcac gggcatcgag gtgatcga 300
aagctggtgg cgtggctatg gccggatggc cattttggca tgttccctgc caactagtt 360
ggagctcatt gagtganctg gangggcacat ctgcccctc cctctnaaca tggctctct 420
attgtggaaa gaagaagcct gggaaattgac attcagacct cttnacggaa taggaccccc 480
agtgangagt aagcctcagg gcttctctcc gctctggcag actaaccctgt caccceaat 540
cgagcaatgg cctggtgatg nccacacatn ctttcttgca ttccccgac cttccagaca 600
gctttggtct ttgcccctga caggatactt gagccnagcc cttgctgtgn ggccaaaccc 660

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WO 99/33982

PCT/US98/27610

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<210> 562

<211> 655

<212> DNA

<213> Homo sapiens

<400> 562

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tgggogggca	gttcctttgc	atgtttcggg	agaggtttgt	tgatttgggg	cttatatgtc	180
aggcctttgg	tttgcgtctt	atttttaggg	ttgtttgggg	gcctgggtgg	tggcctcacc	240
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tnnnannnn	nngacnann	nnnnnaatca	ngannntcna	cannnatcnn	annnnnncnn	600
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<210> 563

<211> 738

<212> DNA

<213> Homo sapiens

<400> 563

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tgccatcgat	gaatgctgca	gaaatgggaa	gatctcaaat	tctttgtctca	aaaacgtgaa	720
cttaacccaa	atgatggt					738

<210> 564

<211> 798

<212> DNA

<213> Homo sapiens

<400> 564

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cgaagtttca	ctcttatccc	ccaggctgga	gtgcaatggt	gcgatactgg	ctcactgcga	180
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WO 99/33982

PCT/US98/27610

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aaaaaaactc	gagcctnina	actatnngng	aggctgtatt	acgtagatcc	agacattgat	420
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<210> 565

<211> 744

<212> DNA

<213> Homo sapiens

<400> 565

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gctagaagta	cttttctgct	ttttggccag	tgcccantgg	aatgcctggg	tggggggaag	660
aagaagggac	tgggttaact	gtggtgcttt	tgttgtaaaa	aggcancctg	ccttctgact	720
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<210> 566

<211> 756

<212> DNA

<213> Homo sapiens

<400> 566

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gtgggtgggg	gtgcttantg	gctatgctca	cccgcctnca	ttangcctcat	tttggctctgc	360
gttttccaaa	tgcttctana	tctaggcatt	tggatcccaa	cctattgccca	cantgcctan	420
aatctncaac	cccgcgcnc	tatgntnana	cctacttggc	acaagaacaa	nngnanaent	480
tgnnnatn	ccanaangnn	naanattaca	nantnttata	ataccaattn	ntnttgangg	540
tgttnnnnnc	anaaaenttt	gntnancngnn	nnnnntatna	atnnataatt	nnnnnttgn	600
nancnannnc	tatgnnaat	taaaangnnnt	tnnncnnnnc	nnnancnnna	nnnnnttan	660
nnantnncnn	ttnnntnnnn	nnnnnnnnnt	tnaanaannt	nnnnnttnat	nnnannnncn	720
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WO 99/33982

PCT/US98/27610

<210> 567
 <211> 746
 <212> DNA
 <213> Homo sapiens

<400> 567
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 cagccagcag gagaggcaag aactggggga acacaggaac ctaggggagg aggggagcgc 180
 tgggcatctct caggctggcg gccaaagcctg cccctggagg cactagagga gggcatctgt 240
 ctgtgggagc ccagagctgc agggaggagg agggggagg tatctggtgt gagcgttgcc 300
 cctgcgacat ttgggaccac acaggtgggc ttctttatc cctgacaaaag cctctgtttc 360
 cagctctctcc gccctctctg gatgagggaa cagaagtgga ggaacaaaaa gaagcagcag 420
 cagcacagct cctgtcgtcg ggtgcggaga cagcctggca aagtcccact cagccatggc 480
 ctgatgcang cccagccct ncttctctgg gtgtcaaatg actgtgtcct ggacatctga 540
 tgcaccacct gccctgcctg ttgcaaacgt gatgtccccg gatggaatgg agaaactagg 600
 agactgggac aagcaaaaang ctgcaaacaa cccagaaccc attcttagaa nactggagaa 660
 atgattgagg aatcattggc accgtggnc ttgtcttcat nacaacaccc ttnnagaaca 720
 acttgggatt gaaaaaccaa gacant 746

<210> 568
 <211> 738
 <212> DNA
 <213> Homo sapiens

<400> 568
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 ctgggacgac tacgttttcc ggataaaaaa ggagaaatga aagaattat gagtggaact 120
 agagaattagg aaagacatga accaacgccc aaaaatgaga agaaggacat ataaagaaaa 180
 agacaaatac aagtgaaaaa aatagactaa tggattaaacg tccctgtcgt gtgacatttt 240
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 gctttttgca ggtgaaatgc ttncacacca gcaggatgca gaaaaatgct ttccaagagt 540
 ttgttgaaatn cagaacatgc atgtttatgc tgcaggaatt aacaaattta tttctcgttg 600
 gcaaaaaagt gttgattgna atgggtccta ttgattaat aaagatgtgt ttgagcctaa 660
 aaaaaaaan nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 720
 nnnnnnnnnn nnnnnnat 738

<210> 569
 <211> 753
 <212> DNA
 <213> Homo sapiens

<400> 569
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 gctggaggag aggagctcag agttctacag agtcttntct gaacaatata agaaagctgc 120
 tgaagagggtg gaagcaaatg tcaagcgata tgaatctcat ccagctctgt ctgactctga 180
 ggccaaaaat ctctcagttt accgtgagaa caccaccag accctcaat gctcgcctct 240
 ggccaccagc tatatgcact gtgtcaatga tgccaaacag agcatgcttg agaaggagg 300

WO 99/33982

PCT/US98/27610

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ataaaaaactt tcagaatgag caaaacacca tcaacgttaa ttccagagat ggaacatttt 360
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gagacatcaa gaatggatgc agcagaatca ttcaacgttt tgaacagcag cagttttgaan 480
ggccaaagcc ttgatcagg gatcccgta taaaggaca ctcttgagta ttagtaaaac 540
ctcttatgat gattaaaaga gaagggcagc cctnttcacc tttttgggtct tctattcaa 600
cttgctgtac cataaaatgg ttctctctcg nacaaagccc catcatcttg tgaacctcac 660
ccttaacaaa gtaggattgg ggttgggggg cctaattaat tggaatgggg ccaaggagaa 720
gagcccgaaa ccttagatnc canggggnana agt 753

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<210> 570

<211> 832

<212> DNA

<213> Homo sapiens

<400> 570

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tnatnaataa ggtttgantt cttatgcttn ccaanngett ggacctannt anccangcgg 60
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gtgacttatt ccagagtggc tcagtttaggg gaactctctc gtaagaaacc ctgggtattg 180
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tttcttttgg gactgtnaag gggaaatggg tttttanaag gtgaaggttt ggtcctgttg 600
gaaggaaaaa aantgtctct gttngggggg acaanaagg n acccttgggg gaggtccatt 660
cgcaatgtgn cctaccaaaa cnnngntctt taanaacacc ngggcctttg nccacggmaa 720
aaaaacctgg gccctcttaa naaaccttgg nanggaacc ccggaataac cctttgggcc 780
ttnccaaatc ttttttccca aagncccc ccggggggccc aaaaaaac ct 832

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<210> 571

<211> 748

<212> DNA

<213> Homo sapiens

<400> 571

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agtnttaatin ntggacttct aangantnng gctnntogn tggaaannnnn cagtnctcta 60
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agccaactat ctttaaaagg ttaagtttat gtttctact atgggaaacc atccccccc 180
aaacttgatg accgcattat gtgcttttat agaacatggc acttctccag gatagcattt 240
attctgtttt gtaagtgtga atgtaattac cctacacaca gcatacacat aatcttcata 300
ttctttgctt tgtctgtga aggcaagggc catgtctatc ttattcgtca ttgattcccc 360
acatccaaca tagtctggg gacagcacca atgcactttt ggtgcataag caaatctgagc 420
atttatagct cttacctaca atatctgata gactaatcaa atatagtagg ttatctgggc 480
ctttttgatt catgtctcta gcttaacttt ttatttgta tctctcactt 540
tgccctttga tatactctta cagtttgcgt cactgagtaa aagaaaaatnt aaacagcaag 600
aagtaaaact gtgttttatg gatttngata acatcttcta aaagaccccc caagatttgtt 660
gatgtctaaa aaaattaaag ggccttcacac tcataataat acttaatagt tcttaaaata 720
ttacaaactg attggaacat tgcctaac 748

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<210> 572

WO 99/33982

PCT/US98/27610

<211> 755

<212> DNA

<213> Homo sapiens

<400> 572

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ggaatgtgag cacaatgcata aatgtcttta aaaagcatgt tgtgatgtac acatttttgta      180
attactctttt ttgttgtttt ttagcaacca ttgttaaaac attccaaata attccacagt      240
cctgaagcag caatcgaatc cctttctcac ttttgaagg tgacttttca ccttaatgca      300
tatcccccct tccatagagg agagggaaaag gtgtaggcct gccttaccga gagccaaaca      360
gagcccgagg agactccgct gtgggaaacc tcattgttct gtacaaagta ctagtcaaac      420
cagaagggtg attccaggag gagttagcca aacaacanca aaacaaaaaa atgtgctggt      480
caagttttca gctttaagat atccttggat aatgttattt ctatctttat ttttttcatt      540
anaagttacc anattaagat ggtaaagcct ctgagaccaa aattttgtcc catctctacc      600
ccctnacaac tgcttacaga atggatcatg tcccccttat gttgaggtga ccacttaatt      660
gctttctgcg ctccctgaaa gaaagaaaag aaagaagact gtgtttttgc cactgattta      720
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<210> 573

<211> 743

<212> DNA

<213> Homo sapiens

<400> 573

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cangtcta at gctgctctn atcggttctt nnnantnaag ntactcgttc tttctncang      60
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gacttggtaa cagacagatt gctggatccc acccctagac tctctgattc agttagtgtt      180
gggttaaggc caagactgaa tttttcaca gtttcccagt ggtgctgata cttctgggtcc      240
aggaacttag tggggagaga acgactaatc tagaccattt cacttccatc tctgagcttc      300
ttgtcactgt cacactgcat ccttttaaca atgcattccc tatcctattg caatactgac      360
atctcatcaa ttttttaaaa catgcgtttt cagaacaact attttatact aaatactcac      420
ttttagta at attttcgaaa ttttgccta tggatctgag atctaacaaa tactattctg      480
gacatgggct acaacagtgt aggcctggaag taaaaatggt aaacccctgt gaccacgtta      540
ttttaaagt ttttttagtt aagaataata tggtcttaga gcagggtctaa acagtagcac      600
tcacatgggg aatgataact tgcctttgca cataaaatgt cctgaaggga aaaaataaag      660
cagaaaattn ncagatgaac tgaaaactctg tacaatgttt gggctgaata ctgccagcgt      720
tgangtctag gaaaatgaac ont                                     743

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<210> 574

<211> 737

<212> DNA

<213> Homo sapiens

<400> 574

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ccgtctaagt ctggnntcta atcgctttct taangctcmn gggctcgntc tcmctncaag      60
cagcccgccg gtgcgaattc ggcacgagg gattacaggc atgaccaccc gcgcccagcc      120
tgtntttctc tatactntgt attttggmct tgtattatgc tctgtatacg ctataattat      180
ttatgtccat gtnctnttct tcaatagact gtgaactctt cgaatgtngg actcctagag      240
ctagatnctc nattatnnnn tattaaattg aatgacttgn aactacagat cctttattta      300
aacttcccaa atttctgctt tatctagcnn actctttaa tctctttatc tcatgtagat      360

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WO 99/33982

PCT/US98/27610

ttcanaggct	gaaataattg	agatttttag	tttgaagaaa	agagaactgn	ggatttaatg	420
gcnttattat	tatatatttt	atggctgttt	gggagtnagg	ttgcagacat	tggtcacttt	480
ccctcctaaat	nectaaatat	ttcctaaaaa	caggncattc	ttntttttnt	tatggagtct	540
ggctctggcn	tccagagctg	antgcgngg	cccactcttg	cttactgcag	ctcccccttc	600
cgattencgc	tggctctcct	ncctngctgc	cgggaggctn	aggccnggga	atcggtgacc	660
ccggaggcgg	agggtncnan	agcctnnacg	ggccctnggn	ctccccgctg	ggtacnngac	720
cggacctccg	ncctgnat					737

<210> 575

<211> 766

<212> DNA

<213> Homo sapiens

<400> 575

gnagttnaaa	agcgmntttt	antcctctcn	aatcngnttg	ggctactngc	tctttctgna	60
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ctctctccctg	ccctccctct	gctccccatc	ccactttctc	atctgcctcc	ttttctcact	180
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ctcttgatcc	cttagtttcta	atctcacctg	ttgtttttca	gagatggagt	ctctcaactct	300
ctggccccagg	ctggagtgca	gtggcatgat	catagctcat	tgcatccttg	aaatcctggg	360
ctcaggtgat	ccnccgcct	gagcctcctg	agtatctggg	actacagatg	cgtgcoccca	420
agcctggcta	attttgtctc	atgtcttcta	aaaattattt	tgtgaagccc	cttcacaaaa	480
aaccttaang	gaaatctgat	gggtgtcagg	aatctaactc	tcctctaaacc	atcctctttt	540
aactgtctct	aaaatatctc	tggtggccctt	tcttagcctt	ttctgtgttc	attcaatgct	600
tcaagcgct	ttttgnttct	aagttgagtn	ctttgggggt	ttgacaggtg	gtgacgtgta	660
gttttgacac	tgtttaacttg	ttnaatacag	tgaaaangtt	tgtagaagtg	aaaatgcttg	720
anaaagaatg	gmaatgcctt	tntacaaata	aaagtnttgt	taaaat		766

<210> 576

<211> 761

<212> DNA

<213> Homo sapiens

<400> 576

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ancacaggcg	ntgngaattc	ggcacgagaa	gataacctct	taatgcattc	agtttgtata	120
tgaaggaaat	gagagcaaat	gtcgtagctg	agtgacactg	gaaagaaagc	gcggccatca	180
accagatcct	tgggcngagg	tgccatgcac	tgctccagtag	tatttattgc	tttagagatt	240
gcttgctgta	cctgtatgtc	gtcccttttt	aaatatgttt	tcctttttct	tgaaactgta	300
taaaagtttt	ttccccetta	gcataagcat	cttatatata	acaactcatt	tgtacaaggt	360
ttttaaagtt	atataataaa	tggtgtatata	tattttttgnt	tccecttttt	gacttttttt	420
ttctgtatga	aaccagatg	tcaccaaatg	gacattaata	gttgcattaa	ggatcagtag	480
cattacaaca	agttgtctta	aaagccatta	tgtaaaaaca	gacttgaaaa	tgagttaggg	540
aatttttagc	acactgtctg	agcacagtgg	gaacctctct	ogtttccctt	ttgaaactcca	600
antggatgac	cctactcctg	cgccccttag	gaccccggac	tgggccgngt	acaaaaacttt	660
accgtgccaa	aattcttaag	tgaatttacc	tttctncttc	tttttgaaagc	tngaaaaattt	720
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<210> 577

<211> 803

<212> DNA

WO 99/33982

PCT/US98/27610

<213> Homo sapiens

<400> 577

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ctgagggcgg	aaatggccaa	ctggggcctg	cagttgctgg	gcttctccat	ggcctctgetg	180
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cagcctctatg	aactatagtg	agtcgtatta	cgtagatcca	gacatgataa	gatcatttgat	360
gagtttggac	aaaccacaac	tagaatgcag	tgaaaaaaat	gctttatttg	tgaattttgt	420
gatgctattg	ctttatttgt	aaccattata	agctgcaata	aacaaagtta	acaacaacaa	480
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tttgcgccnc	tntgcgta	ttcatgggnc	atanncttgn	tttctggng	tgtaaaattg	660
gntaatcccc	ttmacaaaat	ttcncacaca	atcatttacc	aaaccccngg	gaggcctttt	720
aaagnngtna	aaanccctgg	gggtggccct	taatttaagt	ggnnccctaa	ctcncmttta	780
antgcmttg	cccttcaact	ctt				803

<210> 578

<211> 738

<212> DNA

<213> Homo sapiens

<400> 578

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nnnnnnnnnn	nnnnnnaa					738

<210> 579

<211> 758

<212> DNA

<213> Homo sapiens

<400> 579

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ctgccttgga	ccttcccttg	tcaccaaaaca	agcccaacct	gtgcacttcc	accagccttt	360
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WO 99/33982

PCT/US98/27610

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ccttgaggac aagttggaac agaagaccaa gagtggcctc actggatata tcaanggcac 480
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tctggattgt gagaaaaatc cagcaagttc catgaatatt aatccaggt ctgcattggc 600
ccggggcaag agtttaacct ctctggggccc tgcatttctc acatcttggg gtctgtacac 660
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<210> 580

<211> 816

<212> DNA

<213> Homo sapiens

<400> 580

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ataaaattac tatcattata ctttgttcta tcacatact ctaccttga agggatattt 480
cccagttggt atagctacaa aacagaggca gatcatttag cctgcattng atntngantg 540
aaaaataaag ctttgggtng ttaaccact gaaatgttt gcgcctatt agtantngca 600
caacttatcc tatnctggcc aaacatagaa tgttttcggt ttgcaaggta acangatccc 660
ctttacagnt gtaacnaaaa tnancmntaa aaaaactnga gccntntaga acntnntagt 720
ggagtcggan tttaacgttng anccagacc ntggattang gatncttgg atggagtttg 780
gacataccac cancttgaa tggcnantga aaaaaa 816

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<210> 581

<211> 868

<212> DNA

<213> Homo sapiens

<400> 581

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gccttggaat agtaactctt ctcatattgt tgggatctgg ccaccaagtn ccagaatgat 180
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taaaatatcc aancaatggg gtcatcctg gcccaaatgc cagaantcna gagcctaata 660
ggacttccaa tnattaaact tnccaaannc gaaaaaagna gggcnttccn nttatggcaa 720
aaaaatnaaa nnaaaaggan atntggnatn gttngccnaa aaaaaagcc cmntnngaaa 780
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<210> 582

WO 99/33982

PCT/US98/27610

<211> 745
 <212> DNA
 <213> Homo sapiens

<400> 582
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<210> 583
 <211> 748
 <212> DNA
 <213> Homo sapiens

<400> 583
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<210> 584
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 <212> DNA
 <213> Homo sapiens

<400> 584
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 cctcanccag gatattcctt cctcagagaa gccttctgtg accatgctat ctaaaatact 240
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WO 99/33982

PCT/US98/27610

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<210> 585

<211> 745

<212> DNA

<213> Homo sapiens

<400> 585

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<210> 586

<211> 749

<212> DNA

<213> Homo sapiens

<400> 586

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gttgaccttg gctcnaenga catacccant ctgacttnna acngnengct ctnagettac      300
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<210> 587

<211> 783

<212> DNA

WO 99/33982

PCT/US98/27610

<213> Homo sapiens

<400> 587

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<210> 588

<211> 771

<212> DNA

<213> Homo sapiens

<400> 588

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aaaagcttta	aaaagtttta	ttatccanat	ttacaaccca	ctanttaagc	taataaanc	720
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<210> 589

<211> 844

<212> DNA

<213> Homo sapiens

<400> 589

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caactgggtt	cccattggcat	gtggtggcct	tagaggagggt	gttcagcctg	ccaccgtcgg	180
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gggagggaaca	gccaccccg	cccccgctgg	acccccagaa	cctggcaaga	ccgcctgccc	360
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WO 99/33982

PCT/US98/27610

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<210> 590

<211> 767

<212> DNA

<213> Homo sapiens

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atgtgtctac cccaaaggcg acattnttgg caccaaata tccctcttga ccnntttaat 720
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<210> 591

<211> 765

<212> DNA

<213> Homo sapiens

<400> 591

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<210> 592

<211> 757

WO 99/33982

PCT/US98/27610

<212> DNA

<213> Homo sapiens

<400> 592

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<210> 593

<211> 766

<212> DNA

<213> Homo sapiens

<400> 593

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<210> 594

<211> 754

<212> DNA

<213> Homo sapiens

<400> 594

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WO 99/33982

PCT/US98/27610

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<210> 595

<211> 767

<212> DNA

<213> Homo sapiens

<400> 595

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<210> 596

<211> 743

<212> DNA

<213> Homo sapiens

<400> 596

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<210> 597

<211> 786

<212> DNA

<213> Homo sapiens

WO 99/33982

PCT/US98/27610

<400> 597

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<210> 598

<211> 809

<212> DNA

<213> Homo sapiens

<400> 598

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<211> 759

<212> DNA

<213> Homo sapiens

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WO 99/33982

PCT/US98/27610

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<213> Homo sapiens

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<211> 755

<212> DNA

<213> Homo sapiens

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<211> 773

<212> DNA

<213> Homo sapiens

WO 99/33982

PCT/US98/27610

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<211> 784

<212> DNA

<213> Homo sapiens

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<212> DNA

<213> Homo sapiens

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WO 99/33982

PCT/US98/27610

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<211> 759

<212> DNA

<213> Homo sapiens

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<211> 809

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<213> Homo sapiens

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<211> 788

<212> DNA

<213> Homo sapiens

WO 99/33982

PCT/US98/27610

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<211> 796

<212> DNA

<213> Homo sapiens

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<213> Homo sapiens

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WO 99/33982

PCT/US98/27610

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<211> 786

<212> DNA

<213> Homo sapiens

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<212> DNA

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WO 99/33982

PCT/US98/27610

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<210> 613
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 <212> DNA
 <213> Homo sapiens

<400> 613
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 caaattgcca aaagccagag ttgtttatgc tagtgcaact ggtgcttctg aaccacgcaa 180
 catggcctat atgaaccgtc ttggcatatg gggtaggggt actccattta gagaattcag 240
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WO 99/33982

PCT/US98/27610

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<210> 615

<211> 774

<212> DNA

<213> Homo sapiens

<400> 615

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<210> 616

<211> 769

<212> DNA

<213> Homo sapiens

<400> 616

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<210> 617

<211> 766

WO 99/33982

PCT/US98/27610

<212> DNA

<213> Homo sapiens

<400> 617

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<210> 618

<211> 762

<212> DNA

<213> Homo sapiens

<400> 618

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ntaaacttta	tagtngagtc	gtttnacggt	anatcccana	ntttgataan	gatacattgg	720
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<210> 619

<211> 754

<212> DNA

<213> Homo sapiens

<400> 619

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WO 99/33982

PCT/US98/27610

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cangtggaac	accttgatca	aactgacttc	tgaaaaagac	cctntngata	tttgatgcct	720
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<210> 620

<211> 767

<212> DNA

<213> Homo sapiens

<400> 620

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<210> 621

<211> 828

<212> DNA

<213> Homo sapiens

<400> 621

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<210> 622

<211> 784

<212> DNA

WO 99/33982

PCT/US98/27610

<213> Homo sapiens

<400> 622

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acangaaaat agaactttat gttaaaaaat aaaagtctgg tncctctttg ttaaaaaaac      660
nnmctnctn ctcnaaatcc ncnacannnc tnnnaatntn ctaannntag tctnnntnntn      720
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<210> 623

<211> 1164

<212> DNA

<213> Homo sapiens

<400> 623

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<211> 798

<212> DNA

<213> Homo sapiens

<400> 624

WO 99/33982

PCT/US98/27610

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<211> 793

<212> DNA

<213> Homo sapiens

<400> 625

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<211> 825

<212> DNA

<213> Homo sapiens

<400> 626

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WO 99/33982

PCT/US98/27610

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<211> 772

<212> DNA

<213> Homo sapiens

<400> 627

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<210> 628

<211> 808

<212> DNA

<213> Homo sapiens

<400> 628

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<210> 629

<211> 827

<212> DNA

<213> Homo sapiens

WO 99/33982

PCT/US98/27610

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 acannctanc tgnntnctaa tcatgctntg cttntctnang tgancctata gnaacgcant 240
 nagactncan gcnttgctgt gcncacaag gmnacctana ntcatnanga agcmnttgaa 300
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 agggcaanagc gggtnnaant natngntnan ntgnaaanac tntnnnatcc gmnntnctgt 420
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<210> 630
 <211> 793
 <212> DNA
 <213> Homo sapiens

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 ngaagntttt ntaanaagcc accacttagc ngaggcmnct acangcttgg gggnettagc 180
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 aagcttacnc tngactncac nggcaagctg nangcctgtn ctgecttccn ctgcnntnac 360
 aaatngacag tnnagccaag agtcanagna aaaactncaa ggatatactn atcccantct 420
 nttctacacc tntanattcc ntganctatt gctcanaccn atcgtgctggg caaaggcagg 480
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 natntttacn cgaactnttg tgattccaaa ctaaagaaat gngccnnnan gcccntmnt 600
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 caactntng gattacnca actccanaan atccgacggc atnnaanang caaaaacaaa 720
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<210> 631
 <211> 752
 <212> DNA
 <213> Homo sapiens

<400> 631
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 aacataaaa aataagagct ccttaaaagat tataaataaa tgggtgatgt aaagtaatat 180
 caccatcgga cgaagctagg gaatcaacac ttgacagaaa gatcacatatt ttttttatac 240
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 actctataaa gtaaaaggct gatagaatta tatcagcatt ttctagtctc tggctgaatta 360
 tgcatgtggc atccatggct gccttagatc acaaaaatcc caccagatat atgctgttgg 420
 atgaagagtc accaccacct ctgtgaaata gtcttcccc aaaaaatcc aacccaatcc 480

WO 99/33982

PCT/US98/27610

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angtaaagaa  gttcnagacc  agcctgccaa  catggtgaaa  cccccctctn  tacttaaaag  660
taccnagat  gagcccgccc  gttgtggcaa  gcacctgtgg  tcccagccta  cttgggaagc  720
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<210> 632

<211> 751

<212> DNA

<213> Homo sapiens

<400> 632

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agatgccaca  taaaccacag  aaagatgaag  atctgacaca  ggattatgaa  gaatggaaaa  240
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taactggcta  tacattccaa  actgatagta  cattgccatc  tccaggaaga  ttgacggct  360
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aaaaatacca  aaaaatttag  ccangtgttt  gaatggntgc  atgcctgtaa  ttcccagctt  720
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<210> 633

<211> 806

<212> DNA

<213> Homo sapiens

<400> 633

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ccagctcat  gaaacaccaa  aactattata  cgggaggggt  taatagtttt  gatgcccagt  240
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aattactctt  tatggccaaa  ggggctttgc  agatgtaatg  aagttaagga  tctttcgcca  360
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<210> 634

<211> 775

<212> DNA

<213> Homo sapiens

WO 99/33982

PCT/US98/27610

<400> 634

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accagccaca	aaagatcctg	tgtcagaagg	ggaacaggcg	ttggaggctt	ggagtatgct	420
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tattnnctct	aaatttngnn	aaccattttna	taaagnctng	cnantaaaaan	aaaggtttaa	720
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<210> 635

<211> 784

<212> DNA

<213> Homo sapiens

<400> 635

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aatcttcata	tatatanaaa	tggatattaa	tttgctagaa	ttaanagact	gcaggtaaaag	420
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gctggaatga	ggaatggtaa	ctttaggcaa	gatagtcttc	tgnagcggct	gatatgaaca	540
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ttccngttna	tgtggttana	ccccttcgat	naanaanncc	atannttnna	tttggmntg	720
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<210> 636

<211> 765

<212> DNA

<213> Homo sapiens

<400> 636

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agccccactt	ccacaaggac	tggcagcggc	gcgtggccac	gtggttcaac	cagccggccc	180
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caggccaaag	tgcagnggct	tgaaggagta	ccgctccaaa	ctcatcctct	tcccagggaag	480
ccctcmgccc	ccaagaaggg	aagacaagtt	cttgcctgaan	gaacttgaaa	cttggccccc	540

WO 99/33982

PCT/US98/27610

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<210> 637

<211> 853

<212> DNA

<213> Homo sapiens

<400> 637

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<210> 638

<211> 740

<212> DNA

<213> Homo sapiens

<400> 638

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<211> 774

<212> DNA

<213> Homo sapiens

WO 99/33982

PCT/US98/27610

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<210> 640

<211> 743

<212> DNA

<213> Homo sapiens

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<210> 641

<211> 740

<212> DNA

<213> Homo sapiens

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WO 99/33982

PCT/US98/27610

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<210> 642
 <211> 737
 <212> DNA
 <213> Homo sapiens

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nctgacccca	caagggtttc	gtggctgttg
120		
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aggatgaggt	ggaggaggag	agtgacaagg
180		
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agcagccggg	attctggacc	ttcagctact
240		
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<210> 643
 <211> 748
 <212> DNA
 <213> Homo sapiens

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cttcacatgg	aggttactta	gatattgtga
240		
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300		
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gacattgtta	aagtgtcctc	taatgaaggt
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catactccct	taattggaag	agccagngca
420		
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gatcatggng	caagcatcan	cactcattct
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748		

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 <211> 759
 <212> DNA
 <213> Homo sapiens

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WO 99/33982

PCT/US98/27610

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<210> 645

<211> 766

<212> DNA

<213> Homo sapiens

<400> 645

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aagccagagcc	acctangaaa	cagtcacccc	ccttagtaaa	caaaagggaa	nagcatgcac	180
cagaatcatc	cgcaaatnag	acagtcaaca	cgcacaggct	cgaaagagaag		240
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ctnatctctgc	gangatganc	acggtagacg	tnaanatgat	caggcacgct	ctggngagga	360
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acacaggccm	gaaaagaattg	anangaaatt	ggaacacactn	gaagcamaa	acacctaang	660
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<210> 646

<211> 752

<212> DNA

<213> Homo sapiens

<400> 646

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gaagtacttg	caatctgaaa	agggttatgc	tgtggaggtt	cttttagaac	aaaatagatc	300
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gcctctctgc	ctgttgacag	tgcaaggaga	ccatgcctgt	gggagccagg	ctctcgtttg	660
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WO 99/33982

PCT/US98/27610

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<211> 743
<212> DNA
<213> Homo sapiens

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gactgtcaca tgtgtgtttgc tgggtggcttc ccactggcga agagaagcta caaaatatgc    180
tcgatggata gcattcactg gaaccactat gagaagatta taggaaaaac accaagacta     240
gaggactctg ggttcctttt atgcaaaagtc aactcttctg ggtcacagtt acccagcaac    300
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<211> 759
<212> DNA
<213> Homo sapiens

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aatgttttagc tgggagggct gtaggggacc ctgttaaccc cattaaacac agtaaagcat    180
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ccctcctggg tgcggccaga ggccaaggca gtgcgccgag ctccctgaatc ccaagaatgg    300
ttctggcaag tactgtctgt ttgttgtagg ggcaaaagat taaaaataaa cgaggttctg    360
ccatggctaa gccttgtgga aaccagacc caaagccctt gccatgccan gggctcctaac    420
nccagacgct tgttatggag gcaccancng gtantggccc gttaagcan ggccagagtc     480
gggacaaga gcaagantga aacanccaag agacanagga ccatgtctga ccattgggca     540
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<210> 649
<211> 746
<212> DNA
<213> Homo sapiens

<400> 649
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WO 99/33982

PCT/US98/27610

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<210> 650

<211> 789

<212> DNA

<213> Homo sapiens

<400> 650

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<210> 651

<211> 757

<212> DNA

<213> Homo sapiens

<400> 651

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gaacctttaa	aaactatngt	ggagtccega	ttacgttaga	tccagacctt	gataaganac	720
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WO 99/33982

PCT/US98/27610

<210> 652
 <211> 759
 <212> DNA
 <213> Homo sapiens

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<210> 653
 <211> 820
 <212> DNA
 <213> Homo sapiens

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 tnnmtantna tctnaancct aaatgntcac atnnaaactt tanagnncat cnnnnatgna 720
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<210> 654
 <211> 768
 <212> DNA
 <213> Homo sapiens

<400> 654
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WO 99/33982

PCT/US98/27610

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ttttaccaag	taaantgtct	ggaccaacca	tntgcaagtc	caaaamntcg	gaaaaacctg	720
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<210> 655

<211> 752

<212> DNA

<213> Homo sapiens

<400> 655

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<210> 656

<211> 754

<212> DNA

<213> Homo sapiens

<400> 656

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<210> 657

WO 99/33982

PCT/US98/27610

<211> 734
 <212> DNA
 <213> Homo sapiens

<400> 657

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<210> 658
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 <213> Homo sapiens

<400> 658

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<210> 659
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 <212> DNA
 <213> Homo sapiens

<400> 659

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WO 99/33982

PCT/US98/27610

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<210> 660

<211> 734

<212> DNA

<213> Homo sapiens

<400> 660

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<210> 661

<211> 762

<212> DNA

<213> Homo sapiens

<400> 661

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<210> 662

<211> 745

WO 99/33982

PCT/US98/27610

<212> DNA

<213> Homo sapiens

<400> 662

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<210> 663

<211> 748

<212> DNA

<213> Homo sapiens

<400> 663

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<210> 664

<211> 785

<212> DNA

<213> Homo sapiens

<400> 664

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WO 99/33982

PCT/US98/27610

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 <212> DNA
 <213> Homo sapiens

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<210> 667
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WO 99/33982

PCT/US98/27610

<213> Homo sapiens

<400> 667

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<210> 668

<211> 763

<212> DNA

<213> Homo sapiens

<400> 668

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<210> 669

<211> 754

<212> DNA

<213> Homo sapiens

<400> 669

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WO 99/33982

PCT/US98/27610

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<210> 670

<211> 752

<212> DNA

<213> Homo sapiens

<400> 670

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<210> 671

<211> 752

<212> DNA

<213> Homo sapiens

<400> 671

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<210> 672

<211> 792

<212> DNA

<213> Homo sapiens

WO 99/33982

PCT/US98/27610

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ctggacnaca ctggagtgga acactgnctc ccacttttctt gggacttttg agggangtgg      540
aaccggcaca ctggaactct tccgtctcta nggctgcatg gggagccctg gggagcttna      600
atnntggggg gatcccnmaa aangaacccc tgtcccccat anacttgggt ttttngcttt      660
cancccttcc cccctggccc cnnttgacca ctctcatggag tttaattaaa atnngccctg      720
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antnatentn nt                                     792

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<210> 673
<211> 755
<212> DNA
<213> Homo sapiens

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<400> 673
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gatgctgaaa ttgcaaggct gatggaagac ttggacggga acaaggacca ggaggtgaac      180
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ctcgagcctc tagaactata gtgagtcgta ttacgtagat ccagacatga taagatacat      420
tgatgagttt ggacaaacca caactagaat gcagtgaaaa aaatgtctta ttgtgaaat      480
ttgtgatgct attgctttat ttgtaacctat tataagctgc aataaacaag ttaacaacaa      540
caattgcatt cattttatgt ttccaggttca gggggagggt tgggaagttt ttaatttcgc      600
ggcccccggn gccaatgcac tgggcccccg tacccaactt ttggtccctt tantgagggt      660
taattgcncc aatcactggta atagctgttt cctggtgnga aattgtttcc      720
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<210> 674
<211> 753
<212> DNA
<213> Homo sapiens

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<400> 674
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tagctgctat catgacccct ttttaaggca attctaactt ttcataacta catctcaatt      180
agtggctgga aggtacatcg taaaacaaag taaatttttt tatgttcttt tttttggtca      240
caggagtga caagtgaatc aggtttaact tcaccttagt tatggtgctc accaaaagaa      300
gggtatcagc tatttttttt taaattcaaa aagaatatcc cttttatagt ttgtgccttc      360
tgtgagcaaa cttttttagt acgcgtatat atccctctag taatcacacac attttaggat      420
ttagggtgaa ctgcttcttc tttttcttgc aagtttttaa ttcccaactc taagtgaatt      480
tgtggacca aattcaagg aactttttgt gtagttagt cttgcacaa gtgtttgta      540

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WO 99/33982

PCT/US98/27610

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aacaactca aaatggattc ttaggagcat tttaatgttt attaataaac tgaccatttg      600
ctgtanaaag atnanaaaac ttaagctttg ttttactaca acttgtaaca agttgtatga      660
cagggcata tctttgcttn caanattttg ggttgggggc actanggggt caaaacctg      720
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<210> 675

<211> 760

<212> DNA

<213> Homo sapiens

<400> 675

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tgntttctaa acnttgctct cgtntttntt gcaggatccc atctattoga attcgccagc      60
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agctccttgg gcaagctctt tatcctaaga ttctcagtg agccttatag agttgtctgc      180
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tgtcactcca aaacagctgt ttgatgctaa tagcacacat gaggtccttc aaaaattgtct      540
gaggaactac aggacattgg agagatatt atcaaacacc cactacatgc ctgataactta      600
actanggaac tatnaaagtg ggtggtgaag acaagtngga agtaaatgca aaacctattt      660
ccatatatgt ttgmcgcta gattgntncc ancaattngc ntcttggaaat tgttgaattn      720
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<210> 676

<211> 751

<212> DNA

<213> Homo sapiens

<400> 676

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ctcaatctga cttagtataaa ccatgctgta gaatttttgt cttaaaaaga ccacataccc      180
agcaccccat aaataaaaga ttcactctga attgggattc aaagtgtata aattcctttg      240
ttcatactca taaatagcac taaagtgtta taacattttc atttacctat ttttagttcc      300
ttcattttaa cttataaaaa atcttggatt gatattcttt tttttttttt ttgggagcga      360
gtctcgtctc gtcaccagg ctggagtaca gtggctctat ctgggtctac tgcgagctcc      420
gcctnccggg ttacagccat tctctgctct cggcctcccg agtagctggg actgcaggcg      480
cccgccacca caccggcta atttttttgt atttttagta gagaagggtt ttacacctgt      540
tagccaggat ggtctcgatc tctgacctc gtgatccacc tgcctnngcc tccaaaagtgc      600
tggaatttca ggcgtgagcc accgcgcccg ggntcaaat ggatattctt taaccattaa      660
aaggtttact ggggtmccna ttgcacata tattggaac ttggaagggt taatttgaaa      720
caagntttg aagttaactg aaatttgggg a                                     751

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<210> 677

<211> 756

<212> DNA

<213> Homo sapiens

<400> 677

WO 99/33982

PCT/US98/27610

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aaaagtacca ataattgagta ggaaatcact tctgcagtat ttttggagca ttttctctaa 180
gcatgcacata aaagccaaag gtcacaaagg aaaaaactga tagatttgct tgtgatattg 240
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tgtatgaaaa agaggcaaaa caacaagaag aaaagattga aaaaaatgaga gctgaagacg 360
gtgaaaatta tgacattaaa aagcaggcag agatcctaca agaatecagg atgatgatcc 420
cagattgccca gcgcaggttg gaagccgcac atttggatct tcaacggata ctagaaaatg 480
aaaaagactt ggaagaagct gaggaatata aagaagcacg tttagtactg gattcagtg 540
agtttagaag cctgaaactt ttctcgtatg gggtggtttt tgcattaaat nctggggtcc 600
attttacaat ccattatttt tgacctgcgc tatgtgttca agtagtatga gaatgtgatt 660
gntttatctt ggntcatata tattttcttg gctaatttaa tatgtcaaat aaatgagttc 720
atttaaaaaa aaaaaaaaaa acccgagctg ttttnt 756

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<210> 678

<211> 756

<212> DNA

<213> Homo sapiens

<400> 678

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gnnnnnnnnn nnnttnnaat agnnagctac ttgttctttt tgcaggatcc catogattcg 60
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aagccattcc aggaggaact agatccacca ctctctctgc tgggcatgct ccaaaaatgg 180
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atattgaggc aagctgtacc agcagcttct gggggacctg ctcaantggat ggtcccaacc 660
cctgcattta tctctttggg atagttaaag cccctgnacc tggaaactgng tattttcttg 720
tactatctct gtanacattaa ttttttact ttttgg 756

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<210> 679

<211> 747

<212> DNA

<213> Homo sapiens

<400> 679

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tatgcactct atcagccaga atttggcatt tagctcttag ttaaactctg taaggcagac 180
tctattgttt aaagagaagg tgcatttggt cctcaatcaa gcaagagcac ctgtgttgta 240
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cagtgccttt cttgtgttat gaaaggcagg tagatatatt agccataatt aaaaatccat 360
agttaaatgt cacactgacc ttaaactctc ctgtctatgc cctgtatct ctgatgttaa 420
aagttgatt attgggcagt tgtggcagcc tgcctgccta catgctagac aagttgtctt 480
tagtacatag ccacaagttc ttcatctttt aaaatgtttt gacagatcat ctcataataa 540
aaataattca ngaaaactat ggggaaatag ttacatttca caaagatat tttaaactct 600
ttgtaaaact tagataatag agcctancaa gttactttgn actcaattgg atacatttta 660

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WO 99/33982

PCT/US98/27610

tgnttaattt taccaccata catttttatta atcaaaattg gttagcatgt gactcttttt 720
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<210> 680
 <211> 750
 <212> DNA
 <213> Homo sapiens

<400> 680
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 agccttaagg tctgcagttc caccctgccc atcaagccct ttctctcctg ctccctcgag 240
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 attcttgaaa gtgtgtctcc ttgaccttcc tttaatggca acttaactga anaaagggat 660
 gtnctnctat atccaaaatt cagctatttg gcaataaac canatggatt aaaaaaata 720
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<210> 681
 <211> 748
 <212> DNA
 <213> Homo sapiens

<400> 681
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 gccgagattg cactcttgta ctccagcctg ggcaacgagc aaaaaactct gctctaaaaa 180
 aaaaaaaaaa aaagaaaaag aaaaatggct tccaggacag agcatgctca ttgtctggcg 240
 gacagtccca gaaacagacc ctgttagtcc ttctacttac ctgctggatt ttcaagcac 300
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 tctgggtcan gaagaagctg ttcacggtgt gataatactc tttnanttgt gcttctcata 480
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 ccagntgaca naaaaatccm agnatgagat caanaaggat actgggtgtt tctgactttt 600
 acaaaaaatta ctttgntggt ttcatataaa aaaaagcttt aacctantgn ttnctntanc 660
 cttttagaaa ntattaaatt tnaaaatgaa ttcnatanaa atanaannac naaaaaactt 720
 nntnccctta naacttttagt gangcgtt 748

<210> 682
 <211> 755
 <212> DNA
 <213> Homo sapiens

<400> 682
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WO 99/33982

PCT/US98/27610

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catgaccaca gataatcaatg cactgaagcg gcagtactct cgaattaaaa agaagcaaca 180
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gctcaggagg accnncnaag ggcagtttcc ggagcccgnt gttccggaga tgcctgatgtg 660
ggntgtgtct gcanctcang gccaaanttg gggacccctg ggaactgtac cctangggnt 720
ncttgnagnt taaaacttga ccttaanggn ngcct 755

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<210> 683

<211> 755

<212> DNA

<213> Homo sapiens

<400> 683

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acanaattcn ttaatatctc ttctctctgg gcttn 755

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<210> 684

<211> 774

<212> DNA

<213> Homo sapiens

<400> 684

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gaaactctgg agcaactaag tgaatttaat gattcactaa agaaaattat gctctgaaat 180
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gtgtcttctt tctgggggtt cagtatttgc aaagaaantg aagaagaatt ctggaatgac 660
cattcaatta accctnagga aaaaagccga ccttanaaat ttaccttant gcnttgmnnn 720
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WO 99/33982

PCT/US98/27610

<210> 685

<211> 759

<212> DNA

<213> Homo sapiens

<400> 685

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tcattgagta atggatgaag aaagccccc tagaatggca agattacatt tacaaaggag      180
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<210> 686

<211> 749

<212> DNA

<213> Homo sapiens

<400> 686

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ttacatgaag ggctggtttc acatgaatac tatactgaaa tctgtgctct caagatctag      180
cagtgaccag ggctgcccgg cgggggcctct cctggcaagt caggaaagtt tctgttgcta      240
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acagtgacct tctccatggg tcaaggacct cctacaatt tctnctgagt taacttttgt      660
gaaaataatc ctaagggttt ctggcttatt gaggaattn ctacaaacaa caaaccaaca      720
acngaagaga agatcatcaa ccaactgttt      749

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<210> 687

<211> 760

<212> DNA

<213> Homo sapiens

<400> 687

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ttccaaaaat tctctgtatt tttaggttat gcaactaata aaaactacct tacatttaatt      180
aattcacggt tctacacat ggataacag gatatgctac tgatttagga agtttttaag      240
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WO 99/33982

PCT/US98/27610

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taaaattttg gccacttttt tcagatttta catcattctt gctgaacttc aactgaaat 480
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naaaagctct taaattgatt ttacagtcct ggaatgcttg gatgnttaa aantanaaca 720
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<210> 688

<211> 752

<212> DNA

<213> Homo sapiens

<400> 688

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tgttccagaa ccttattttg gggagtaaag tcaattgggc agaggatcct gcccttaagg 180
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tattttacat ttctggcaat ctcaactctt atttggaaata cttctgtgca tttgtctgtc 300
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aagtagaaac cgggtttcac ccgtgttgcc caagctgctc tnaaaactcc tgagctcaag 660
cagtcacccc gnettngeta ccggantgct aggattcaga cgttaagcccc cgaancctgg 720
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<210> 689

<211> 806

<212> DNA

<213> Homo sapiens

<400> 689

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<210> 690

WO 99/33982

PCT/US98/27610

<211> 772

<212> DNA

<213> Homo sapiens

<400> 690

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tcagcttctt caagocacaag ctgcccctca gccctacaaa gaaggtgctg ctgattgtgc      180
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gggaagcttt aagnnctctc nanangccac ttaccaaac ttgaggggnt ccaaangccc      720
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<210> 691

<211> 755

<212> DNA

<213> Homo sapiens

<400> 691

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gatgttactg atattcgtaa aatgaatatt ttttgttttg ttttgtttta tttttttgag      180
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gttgccacag ctggtctcaa actcctgacc tcaactcctc cacacctgta atctcagcac      420
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<210> 692

<211> 748

<212> DNA

<213> Homo sapiens

<400> 692

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agaaacacag aacaagtttg cctctcctta gtttttccag aaatgacttc agtatcttga      180
gcatcctcag aaaaagtatt ggaatggaac tatccaagat cagatgcca gttatatatta      240
atgagcctct gagcttcta cagcgctaa ctgaatacat ggagcalact tacctcctcc      300
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WO 99/33982

PCT/US98/27610

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atcacccacc  aatcagtgca  tttcatgctg  aaggattaaa  caatgacttc  atctttcatg  540
gctctatcta  tcccaaaactg  aaattctggg  ggaagagtgt  agaacagaa  ccaaaggaa  600
catcaccttg  gagctncttg  aacacaatga  ggcatatata  tggacaaatc  cactgctgt  660
gtgcataata  tcattgmggg  taaactgttg  atcgaaacgt  ntggcaatgt  ggaaattnta  720
accncagaat  ggggacaaat  ntgtgttg  748

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<210> 693

<211> 881

<212> DNA

<213> Homo sapiens

<400> 693

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ctttcaggac  aggtcaanca  agtcagagga  tgaacaanat  atgtgatanc  atgtgatanc  480
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tataanattt  tatgcantnc  ncacaatna  tataanangg  tcttnaaaac  gngnnccaat  840
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<210> 694

<211> 742

<212> DNA

<213> Homo sapiens

<400> 694

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agttgatagt  agattgcatg  gtttcatggt  tctcatatt  ggtttattaa  ttctatttaa  180
tcaaggaaaa  taactctaga  ttccataaag  ttctcattta  tttttatggt  actactaggt  240
gagatagcac  attacatact  ttactatcca  aatatttatt  tagcagcttc  ccatagtacc  300
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gggggttttt  aaaaactgag  gatatacanta  ataaattgca  gaatttttg  caaagctttc  420
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<210> 695

WO 99/33982

PCT/US98/27610

<211> 745

<212> DNA

<213> Homo sapiens

<400> 695

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aatcacgttag	tccttctctga	aaccactaag	aggaaaaatg	tctgtgacac	tgcatacaga	180
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ctatggcaaa	cagcccacatt	tggacatgaa	atacacccga	tttggaaaagg	taatatagtg	540
tctggaaact	ctagatgagt	tggagaaagt	tgccagtaaa	tgagaaaagc	ataccgacct	600
cttaatgatg	tacacattaa	gggcccnaac	tattcatgcc	aacctatttg	ctcagtagct	660
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<210> 696

<211> 795

<212> DNA

<213> Homo sapiens

<400> 696

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atanctgcct	ccggggagcc	gcttgatcac	aggactagca	gtgagcaggc	agatccctca	420
gcacctgcct	ctgcccctac	cagcttgcgt	tcccctgagg	cctnacacct	ccggaatgac	480
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<210> 697

<211> 734

<212> DNA

<213> Homo sapiens

<400> 697

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ccatccaagt	catctccatg	gctcctgggt	cccctggta	gcattggagt	aggaggctcat	180
caatcatcat	gctgggggtg	gtgcgagagg	ggccaacagc	ctgaaaccaa	atggatctga	240
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WO 99/33982

PCT/US98/27610

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ccttgatgtc ttcttcatta acactgtcac gtctcaccag gaatacagtg acattaaaaag 480
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gttttccatg ttttgggtct tatttttctn ttgcaatctg catttaagna antgcmttn 720
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<210> 698

<211> 728

<212> DNA

<213> Homo sapiens

<400> 698

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<210> 699

<211> 746

<212> DNA

<213> Homo sapiens

<400> 699

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<210> 700

<211> 759

WO 99/33982

PCT/US98/27610

<212> DNA

<213> Homo sapiens

<400> 700

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<210> 701

<211> 751

<212> DNA

<213> Homo sapiens

<400> 701

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<210> 702

<211> 748

<212> DNA

<213> Homo sapiens

<400> 702

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gaatcagtc	atcctgatcg	aaaggtggaa	aaggtttata	agaatgggtg	cctgtttata	180
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WO 99/33982

PCT/US98/27610

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<210> 703

<211> 769

<212> DNA

<213> Homo sapiens

<400> 703

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tactacagaa gaagcagtac agaagttggg ggaactgaagg agagggagcc actgcaggtg 180
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ttttgtana aaccaaggtt ttgccatgtt tnccaggctg gntcnngaac ttctgggctt 720
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<210> 704

<211> 759

<212> DNA

<213> Homo sapiens

<400> 704

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tcgctagccc tcgcgcagct cgccgcgcgg agaagccagc tctcccttgg cagtgtatttc 540
ggaaatgtgt caaggaatt ccaaaaggtg aaacgcagcc aactggctca cggcaaaaaga 600
gtggtcngaa aaaaagcgtt gcccttaca cgaagcacca gacactggag ctggaagaan 660
ggagtttctg ttcaatatgt acccttactc gaaaagcggg gcctagagaa taacccgcan 720
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<210> 705

<211> 777

<212> DNA

<213> Homo sapiens

WO 99/33982

PCT/US98/27610

<400> 705

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aggtgctcgc cgtgcgcgtg gtccactctgc tctacgacct ggtcacggag aagatgttgc      180
ccgaggagga ggtcggagctg acccaggaga tgtcccaga gaagctgcag cagtatcgcc      240
aggtacacct cctgccaggc ctgtgggaac agggctgggt cgagatcagc gcccaacctcc      300
tggcgctgcc cgagcatgat gcccgtgaga aggtgctgca gacactgggc gtccctcctga      360
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aggtcgagta ccaggtgctg gccagcctgg agctgcaggga tggtagaggag gagggtactac      480
tccaggagct actgggctct gtcaacagct tgctgaaggga gctgagatga gggcccacac      540
cangactgga ctgggatgcc cgctagttaa gcttgaaggg tgcccaacctg ggggtgggct      600
ttcttaagca tggaggacat ttttggcaat gcttgggcttt gggccattta aatggggaac      660
cttgaaggcc caaaaaaaa aaaaaantna tntnaaaaaa aaactnnac cttttaaaac      720
ttttaantgm ngnccgnttt tacmttanat tccagacttg attaggaatc cattttt      777

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<210> 706

<211> 760

<212> DNA

<213> Homo sapiens

<400> 706

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gntttgaat ncenntnttt caaatnctng gctacttgtt ctttttgcag gatcccatcg      60
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tgccagaaac atatatatca tttcagactt gaaaacatgc ttcaatttca attcagcaac      180
attatcgaac atatatagact gcaaaattgc aaagagaaaa ttatatcaga caatggcatt      240
ctgctgtggt tattcaggctt gcatataaag gaattgaaagc aagacaactt ttaagggaag      300
aacacaaagc ttctattgta atacaaggca cctacagaat gtataggcag tattgtttct      360
acaaaaagct tcagtgggct acaaaaaatca tacaagaaaa atatatagca aataaaaaa      420
aacagaaagt atttcaacac aatgaactta agaaagagac ttgtgttcag gcaggttttc      480
aggacatgaa cataaaaaaa cagattcagg aacagcacca ggctgccatt attattcaga      540
agcattgtaa agcctttaaa ataaggaagc attatctcca cattagagca acagtagttt      600
ctatttcaag aagatacaga aaactaaactg cagtgcgctcc ccaacaagtt atttgtatac      660
agtccttatta cagangctttt aaagtcccaa aaggatattc aaaaaatcgc caccgggctt      720
gccacactta attcagncat tctatcnaat gccccagggc      760

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<210> 707

<211> 856

<212> DNA

<213> Homo sapiens

<400> 707

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gttgctttga agcctttgaa atnctntgtt tnaaatnctt ggctttngnt ctntttgcag      60
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agtggccccc gctccccacc ccccacggcc gaacagcagg ggcagagcag tctggagggtg      180
tgntccccc ttgatgaaga gcaggcgact ggnattggaga gggagatcat gctggctgna      240
aagaanggac tggacgcata caatgtactg gccncaagg gancctcagg caccagangaa      300
gaccaaaant tantncccta catntccaaac aagagaatag naagctgcat ntgtgaanag      360
gacaaatcca gntcnaantg gttttggctn nacaaaangcc agnncgancc atgccccnn      420
tttgnaacce attacaanct gntgccccan tagctggcac actgancncc tnnctetaat      480
tacttaaaat natgctgtan aagtatantn ttncagaan agactaanca ntncatngnc      540
tactttccca aaaaaaantg anaaaaatna taaaantcaa antaaatca aaatnannan      600

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WO 99/33982

PCT/US98/27610

ataananancan	tannaanatta	tatttcnnan	atantanann	nancnnttta	naannanatta	660
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nananannat	atattannan	anantnaent	aaactnnnnt	naatnntcca	nanacttnaa	780
naanaataag	nnntnatna	nnnnttangn	ntnatatann	tttnatann	nnnnacnata	840
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<210> 708

<211> 766

<212> DNA

<213> Homo sapiens

<400> 708

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agccttagtg	gcccgcattt	gttgaatate	tactgtgtgc	caagcagtg	gtcacacatt	180
tatgaagtag	gtattattat	catccccatt	ttacaggtga	agaaactgag	tctctgagag	240
accaactttt	ccaaggtcac	acagaggttg	gatccagccc	acttccgtct	gaccccaagc	300
cctgtctgtt	aacccccctg	ccattgtggg	gaggttcctg	cccactctgg	agttctctgg	360
tctgcgtcag	tcttcaggag	aagaagaagt	gggggtgatg	ctccaaatat	tgaggctccc	420
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ccagatctga	ggagcaata	ggttcttgg	ctgagatctc	atgggatcag	gttgccagcc	540
ctgcaaaccc	ccgctcangt	ctagaggaca	tggagctgcc	tttcaagggt	catttgcctc	600
ctttacagac	ctggactctg	tnctctggct	actttggccc	gtcccgaact	cggggaatcg	660
tnctacactt	gtaggggcaa	aaccccgggt	tgactctctc	cggttcccta	cccttaacca	720
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<210> 709

<211> 743

<212> DNA

<213> Homo sapiens

<400> 709

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gaattccgca	cgaggttttt	tttttttttt	tttggagaat	gaatgcaaga	tttatgtagt	120
gtgggaagta	gctctcagca	gatggctggg	gagccagaag	ggggatagca	tggggaagta	180
gtcttccctc	ggagtctggc	tgctcagcag	ccgggatctc	ctactgtcc	tgcccgagtt	240
tcccttggcg	tccgaatcgt	tccaccatca	atggcctgcc	agcgtctctc	gatgtgtctc	300
tctgccagtg	gtttctctct	gacgtccagc	cgtctgtgtg	tgtgcccgct	ggggctctcag	360
ggtttttata	ggcagacgaat	gggtggcatg	gcaggccaga	gtggtcttgg	aaaatgcaac	420
atttgggcaa	gaagacagga	gtccttgttc	tcatttagtc	catgggcaca	agcctgaggg	480
tggagccctt	gccagtgacc	ctgccccttc	ctaccagaca	cttccctgtc	cccccccat	540
atcaccgctg	ccatcttctc	cttgatgagg	aatacaactc	ccaattcagt	gnttgccttg	600
gggaagatgc	aatcctcttt	atgacaagtt	tctanaaagt	tgataagaaa	aatggggacc	660
tgctaagggg	ctagtatctc	atttaatact	ctatagaata	ttatgnggtt	ttccccttta	720
ngttttaaat	gttgaananc	nan				743

<210> 710

<211> 753

<212> DNA

<213> Homo sapiens

WO 99/33982

PCT/US98/27610

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<400> 710
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tcagacatctt tctgtgctctc cgagccttgt atttacatcac tagctgaaac tgcgaagtga      180
aatgaatgga gctgtagtata ttgtccttat cctaattttt ctgtgaggag gagaaaaaca      240
cttgtgcttc aaataagcag atgtgaaaaa actctctcact aatcaaaatg ttaccactata      300
ggttatgaga gtctgcctct catagggcagt gaatctgata tgtatactta gtaataaag      360
tctatttagt ttgacaaaac cttagagcag aatttttgca gcttagtcca ggaatgatcac      420
tagcaatgcc aaactctcatt ttttattgaa ctggatccca agaaggcctg ctgtgtctat      480
ttcagtatag actctcctac caatatattt atgctccaaag tcactacacc cagaagtgtat      540
gcagtggggg aaatgcaaag acaacatcac tgaagattc acagaatgga tcttttgtta      600
aatattttat attgacttaa ggaaaacett tcattgggaa ttaattaaat taagtctcta      660
atatcctgga agacagtaaa aantnaagcn ggtgntctca antttgaacc cggcmattng      720
naatttcatt ataggaaattt ctgaaaaataa tcc                                     753

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<210> 711
<211> 718
<212> DNA
<213> Homo sapiens

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<400> 711
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tgtcaattact ttctcattggc attgaaactga gaaataacaa acaagcttta agtgggaaat      180
taaaaaaaag aagtaaaccta tgtagatcca aacttaaaat gtgagaaatt attgaaattt      240
cattttctac aaacttgaaa ttagcctgct aatgttaaag ttgttttaat aatgctgaca      300
aatgtcagtt acgtttgcaa aggagtgtat ggttctaggt atttgctcac tgttaaccgt      360
tgagaaaaaa atgttcaggt tagcaagctc attgaaatag agacctcctt agtttacagc      420
aaagaataaa tagctgatga ctggagattg ggactaaggt tttatttatt tatattcttt      480
gaaagaaatc ggacagttta taagtgggtt gtggttagagt tgaaggatgt ctgagagatg      540
gaaagagagt gacaaaggag gagaaggaaat agtatttctt ttttagtatt gntttgaaat      600
taaaactctg ntattttaat atggtaaaga gcaagaattt gggttgggcc gngtgcactc      660
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<210> 712
<211> 783
<212> DNA
<213> Homo sapiens

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<400> 712
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cttggaaacat ttgtgcaatg ctggtgggaa tgtcaaccgc tgcggccctc tggaataagc      180
ctggcagctc ctccaagagt taccngtga cccancaatt ccactcctag ctccaccac      240
aggaattgaa agcaaaacgc caaacagatg cctgtncacc aaagttcacg gcagcatnct      300
tcgncatagt ggcagcatcc gtctgcacag cggcatcacg ctctcatcac gggcagcatc      360
cctgtctcac aagcggcagc atccttcgcc acagnggcan gcactctgct tcacancggn      420
agcatccttc gacaaagcgg cagcatnctt cgtnatagcn gcagcatctt ttgccatanc      480
cgccaaggtg gaaacccctgt ccatccactg aggcgtgcat agactaaaca tgggcagtc      540
agcactggaa ttccaagcgg tacaacggng nccaamgtca aaanagatc aggcacctga      600
ngcacctgng cnganaacaa gaacmngcga nnccaanact tttnagacat tatgtcctta      660

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WO 99/33982

PCT/US98/27610

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agtngaaaaa cccagngcac caacgggaaaa ccmgaccgnc ntgnanccct gnttaacntt      720
nantnngttn cccgaaaaatg ggggcacntt nccaaaaagg ggaataaaa gggagaattn      780
cct                                                                    783

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<210> 713
<211> 765
<212> DNA
<213> Homo sapiens

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<400> 713
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atgaagagag aggacatcta cacttttagat gaagagttac ccaagagagt gaaagctcga      180
ttttccacag cctctgacat gcgatttgaa gacacgtttt atggagcaga cattatccaa      240
ggggagagaaa agagacaaa agtgctgagc tccaggttta agaatgaata tctggccgac      300
cctgataacc gcactttttt gaagagctct ttccagaaga agtgccagaa gagacagtga      360
ctgtcataca tcgctgcagg ccacagagca gcttgggttg gaagagagaa gatgaaggga      420
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tggttaaatg ggtttccaga gtttgggtcac caaaaataca aaatacaccc aatgaattgg      540
acgcagcaat ctgaaatcat ctctagtctt gcttctcttg tgagcagttg tctttctatg      600
atccccaaa agtgttttct aaagtnaaaa ggaaaattcc tagtggattt cancccccaa      660
gggaaaaaaa cccacttgnc cacannagga agccnggntn ccccttngtt ccggcttaan      720
ggccccctgt tcaggaaaac acactggggg anctnttttt tttttt                    765

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<210> 714
<211> 740
<212> DNA
<213> Homo sapiens

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<400> 714
gtttgaannc cttngntttc naatgctnng ctacttgttc tttntgcagg atcccacga      60
ttcgccaaaa gcttgtggca aatttgaaat ttctgccatt agggacctta caactggcta      120
tgatgatagc caacctgata aaaaagctgt tcttcccact agtaaaagca gccaaatgat      180
caccctcacc tttgtcaatg gaggcgtggc caccatgcgc accagtggga cagagcccaa      240
aatcaagtac tatgcagagc tgtgtgcccc acctgggaac agtgatccct agcagctgaa      300
gaaggaactg aatgaactgg tcagtgtcat tgaagaacat ttttccagc cacagaagta      360
caatctgcag ccaaaagcag actaaaatag tcagccttg ggtatacttg catttacceta      420
caataaagct gggtttaact ttgttaagcaa tatttttaag ggccaaatga ttcaaaacat      480
cacaggtatt tatgtgtttt acaaaagacc acattctcca ttgtttcatg tttgaccttt      540
aaggtgaaaa aagaaaaatg ccaaaaccaa caaactaaca ttctactaa aaagtggagc      600
ttggacatat ttgaaatttt tgtaagtga agatttttaa actgactaac ttaaaaaaat      660
agattgtaat tgatgtgcct taatttgcat aaatcataaa tgatgtcct cctctgaatt      720
ggtttaagtgt gtgcttgaan

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<210> 715
<211> 708
<212> DNA
<213> Homo sapiens

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<400> 715
tttgcataat gcttggtcac ttgttctttt tgcaggatcc catcgattcg aattggcac      60

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WO 99/33982

PCT/US98/27610

gagggaggct	agactcaagc	tgtctggaga	gtgtgaaaca	aaagtgtgtg	aagagtgtga	120
actgtgtgac	tgagcttgat	ggccaagtgt	aaaactctta	tttggatctg	gtctgccttg	180
ctggtaacca	ggaagacctt	agtaaggact	ctctagggtc	taccaaatca	agcaaaattg	240
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aagagaatag	ttccccagag	aataaaaact	ggttgttgcc	catggcagcc	aaacgggaag	420
ctgagaaatc	atctccacga	agtcctgtcat	cccagacacc	caattccagg	agacagagcg	480
gaaagacatt	gccaagcccg	gtcaccatca	cgcccagctc	catgaggaaa	atctgcacat	540
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tctaactcga	tgagttactg	agctttggtc	ccttaaaaaca	agctgacttg	gtccctaaac	660
cagatgaaaa	tcagatgctc	ctatacttgg	ctttaagaac	tgctttcm		708

<210> 716

<211> 730

<212> DNA

<213> Homo sapiens

<400> 716

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actttctgtg	aatggccagg	tagtaaaatg	ttctgtcttt	gaaggcatat	ggctctctgc	180
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tcaacagatca	cagttttctgc	ttttgtgtcgc	aaataactga	accctctcct	agttcagagc	360
atttgatacc	gtaaatattta	aagctcactt	gtaaaaactt	gtttgtgtgc	tcocctcacta	420
gtatctcaaa	cagaattgtct	ctcccaataa	tacctaaatt	ccatattctt	tgaagcacia	480
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taaaaaagag	acccttttta	tgagactcac	aataggataa	aagagcccat	gcctattttt	660
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ntgcttaatin						730

<210> 717

<211> 728

<212> DNA

<213> Homo sapiens

<400> 717

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gcaatgactg	gcctcagcaa	gggggacagt	taggacctgt	acatcccaag	tcactaaagcc	120
acataggata	agtaattgggt	ggacagaagc	gggaaaggag	aagggcaggg	cacattgttta	180
aaacttgaac	tttctgaggg	taagactgga	aaaggaaatg	tttcagctga	tatattttga	240
taccagttga	ctatttttga	gaaaaaaa	caaatggcct	ttaaacatca	cagttgtgata	300
cagtcctaact	cagaattaga	gacaggcaaa	acagaaatcc	atcttaaaaa	ataaataaat	360
aaaataaaat	aaatgacatc	actttgggtc	agagctctaa	aattggaggga	ggaagccatt	420
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tggattttgt	tactaanccc	agttgcctct	ttnaaaaaca	cttgtcaact	ttgtctaatc	660
accctcagct	tttttttaaa	aacctctnct	ctacccctnt	ctcttcagaa	caccaaagtg	720
gncttttn						728

WO 99/33982

PCT/US98/27610

<210> 718
 <211> 730
 <212> DNA
 <213> Homo sapiens

<400> 718
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 aattcggcac gatctagata ttgcccacac gctgccacac gtgcacatac ctttccacca 120
 gtcacatgtg agagggcaga ttttccaaat gctcatcacc acttggcact gtgtggacta 180
 taattttggc cagttaggaa atggcatctc atgtttttca tcttaatttg cgtcagcctg 240
 attactcatt gaaacttggt aggttgagaa actttttcta agcttatttg ccatccaagt 300
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 cttttttcca gctgacttgt aggaactcta catcttatca atattaatca tttatcgaaa 420
 actatttggg tgcctatctc ttctcctagt caatgttttt tgtttgtgat atcttttata 480
 atatataagt ttttaagtgt ggcagaagta aagttaatct ttttggctgt gttgtgtgtc 540
 ttgtttgatg taaagatagt ttctgtaata gttttgcagt ttgattgggtc atctttcagg 600
 cttcaattac aacctgcaca ttcatccctc tatctctctt ctactctggt ttttctccat 660
 agcaactatc atccaataat atggcatgca cttatttaat ctggttttga tatataattt 720
 ngctggtagc 730

<210> 719
 <211> 733
 <212> DNA
 <213> Homo sapiens

<400> 719
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 aacaggagag aggagaaaga agaaacgccta gtaattccaa gcactggaat taagtgcct 120
 tcatcagtg ttgcttcaga gtttgaggaa gatgttggat tgttaaataa agcagctcca 180
 gtttcaggac ctgcactgga ttttgatcct gacattgttg cagctcttga tgaatatttt 240
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 aacaggagag gaagagggaa tggatataca gaaatctgag aatgaagatg acagcgagtg 360
 ggaagatgtg gatgatgaga agggagatag caatgatgac tatgactctg caggcctatt 420
 gtcagatgaa gactgtatgt ctgtgcccggt aaaaactcac agagctatag cagatcactt 480
 gttctggagt gaggaaacaa agactgcgctt cacggagtat tcatgacttt nctcagtcct 540
 gaggagaagt gaacagcttg accctacatg atgagangtt tgagaaagtt ttatgacca 600
 tattgatgat gatgaaattg ggagctctgg ataatgccag aatttggaaa ggttctattc 660
 aagtgggaca gcaattcgct ttcnaggag ttttgaatga ctactattaa agagaangcc 720
 caanaattnt ntt 733

<210> 720
 <211> 740
 <212> DNA
 <213> Homo sapiens

<400> 720
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 gaactggagg ccaagatggt gggccagaag gctgaggaaa aggagaacca ttgtcccaca 180
 atgtctcggc ccctttcaca tgcacagtc acaggggcaa agccccgaa aaaggctgtg 240
 gtgatgcccc tacagetaat tcaggagcag gcagcatccc caaatgccga gatccacatc 300

WO 99/33982

PCT/US98/27610

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ctgaagaata aaggccgga gagaaagctg gagtccctgg atgccctaga gctcaggagg 360
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aaaatactgg atctgctgaa cgaaggctca gcccgagatc tccgcagtct tcaacgcatt 480
ggccccaaga aggccagact aatcgtgggc tggcgggagc ttcacggncc ctccaccagg 540
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caaacattct gggctctcggc ggccgccanc gctntggcgc cttctgacgc tgcgttctac 660
ttncgncctt tcaaatcttt ggnataaccc ccgtgtttgm gtataatcca gtttttgttc 720
cgntaaaaaa aaaaaaaaaa 740

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<210> 721

<211> 736

<212> DNA

<213> Homo sapiens

<400> 721

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aatgttttta atatacatc ttattttgtc ccacccctcc agaaataagc tggaaatcttt 180
aacttttttg ggggtctttt ttggtgtttt aatgggcccc gaactgtggg ttaaattttt 240
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tgaggaatag aaaaaggttta tactttttta aaaaaaaaaa cmaaanccaa aaaaccaaaa 660
cttcaaatgg aataaattat tcatgaagcc cttaaaaaaa aaaaaaaaaa aactcgaaac 720
tntaaaactn tngnng 736

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<210> 722

<211> 751

<212> DNA

<213> Homo sapiens

<400> 722

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cacatctaaa acatactttt acagcaacat ctgactggtt gtttgaccaa caaactgggc 180
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gcatactggt tgtatttgat ccnctagat gacatgtaag agaaaacttt attgnggact 660
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attacatagc taactctcag ctgctttcaa t 751

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<210> 723

<211> 749

WO 99/33982

PCT/US98/27610

<212> DNA

<213> Homo sapiens

<400> 723

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ccacagctgt	ggtgagcttc	ttggaggagg	cagggtccc	aatgcgcaag	ttgtggctga	180
cctacagctc	ccagagcaca	gccatctcgg	gcgcactgct	gggcagctgc	tgccccagc	240
tcaggctctc	ggaggtgagc	accggcatca	accgtaatag	cattccccct	cagctgctgc	300
tcgaggctct	gcanaaaggc	tgccctcagc	tcagagctgg	accttgcccc	cagggtgctgc	360
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tctgggctgc	tatggcacgt	cagaccggct	gacttttacc	aangagggca	agmccccctt	660
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<210> 724

<211> 761

<212> DNA

<213> Homo sapiens

<400> 724

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agaaattgta	actaaagata	gattgtttaa	agcaaaagcaa	gaaactctgc	aagaaatgga	180
acaaaagtga	gaagcctcag	gaaagcccaa	cagagagtgt	gcaccccaga	ttcctttaga	240
tactctctatt	gctaactgaa	ggacagtgtc	acatttgaa	actctgaagg	accgtcaacc	300
aggtgatttg	tggggcccga	tgacacatctc	atccctggaa	tatgctgcant	gagacattac	360
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tccaagctgg	tcagcactgg	attctggact	tttgaatctc	aagagcgaaa	agtttggaac	600
cagtagagct	ttttgaatta	ttttttgatg	atgaaacatt	caacttaatt	gtcaatgaaa	660
cnataatta	tgcttctcag	aaaaatgtca	gctttggaag	tcagttcag	gaaaaaaan	720
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<210> 725

<211> 760

<212> DNA

<213> Homo sapiens

<400> 725

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gaanttcaga	ggaagtaact	ggaaagccag	aagatcatgg	tataaaaggag	aaaggggtcc	180
cagtcagcgg	cgaggagcgg	aaagagccag	agagttggga	tgggggcagg	ctggggggcag	240
tggaagagc	gaggagcagg	gaagaggaga	atgagcatca	tgggccttca	atgcccgctc	300
tgatagcccc	tgaggagctc	cctcactgtg	acctgtttcc	aggtgectca	tatctcgtga	360
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WO 99/33982

PCT/US98/27610

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catgtttatc cagttcaatg tatttttaaa tttttccttg agacttcttt gactgataga 600
ttattgtgaa gtgtgttttt aaatttncaa atgtttangg attttcatat ctttcttatg 660
ctgatttcca attggatttc ttacaatgat ttttgggttt catctgctct tggatgatta 720
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<210> 726

<211> 741

<212> DNA

<213> Homo sapiens

<400> 726

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gatggcaatt tgaagtgcct ataaaaatag actaatctac attgcttttc tccgtcagag 180
tctaatacct tttatgcctt gataattagc agtttgtcta cttggtcact aggaatgaaa 240
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tctcatcgca atctctctct catgggttca agcaattctc ctacttcagc ctcccaagt 600
gctgggatta caggtcatgt ctaatttggg gtttttaata gagatgagg gtttccatgt 660
tggtcangct ggtctcaaac tctgcctta ngtgatcgcc tcggcctnct aaagtctgg 720
aattcaggca tgaanmcca t 741

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<210> 727

<211> 751

<212> DNA

<213> Homo sapiens

<400> 727

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ccttctctcn aangctntgt tgaacnctt tcmnnatcgc gcttgcgctt tgagctagga 60
taaaaattgg gtaaaaggac atttgcttac ctgmnnatgc aatcactnnt tgaatgtga 120
tcttgcctac tcatcaagaa acttgttttc tggatgaata ctgggagaat aaaatgagaa 180
ctctggagtg agctaaattg atcccaatna agtttttctg cttagcagac agaaggtata 240
attntttgac accctttccc acctggtgcc tatgctaggc ttgtcctgan aacatnctc 300
agtaacttga tattcacatg acctacagga tgteccatct gcagggctga gtcagttggg 360
gaacaccaga ggctacacag tagctattcc tgctactcgg ttaatgagct tggcaggttc 420
ttgtctctac tgaattctta tcatggaaac agcagcagca gccgctagga aatcttcaag 480
tgtagnngcc tgtgtcaacc cagtggtaaa tcccttagat ccctgctggg tctctgcgaa 540
aacctcctga tnttgggtga catgtatant ttgcctttga cntttaacgc tttctacgat 600
anggtaanca cncntttaat ttangcnctg gancattaac tttctttgca aaggctactt 660
atngcngnc acaantgcag cctcggacan ancmnangnn atatcctggt ggccatggct 720
ntgatgttgc acanccgata ngccttctnc g 751

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<210> 728

<211> 765

<212> DNA

<213> Homo sapiens

WO 99/33982

PCT/US98/27610

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ggacatgctgt gagcagatgg acctgatgga catatccggac cangaggccc tggacgtctt      180
cctgaactctt ggaggagaag agaacactgt gctgtccccc gcccttagggc ctggaatccag      240
taacctgtcac aatganatta cctccacaggt tccaaatncc tcagaattaa gagccaance      300
nccctcttnt tccctnacct gcaccgactn ggncccccng nacatcannng aggggtgggga      360
gtncnccmnt gttcagtcog atgaggagga anttcangtg gacactgncc tgnccacatn      420
acacactnac agatgagcca ctcnngatgg tgnthangac agcaactntt aaattgggac      480
atggggcgtng ntntggccaca ctggaatcca nntttggctg tatgcggaat ttcacctgcn      540
aagccaggtt ntntnataga cgttcttgat tattacataa ttgccaatca tgtggtgagn      600
aacttgttng aacantttaa caattaantg tgaagaccgt acaangaatt agttaaangc      660
natnnagggc taacaaagct attactnttg annnaantta angnatntaa nntttctnctn      720
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<210> 729

<211> 743

<212> DNA

<213> Homo sapiens

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<400> 729
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acgaggagatt cctctgggatg tcatgtgaggc tgggttgaaga ccagaggttaa actgcagaggt      120
tcacacacccc caccatgtcc caggtgatgt ccagcccactt gctggcagga ggccatgctg      180
tcagcttggtc gccttggatg gagcccagga ggacccctgca cccagcacc cagcccagcc      240
tgccaccccca gtgttcttac tacaccaagg aaggctgggg agcccaggcc ctgatggccc      300
ccgtgccctg catggggccc cctggccgag tccagcaagc cccacaggtg gaggccaaag      360
ccacctgctt cctgcgctcc cctggtgaga aggccttggg gaccccagag gaccttgact      420
cctacattga ctctcactg gagagcctca atcagatgat cctggaactg gaccccacct      480
tccaaactgct tcccccangg actgggggct cccangctga nctggcccag agccacatgt      540
caatgagaaa gaaggaggaa tctgaacctt ggttaaggat ttggggcaca gtaccaggaa      600
gggggcttgg tgccagacgt tatgaggaag aaggattttc ctatgtacag agaangggac      660
cctgtntctg tgggaagtgc ttgtgcaaac ctaaccaagt tactaacccc tctgnttctt      720
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<210> 730

<211> 744

<212> DNA

<213> Homo sapiens

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<400> 730
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gcacgagggt tccccaaga gtttggggcg cggacnnmag taccttgcgt gcagttatgt      120
cggcgtntgt agtgtntgtc atttcgcggt tcttacaaca gtacttgagc tccactcgc      180
agcgtctgaa gttgtcggac gcgtacctgc tgtataactc gctgaccogg gcgctgcagc      240
acggtttactg tctcctcgtg gggaccttcc ccttcaactn ttttctctng ggccttnact      300
cttgtgtggn tgagtttnat cctagcggtt tgccctgataa tcmgntcaa cccacnagaa      360
aaagcngatt tccaaggctt ctgcccagag cnagcctttg ntgannttct ctttccagc      420
accatcctgc accctgttgt natnancnta ggtgntcgaa tcattctcan ttncntaatt      480
gangagtang anaactaaaag aatgttgact ctttgaatct gctggataag agactngaga      540
tggcagctta ttggacacat ggattttctt cngatntgca cttactgcta gcntngctan      600

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WO 99/33982

PCT/US98/27610

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ctatgcagga gaaaagccca tagttactgc gtgtnacaac aactntctaa cnaacattca      660
ttaatccann ngannccctt caangaatgg taancctatg ccnttcaana tactgaactt      720
mntgcactt ntggcaaaaa aaat                                         744

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<210> 731
<211> 746
<212> DNA
<213> Homo sapiens

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<400> 731
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tataactgat ttatgatatt tttcttttaa tttcagactt cagtgaaagt ccttatgact      540
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tataaggact gcaaatgatg gccagggggt agtcngactt gggatgggag agaaccagg      660
actgagcatt ctctgggtgt gcacctgcag atgtgaagga agttgttgag aanggtgtcc      720
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<210> 732
<211> 756
<212> DNA
<213> Homo sapiens

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<400> 732
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tgaatgagaa gaagaaaaac aatgtgggaa ttggggagat aaaggatata cggttgtgtg      180
ggatccacca aaatggaggc ttccaccaag tgtggtttgc catgaagacc ttccttaacg      240
ccagcatctt catcattatg gtgtggtatt ggaggaggat caccatgatg tcccgacccc      300
cagtgctctt ggaaaaagtc atctttgccc ttgggatttc catgaccttt atcaatatcc      360
cagtggaatg gttttccatc gggtttgact ggacctggat gctgctgttt ggtgacatcc      420
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ccgntggctc ctctgccttc ttcatatttg acatgtgtga gaaagggcta caactnacga      600
atcccttcta cagtatctgg actacagaca ttggaaacana gctggccatg gmttcatca      660
tcgtggctgg aatctgcctc tgcccttact tctgtttct atgcttnatg gnatttcaag      720
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<210> 733
<211> 742
<212> DNA
<213> Homo sapiens

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<400> 733
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WO 99/33982

PCT/US98/27610

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cctacgtgcc tcggattctg aacggcttgg cctcggagag gacagcactg tctccgcagc 240
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gtggactttt cgcgcccaaa actgatgagt nccggagaat atatggagag agagatgtaa 660
aaaaaaaaaa nnnnnnnnnn nntannnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 720
nnnnnnnnna annnnnanan tc 742

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<210> 734

<211> 749

<212> DNA

<213> Homo sapiens

<400> 734

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tcgttcaatc accttttcaa agttagatgt agattgcatg gtttcattgt tctcatatt 180
gtttatttaa ttctatttaa tcaaggaaaa taacttcaga tccataaag ttacagttta 240
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ataactttan gtaattatng gaactcctca aagaggagaa agtaattttt tncagacatt 660
ttctcaatct gggnccttca cacactantt tncatagtc agaactcgtt tttaccatt 720
gggctgngaa tgtccaatat cagtctcgg 749

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<210> 735

<211> 770

<212> DNA

<213> Homo sapiens

<400> 735

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ccgcccgact tggccccgca aagtgcctgg attacaagca tgagccagc gctggtcgtg 240
atcttcat ttaccatgg cactttacc aagtaagtaa ttaggggaaa gctcgtgct 300
gtaccacact gttcatttg ggaactgtgg gaaacggagc caacggacct aagtcacct 360
tgacagttag ttcatatca ttccagttag gtattttctt cttaactctga ataaaccaga 420
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tttatgtatg cttncttatg aattactgaa cgaacactgg aatgggactc acgtatcctg 540
aggacatctc tcaactgtg ccttantttc cctctgttaa aattagggtg ccaactaaat 600
gatctacaag gtccttttnc aagcgccogn cattctgtaa ttacatcgt tgaactgna 660
ttaaacatac accagtgaac tggcangcat tgggaatgta accttccag taaaattgct 720

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WO 99/33982

PCT/US98/27610

tnggttttgggt tcaaaaataca cnttgaactt cttttcaaag acnggttngg

770

<210> 736

<211> 746

<212> DNA

<213> Homo sapiens

<400> 736

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gatatgacat	tgccatctnc	aggaagactt	gacggcttgg	ggattttggt	taaaactttta	180
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agccttatgt	gctttcttac	aaaatggaat	tggaggccgg	gcgcagtgcc	tcacgcctgt	360
aatcccgaca	ctttggggagg	ccaaggtggg	tggatcacct	gaggtcagga	nctcgagacc	420
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<210> 737

<211> 751

<212> DNA

<213> Homo sapiens

<400> 737

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<211> 795

<212> DNA

<213> Homo sapiens

<400> 738

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WO 99/33982

PCT/US98/27610

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<210> 739

<211> 763

<212> DNA

<213> Homo sapiens

<400> 739

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<210> 740

<211> 765

<212> DNA

<213> Homo sapiens

<400> 740

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WO 99/33982

PCT/US98/27610

<210> 741

<211> 753

<212> DNA

<213> Homo sapiens

<400> 741

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<210> 742

<211> 767

<212> DNA

<213> Homo sapiens

<400> 742

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<210> 743

<211> 768

<212> DNA

<213> Homo sapiens

<400> 743

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WO 99/33982

PCT/US98/27610

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gnactatgtc	catgnaaggg	gaacatntan	tgttgganna	tgcnatgcaa	ncntnnccnt	720
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<210> 744

<211> 757

<212> DNA

<213> Homo sapiens

<400> 744

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caaacatctt	ttcctttgct	ctatnggaac	atttttaagg	ttggtttgca	caactgggtt	720
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<210> 745

<211> 751

<212> DNA

<213> Homo sapiens

<400> 745

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<210> 746

<211> 760

WO 99/33982

PCT/US98/27610

<212> DNA

<213> Homo sapiens

<400> 746

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<210> 747

<211> 786

<212> DNA

<213> Homo sapiens

<400> 747

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<211> 722

<212> DNA

<213> Homo sapiens

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WO 99/33982

PCT/US98/27610

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<210> 749

<211> 821

<212> DNA

<213> Homo sapiens

<400> 749

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<210> 750

<211> 770

<212> DNA

<213> Homo sapiens

<400> 750

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<210> 751

<211> 774

WO 99/33982

PCT/US98/27610

<212> DNA

<213> Homo sapiens

<400> 751

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<210> 752

<211> 778

<212> DNA

<213> Homo sapiens

<400> 752

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caatattgta	aatacataaa	aaatatacaa	atttttggct	gctgtgaaga	tgtaatttta	480
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aaatacaagg	agactgactt	ggacaccgtt	tggaaaatgg	gtaaaaacgg	tggnttactgt	720
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<210> 753

<211> 775

<212> DNA

<213> Homo sapiens

<400> 753

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WO 99/33982

PCT/US98/27610

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<210> 754

<211> 1032

<212> DNA

<213> Homo sapiens

<400> 754

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<210> 755

<211> 798

<212> DNA

<213> Homo sapiens

<400> 755

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WO 99/33982

PCT/US98/27610

ngtcgattnn cgnncanc

798

<210> 756

<211> 834

<212> DNA

<213> Homo sapiens

<400> 756

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<210> 757

<211> 1062

<212> DNA

<213> Homo sapiens

<400> 757

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<210> 758

<211> 845

<212> DNA

WO 99/33982

PCT/US98/27610

<213> Homo sapiens

<400> 758

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<210> 759

<211> 947

<212> DNA

<213> Homo sapiens

<400> 759

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<210> 760

<211> 759

<212> DNA

<213> Homo sapiens

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WO 99/33982

PCT/US98/27610

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<210> 761

<211> 752

<212> DNA

<213> Homo sapiens

<400> 761

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<210> 762

<211> 1032

<212> DNA

<213> Homo sapiens

<400> 762

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WO 99/33982

PCT/US98/27610

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<211> 817

<212> DNA

<213> Homo sapiens

<400> 763

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<210> 764

<211> 777

<212> DNA

<213> Homo sapiens

<400> 764

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<210> 765

<211> 774

<212> DNA

<213> Homo sapiens

WO 99/33982

PCT/US98/27610

<400> 765

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catatttgaa aaatcctggg agaanggact atttggtctc ttttgccaac ttacttcata      720
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<210> 766

<211> 779

<212> DNA

<213> Homo sapiens

<400> 766

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attcctcttg tcatgtcagt accttatgtc tggggccanc tgaacagaga catgattgna      660
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<210> 767

<211> 799

<212> DNA

<213> Homo sapiens

<400> 767

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gatccaccca ggatgacaaa agatcaccaa ggggaaagaa aacatttttt atctttacag      360
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tgatagctac agtttttaaa tgtataacct gaaaaatgaag gtttaatttg catgtgaaag      540
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WO 99/33982

PCT/US98/27610

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cactttcata ttaagtagca tgtgtatgaa ttttaagattt tcatatttgn tngtctgggt      660
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<210> 768

<211> 826

<212> DNA

<213> Homo sapiens

<400> 768

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catttttggg ggatagcct nnnngnacnt ttttaaaaaa gtttatnagt tngntatggg      720
naaaaacaa ttttctctan tttttaaagt ggntaataaa tnaaantctc aatggnaaaa      780
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<210> 769

<211> 802

<212> DNA

<213> Homo sapiens

<400> 769

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<210> 770

<211> 1157

<212> DNA

<213> Homo sapiens

WO 99/33982

PCT/US98/27610

<400> 770

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<210> 771

<211> 760

<212> DNA

<213> Homo sapiens

<400> 771

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tttatagcag agtttctcac acctggcgag ctgtggcatg cttttaaaca gagttcattt 240
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acagcgtcgg taaattaagg ggtgatcacc aagtttcata atattttccc ttataaaaag 360
gatttgttgg ccaggttcagc tgggttcacg ctgtaatccc agcagttttg gaggctgagg 420
tgggtggatc acctgaggtc aggaagttcga gaccaacctg accaacatgg tagacccecc 480
gtctctacta aaaaataaaa aaaaatttagc tgggagtggn ggtgggcacc tgtaactccta 540
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agccccgatg cgtgccattg cactccaacc agggcaacaa gagtgaaact ccatctctaa 660
aaanaaaaaa gaaaactcga gcctctagaa ctatagtggc tcgtattacg tagatccaga 720
catgataaga tacattgatg aattttggac aaaceccann 760

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<210> 772

<211> 777

<212> DNA

<213> Homo sapiens

<400> 772

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gaaancccat ttnnnnnntc cnccttcaat cccttggnta ctcgntcttt ntgcaggate 60
ccatcgatcc gaattcggca cgagctctac taataatata aaaaattagc gggcgtgggt 120
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WO 99/33982

PCT/US98/27610

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ctacttttcc agtagttttg cactttctcc gaggtanttt ggctgctctt tcagtaatgc 480
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gngtttcaaa ctgggtatttt ttaaaaaaca aatcaatgta aggactgaag ttgaaatanc 660
caatgtaata aagttaatta ggggtatttt taaaaaaaan aaaaataana actcnagccc 720
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<210> 773

<211> 782

<212> DNA

<213> Homo sapiens

<400> 773

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caatgacagg ttcattttgn tggccttggt atnggctctt naaaggncct tnccccatna 660
aggaagcng tggaactttc atcttgnccg gnantcgang atnaaaaagn atncgaacc 720
cggggaaggg gaaaaactcn aannctgact tcccggttcc caaacacagn ttgnaacaaa 780
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<210> 774

<211> 793

<212> DNA

<213> Homo sapiens

<400> 774

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tttgagtgtg ctaatcatgc ttttctgctt gtgggctatc ngcactgact cagcctctgg 240
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WO 99/33982

PCT/US98/27610

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793

<210> 775

<211> 1009

<212> DNA

<213> Homo sapiens

<400> 775

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nannggcnc	cttcgggggn	ccngtgnata	gncnatnctt	gtntntanaa	agntggnnnt	180
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<210> 776

<211> 785

<212> DNA

<213> Homo sapiens

<400> 776

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<210> 777

<211> 1366

<212> DNA

<213> Homo sapiens

WO 99/33982

PCT/US98/27610

<400> 777

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<210> 778

<211> 775

<212> DNA

<213> Homo sapiens

<400> 778

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<210> 779

<211> 781

<212> DNA

<213> Homo sapiens

<400> 779

WO 99/33982

PCT/US98/27610

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aaagaagctg caaggtggat ggatgaggcc caggccttgg acacagcaga cagattatc      420
aactccaaat gtgcaaaata catgctaaaa gccaacctga ttaagaagc tgaagaatg      480
tgctcaaatg ttacaaggga aggaacatca gcggtagaga atttgaatga aatgcagtcg      540
atgtgggtcc aaacagaatg tgcccaggct tataaagcaa tgaataaatt tggtagaagca      600
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ctttcataca tactggatga aggaagatta cccttagatc atatgtggac ttattnaaac      720
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<210> 780

<211> 783

<212> DNA

<213> Homo sapiens

<400> 780

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atatcaagta atagatcaca tattgtgaaa tctccagtta acagggaatt gaagtattatg      360
catactccac atcagttcct tcttctcago agtccaccag ccaagaatc caattttaga      420
gctgctaaaa aactctttgg aagcaccttt gcatctcatg gctcacacat tgaaaacttg      480
cactccatcc tgaggaaatg tctgggtgtt gcttctaata cagcatgtga gctccatggt      540
gcaatgtatg gaagtggaaat ctatcttagt ccaatgtcaa gcatatcatt tggtaactag      600
ggatgaacaa gaaacagaaag gtgtcagcca aggacgagcc agcttcaagc agtaaaagca      660
gcaaatacat cacagtcaac ggaaaaaagg acagcaatcc caattctctg caaagccgta      720
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<210> 781

<211> 796

<212> DNA

<213> Homo sapiens

<400> 781

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accgcctccc acccttttca aacccccagg cccttgcctg tgagatttggg cttgggttagg      480
gacagaagag gccccaatc cctcccccat gcttctgac cctgttttgg ccaaaaggca      540

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WO 99/33982

PCT/US98/27610

tctttgatgg	tacaaagcag	angcttcggg	anaagcttcc	gtcacaaacac	tncaaggtcc	600
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annccccacc	tnnggggccca	tttttcccaa	ttaaacttacc	ccccaacccca	agncanggtt	720
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<210> 782

<211> 886

<212> DNA

<213> Homo sapiens

<400> 782

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ggacacnctt	ntaanmnnan	nagngmnnngt	tttngnganan	agggnnnnna	gnsgnannna	180
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nncnngnnnn	ggaaaagann	ggaggggagg	ncgaaggcaa	aggggggann	cgnnannncc	540
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gggcgagggg	agcanaannn	nnccnnagnc	aanngaaggg	gananaagag	ngggaaaaann	660
aannagaaag	agggaaaaana	agnnaaggaa	anaaaagang	ngnnnaannng	gganaaaaaana	720
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nggggagggg	ngananaanag	ngaannagac	aaggaanagn	gaannagnng	anagnannng	840
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<210> 783

<211> 805

<212> DNA

<213> Homo sapiens

<400> 783

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ggttatttgg	taaataaaata	gactggtaact	ttaggaattt	taaaatgttg	atcattgtac	420
tactaataac	tatntatctt	atatttacta	tctactaagt	aattttacatg	tattttctctg	480
tactgactgt	aaacctttcg	gggtgtgggtg	ttttaagtgc	cattttactg	ataaagaaac	540
tgangcttaa	atagntgaaa	tanntcacc	tggttagtgag	tgggcacaatg	acaagtcaann	600
atcttangg	tgccnamtgc	caaaaannact	ttaaanttnn	agnatnatgg	annnttttnc	660
cttatggcnc	nnnaaatctg	gggagccatt	attgaaatcc	nttacnactn	angaattgnc	720
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<210> 784

<211> 776

WO 99/33982

PCT/US98/27610

<212> DNA

<213> Homo sapiens

<400> 784

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gcagngtgcc	aaaggtgaaa	angntgcttn	ctctaacaga	gaaattctta	ngactccag	240
tcgtanaaaa	acgtctttac	aacctgaata	agatnganga	attgngaaca	taccatggcc	300
tattggatga	atcatttgcc	ggnggctana	ncagactgta	gggtttgtga	tggatntatg	360
gagtatgtgg	gtatagaaat	catgaatntn	ccatttgnnn	ncagagattc	aagcntanac	420
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tgtgcccaga	tatgtntttg	aaatggcagn	tccctggggg	catgtntcta	ctggcaaaat	540
ttgctatagn	gmnactattg	nantgtaatt	ataaaaatna	tcannattat	ncaccgattn	600
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aantntagaa	cngatgtctg	ggcttaaaaa	tttatcnggg	accacnatt	angaaaactna	720
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<210> 785

<211> 778

<212> DNA

<213> Homo sapiens

<400> 785

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gcagtgaaca	gagttatgga	gcagcaaaaa	cacagatcta	tttggaaaaa	gagaaaacat	300
atgcgttgta	ttttgcttca	attataaaat	accatcctct	caaaggtggt	tctaaattac	360
aaaggacctt	gattttctagg	tagattctgg	gtagagactt	cctttcatac	tgaggcatta	420
atgacacctt	ttaacctggg	aagcaatatg	actggagttg	tactttgaga	agattaatca	480
ggtttgggtg	cagaatgaaa	gagaagatga	agtcaagaga	ttggtttaga	ggctctagca	540
gaagcttagt	catattttca	aatgatcaaa	tatcaagaaa	aattctgagc	tgataaactt	600
gtataaagta	attttctagt	atttttttca	tggttatgat	aaaagaactg	gatttagcaga	660
aacttttacc	ctgaatcaag	atttaatttt	tctttgagct	catcttaagg	atatcggaac	720
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<210> 786

<211> 805

<212> DNA

<213> Homo sapiens

<400> 786

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ttattaaagt	atcgagagac	aaaatatcag	acagcaatga	ccaagagta	gcaaatgtgt	360
atgcaaaagg	gctatcaagg	ggaggtcttt	tacagagAAC	taagggaagag	aaggaggtgt	420

WO 99/33982

PCT/US98/27610

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gaagtatttt gctgagcaaa catttgaatg cctgtatgta ccgtaatcct ctatcactgg 540
ggcccccaac cccggtacca gcccgtagcc tgcaggagac tgggcccgcac agcaggaggt 600
gagcagtggt tgggcaagcg accattccca cctgagcttc cctcctctgc agatcagcag 660
cagcgtaga ttctcataga agtgcaaaac cctattgtaa actgcccatg ccaaggggac 720
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<210> 787

<211> 775

<212> DNA

<213> Homo sapiens

<400> 787

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tacagagaac taaggaagag aaggagggtt ttaagagac ttgagatcag aaaagatca 420
agaacaactt gaactcctaaa gtatgaattt gaagtatttt gctgagcaaa catttgaagt 480
cctgtatgta ccgtaatcct ctatcaactg gggtcccaac cccggtacca gcccgtaggg 540
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ccctattgta aactgccatg cnagggatct aggtttgcacg ctccctatga ggaattgaat 720
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<210> 788

<211> 774

<212> DNA

<213> Homo sapiens

<400> 788

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gcttgggaaga aacaaattta taggttatat ttccctctta aattaaanaa acaacttcc 600
tctggcagta gtttggtgaa ttcccttctat tgnaatgata ccatgattac aggatcaaaa 660
atgcttaact tacttgccat tctgctcaca tcatcacagg ttgtnttttt tttaaagcac 720
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<210> 789

<211> 773

<212> DNA

WO 99/33982

PCT/US98/27610

<213> Homo sapiens

<400> 789

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acattanttt	ngggtcocag	actacttgge	acanccttat	nacgaaactg	gncngtncnt	600
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netctttntc	anganagctn	nngatccata	ngacntgctg	ganatnttta	aggaancttc	720
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<210> 790

<211> 953

<212> DNA

<213> Homo sapiens

<400> 790

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aaaantggna	ttngaattgn	nagaaaaang	gatananaan	aaaanccaat	nntaannacc	720
nanncctctc	ggantctnac	tatctccact	acntactntt	acntatngcg	ntaanaatnaa	780
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<210> 791

<211> 798

<212> DNA

<213> Homo sapiens

<400> 791

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gggtgtatcc	cttgggggat	ggtt tggggc	gaatggggag	tggaatattt	gnccttnccc	180
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WO 99/33982

PCT/US98/27610

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<210> 792

<211> 788

<212> DNA

<213> Homo sapiens

<400> 792

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<210> 793

<211> 806

<212> DNA

<213> Homo sapiens

<400> 793

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WO 99/33982

PCT/US98/27610

<210> 794
 <211> 815
 <212> DNA
 <213> Homo sapiens

<400> 794

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<210> 795
 <211> 1050
 <212> DNA
 <213> Homo sapiens

<400> 795

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<210> 796
 <211> 884
 <212> DNA
 <213> Homo sapiens

WO 99/33982

PCT/US98/27610

<400> 796

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<210> 797

<211> 773

<212> DNA

<213> Homo sapiens

<400> 797

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aatatcaaaa	atgggtgatg	tataatgtct	ctttagtttt	tttggtattt	ggcctctttt	480
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<210> 798

<211> 812

<212> DNA

<213> Homo sapiens

<400> 798

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WO 99/33982

PCT/US98/27610

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<210> 799

<211> 758

<212> DNA

<213> Homo sapiens

<400> 799

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<210> 800

<211> 770

<212> DNA

<213> Homo sapiens

<400> 800

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<210> 801

<211> 573

<212> DNA

<213> Homo sapiens

WO 99/33982

PCT/US98/27610

<400> 801

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<210> 802

<211> 1390

<212> DNA

<213> Homo sapiens

<400> 802

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<210> 803

<211> 947

<212> DNA

<213> Homo sapiens

<400> 803

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WO 99/33982

PCT/US98/27610

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<210> 804

<211> 532

<212> DNA

<213> Homo sapiens

<400> 804

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<210> 805

<211> 552

<212> DNA

<213> Homo sapiens

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<210> 806

<211> 1646

<212> DNA

WO 99/33982

PCT/US98/27610

<213> Homo sapiens

<400> 806

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<210> 807

<211> 1029

<212> DNA

<213> Homo sapiens

<400> 807

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catctgtccc	aaagctgcac	caagggggtg	cagcaacccc	aacctactga	ctcactttgg	600
gaccacaggc	ccatctagt	caaatgaggc	ccagaaagga	gaatgtcttt	gtcacaagca	660
cacagttagc	tgaagtaacc	tatgtaatg	agggctcagg	tgggctgag	ggatgancca	720
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WO 99/33982

PCT/US98/27610

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<210> 808

<211> 836

<212> DNA

<213> Homo sapiens

<400> 808

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<210> 809

<211> 1844

<212> DNA

<213> Homo sapiens

<400> 809

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WO 99/33982

PCT/US98/27610

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<210> 810
<211> 489
<212> DNA
<213> Homo sapiens

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<400> 810
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aaaaartctt gcttgaattt caccctggcr atgtaaaytg akagcttate ttcacagatg 180
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<210> 811
<211> 471
<212> DNA
<213> Homo sapiens

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<400> 811
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<210> 812
<211> 579
<212> DNA
<213> Homo sapiens

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<400> 812

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WO 99/33982

PCT/US98/27610

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ctctckgnwg sarccrrsrs akamragkym sssatcnag scagcscwnk arskstsgca 480
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<210> 813
 <211> 562
 <212> DNA
 <213> Homo sapiens

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<400> 813
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tgggtgcctt ggagtcctcg tagscctaaa caagtatac tgggcttgcc aggcagttgt 240
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tccccagccc ctaaaaactcc tccccaaaac actctgaaaa aaattttttt aaaaacaarg 360
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cgtgcaggt cctagagcac gagagccggg cgtggccttg gtcaggcctg cagctgtgcc 480
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<210> 814
 <211> 594
 <212> DNA
 <213> Homo sapiens

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<400> 814
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<210> 815
 <211> 812
 <212> DNA
 <213> Homo sapiens

<400> 815

WO 99/33982

PCT/US98/27610

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<210> 816

<211> 999

<212> DNA

<213> Homo sapiens

<400> 816

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<210> 817

<211> 653

<212> DNA

<213> Homo sapiens

<400> 817

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WO 99/33982

PCT/US98/27610

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<210> 818

<211> 1225

<212> DNA

<213> Homo sapiens

<400> 818

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<210> 819

<211> 1024

<212> DNA

<213> Homo sapiens

<400> 819

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WO 99/33982

PCT/US98/27610

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<210> 820
<211> 631
<212> DNA
<213> Homo sapiens

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<210> 821
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<212> DNA
<213> Homo sapiens

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<210> 822
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<212> DNA
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<400> 822
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WO 99/33982

PCT/US98/27610

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<211> 899

<212> DNA

<213> Homo sapiens

<400> 823

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<210> 824

<211> 1980

<212> DNA

<213> Homo sapiens

<400> 824

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WO 99/33982

PCT/US98/27610

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<211> 333

<212> DNA

<213> Homo sapiens

<400> 825

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<210> 826

<211> 658

<212> DNA

<213> Homo sapiens

<400> 826

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WO 99/33982

PCT/US98/27610

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<210> 827

<211> 453

<212> DNA

<213> Homo sapiens

<400> 827

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actctttcac	agtcactctg	gtttttaga	gggaacataa	ctggacattc	tggtcagggt	360
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<210> 828

<211> 657

<212> DNA

<213> Homo sapiens

<400> 828

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<210> 829

<211> 775

<212> DNA

<213> Homo sapiens

<400> 829

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WO 99/33982

PCT/US98/27610

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<210> 830

<211> 413

<212> DNA

<213> Homo sapiens

<400> 830

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<210> 831

<211> 876

<212> DNA

<213> Homo sapiens

<400> 831

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<210> 832

<211> 768

<212> DNA

<213> Homo sapiens

<400> 832

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PCT/US98/27610

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<212> DNA
<213> Homo sapiens
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269

WO 99/33982

PCT/US98/27610

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<210> 835

<211> 542

<212> DNA

<213> Homo sapiens

<400> 835

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<210> 836

<211> 542

<212> DNA

<213> Homo sapiens

<400> 836

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<210> 837

<211> 719

<212> DNA

<213> Homo sapiens

WO 99/33982

PCT/US98/27610

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<210> 838

<211> 579

<212> DNA

<213> Homo sapiens

<400> 838

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<210> 839

<211> 1172

<212> DNA

<213> Homo sapiens

<400> 839

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WO 99/33982

PCT/US98/27610

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<211> 1145

<212> DNA

<213> Homo sapiens

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<211> 642

<212> DNA

<213> Homo sapiens

<400> 841

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WO 99/33982

PCT/US98/27610

<210> 842
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<210> 844
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WO 99/33982

PCT/US98/27610

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